# EXHIBIT 23

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#### (54) PROBES AND DECODER **OLIGONUCLEOTIDES**

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#### **Publication Classification**

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			B05D	3/00

(57) ABSTRACT

The present invention is directed to improved methods and compositions for the use of adapter sequences on arrays in a variety of multiplexed nucleic acid reactions, including synthesis reactions, amplification reactions, and genotyping reactions.

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#### Description of algorithm to select "best" oligonucleotide adapter sequences.

Requirements for good sequences:

- Generates adequate hybridization signal intensity when employed in an experiment.
- Exhibits minimal cross-reactivity with other adapter sequences.
- Unique within the human genome sequence. This requirement can be extended to the genomic sequence of other organisms such as the fruit fly, the mouse, etc.

One method of generating sequences that meet the above requirements is to randomly generate sequences of given lengths and than pass these filters through a set of heuristic acceptance filters. In particular, the 24-mer Illumina Adapter sequences (IllumaCodes) were chosen as follows.

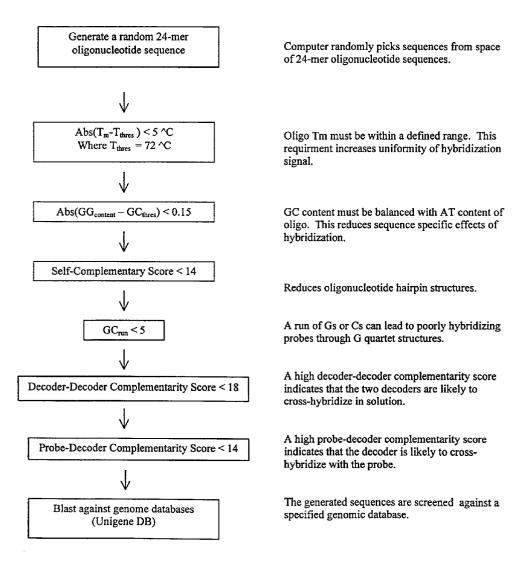


FIGURE 1

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# Flow Diagram for selection of probes sequences

Synthesize 768 oligo decoder sets on Oligator

 $\mathbf{1}$ 

Individually label decoders with two colors in HT format



QC: RP HPLC ~ 8 decoders/ plate



Pool decoders into 2 color -10 stage decode mix

 $\bigvee$ 

Decode 768 bead series on array blocks in sets of 96 (by plate)



Select probe based upon decoding (good clustering) and normalization intensity

FIGURE 2

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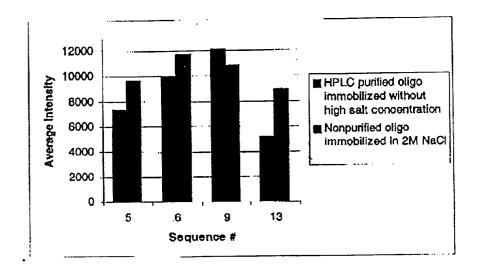
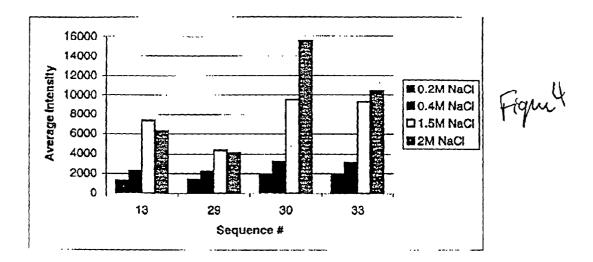


Figure 3

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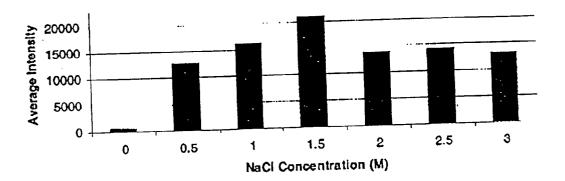


Figure 5

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#### PROBES AND DECODER OLIGONUCLEOTIDES

[0001] This application claims the benefit of U.S. Ser. Nos. 60/227,948 filed Aug. 25, 2000 and 60/228,854, filed Aug. 29, 2001, both of which are expressly incorporated herein by reference.

#### FIELD OF THE INVENTION

[0002] The present invention is directed to methods and compositions for the use of adapter sequences on arrays in a variety of nucleic acid reactions, including synthesis reactions, amplification reactions, and genotyping reactions.

#### BACKGROUND OF THE INVENTION

[0003] The detection of specific nucleic acids is an important tool for diagnostic medicine and molecular biology research. Gene probe assays currently play roles in identifying infectious organisms such as bacteria and viruses, in probing the expression of normal and mutant genes and identifying mutant genes such as oncogenes, in typing tissue for compatibility preceding tissue transplantation, in matching tissue or blood samples for forensic medicine, and for exploring homology among genes from different species.

[0004] Ideally, a gene probe assay should be sensitive, specific and easily automatable (for a review, see Nickerson, Current Opinion in Biotechnology 4:48-51 (1993)). The requirement for sensitivity (i.e. low detection limits) has been greatly alleviated by the development of the polymerase chain reaction (PCR) and other amplification technologies which allow researchers to amplify exponentially a specific nucleic acid sequence before analysis (for a review, see Abramson et al., Current Opinion in Biotechnology, 4:41-47 (1993)).

[0005] Specificity, in contrast, remains a problem in many currently available gene probe assays. The extent of molecular complementarity between probe and target defines the specificity of the interaction. Variations in the concentrations of probes, of targets and of salts in the hybridization medium, in the reaction temperature, and in the length of the probe may alter or influence the specificity of the probe/target interaction.

[0006] It may be possible under some circumstances to distinguish targets with perfect complementarity from targets with mismatches, although this is generally very difficult using traditional technology, since small variations in the reaction conditions will alter the hybridization. New experimental techniques for mismatch detection with standard probes include DNA ligation assays where single point mismatches prevent ligation and probe digestion assays in which mismatches create sites for probe cleavage.

[0007] Recent focus has been on the analysis of the relationship between genetic variation and phenotype by making use of polymorphic DNA markers. Previous work utilized short tandem repeats (STRs) as polymorphic positional markers; however, recent focus is on the use of single nucleotide polymorphisms (SNPs), which occur at an average frequency of more than 1 per kilobase in human genomic DNA. Some SNPs, particularly those in and around coding sequences, are likely to be the direct cause of therapeutically relevant phenotypic variants and/or disease predisposition. There are a number of well known polymorphisms that cause clinically important phenotypes; for

example, the apoE2/3/4 variants are associated with different relative risk of Alzheimer's and other diseases (see Cordor et al., Science 261(1993). Multiplex PCR amplification of SNP loci with subsequent hybridization to oligonucleotide arrays has been shown to be an accurate and reliable method of simultaneously genotyping at least hundreds of SNPs; see Wang et al., Science, 280:1077 (1998); see also Schafer et al., Nature Biotechnology 16:33-39 (1998). The compositions of the present invention may easily be substituted for the arrays of the prior art.

[0008] There are a variety of particular techniques that are used to detect sequence, including mutations and SNPs. These include, but are not limited to, ligation based assays, cleavage based assays (mismatch and invasive cleavage such as Invader<sup>TM</sup>), single base extension methods (see WO 92/15712, EP 0 371 437 B1, EP 0317 074 B1; Pastinen et al., Genome Res. 7:606-614 (1997); Syvänen, Clinica Chimica Acta 226:225-236 (1994); and WO 91/13075), and competitive probe analysis (e.g. competitive sequencing by hybridization; see below).

[0009] Oligonucleotide ligation amplification ("OLA", which is referred as the ligation chain reaction (LCR) when two-stranded reactions or nested reactions are done) involves the ligation of two smaller probes into a single long probe, using the target sequence as the template. See generally U.S. Pat. Nos. 5,185,243, 5,679,524 and 5,573,907; EP 0 320 308 B1; EP 0 336 731 B1; EP 0 439 182 B1; WO 90/01069; WO 89/12696; WO 97/31256 and WO 89/09835, all of which are incorporated by reference.

[0010] Invasive cleavage technology is based on structure-specific nucleases that cleave nucleic acids in a site-specific manner. Two probes are used: an "invader" probe and a "signalling" probe, that adjacently hybridize to a target sequence with a non-complementary overlap. The enzyme cleaves at the overlap due to its recognition of the "tail", and releases the "tail" with a label. This can then be detected. The Invader™ technology is described in U.S. Pat. Nos. 5,846,717; 5,614,402; 5,719,028; 5,541,311; and 5,843,669, all of which are hereby incorporated by reference.

[0011] An additional technique utilizes sequencing by hybridization. For example, sequencing by hybridization has been described (Drmanac et al., Genomics 4:114 (1989); Koster et al., Nature Biotechnology 14:1123 (1996); U.S. Pat. Nos. 5,525,464; 5,202,231 and 5,695,940, among others, all of which are hereby expressly incorporated by reference in their entirety).

[0012] Sensitivity, i.e. detection limits, remain a significant obstacle in nucleic acid detection systems, and a variety of techniques have been developed to address this issue. Briefly, these techniques can be classified as either target amplification or signal amplification. Target amplification involves the amplification (i.e. replication) of the target sequence to be detected, resulting in a significant increase in the number of target molecules. Target amplification strategies include the polymerase chain reaction (PCR), strand displacement amplification (SDA), and nucleic acid sequence based amplification (NASBA).

[0013] Alternatively, rather than amplify the target, alternate techniques use the target as a template to replicate a signalling probe, allowing a small number of target molecules to result in a large number of signalling probes, that

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then can be detected. Signal amplification strategies include the ligase chain reaction (LCR), cycling probe technology (CPT), invasive cleavage techniques such as Invader technology, Q-Beta replicase (Q $\beta$ R) technology, and the use of "amplification probes" such as "branched DNA" that result in multiple label probes binding to a single target sequence.

[0014] The polymerase chain reaction (PCR) is widely used and described, and involves the use of primer extension combined with thermal cycling to amplify a target sequence; see U.S. Pat. Nos. 4,683,195 and 4,683,202, and PCR Essential Data, J. W. Wiley & sons, Ed. C. R. Newton, 1995, all of which are incorporated by reference. In addition, there are a number of variations of PCR which also find use in the invention, including "quantitative competitive PCR" or "QC-PCR", "arbitrarily primed PCR" or "AP-PCR", "immuno-PCR", "Alu-PCR", "PCR single strand conformational polymorphism" or "PCR-SSCP", allelic PCR (see Newton et al. Nucl. Acid Res. 17:2503 91989); "reverse transcriptase PCR" or "RT-PCR", "biotin capture PCR", "vectorette PCR". "panhandle PCR", and "PCR select cDNA subtraction", among others.

[0015] Strand displacement amplification (SDA) is generally described in Walker et al., in Molecular Methods for Virus Detection, Academic Press, Inc., 1995, and U.S. Pat. Nos. 5,455,166 and 5,130,238, all of which are hereby incorporated by reference.

[0016] Nucleic acid sequence based amplification (NASBA) is generally described in U.S. Pat. No. 5,409,818 and "Profiting from Gene-based Diagnostics", CTB International Publishing Inc., N.J., 1996, both of which are incorporated by reference.

[0017] Cycling probe technology (CPT) is a nucleic acid detection system based on signal or probe amplification rather than target amplification, such as is done in polymerase chain reactions (PCR). Cycling probe technology relies on a molar excess of labeled probe which contains a scissile linkage of RNA. Upon hybridization of the probe to the target, the resulting hybrid contains a portion of RNA:DNA. This area of RNA:DNA duplex is recognized by RNAseH and the RNA is excised, resulting in cleavage of the probe. The probe now consists of two smaller sequences which may be released, thus leaving the target intact for repeated rounds of the reaction. The unreacted probe is removed and the label is then detected. CPT is generally described in U.S. Pat. Nos. 5,011,769, 5,403,711, 5,660,988, and 4,876,187, and PCT published applications WO 95/05480, WO 95/1416, and WO 95/00667, all of which are specifically incorporated herein by reference.

[0018] The oligonucleotide ligation assay (OLA) involve the ligation of at least two smaller probes into a single long probe, using the target sequence as the template for the ligase. See generally U.S. Pat. Nos. 5,185,243, 5,679,524 and 5,573,907; EP 0 320 308 B1; EP 0 336 731 B1; EP 0 439 182 B1; WO 90/01069; WO 89/12696; and WO 89/09835, all of which are incorporated by reference.

[0019] Invader™ technology is based on structure-specific polymerases that cleave nucleic acids in a site-specific manner. Two probes are used: an "invader" probe and a "signalling" probe, that adjacently hybridize to a target sequence with overlap. For mismatch discrimination, the

invader technology relies on complementarity at the overlap position where cleavage occurs. The enzyme cleaves at the overlap, and releases the "ail" which may or may not be labeled. This can then be detected. The Invader™ technology is described in U.S. Pat. Nos. 5,846,717; 5,614,402; 5,719,028; 5,541,311; and 5,843,669, all of which are hereby incorporated by reference.

[0020] "Branched DNA" signal amplification relies on the synthesis of branched nucleic acids, containing a multiplicity of nucleic acid "arms" that function to increase the amount of label that can be put onto one probe. This technology is generally described in U.S. Pat. Nos. 5,681, 702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference.

[0021] Similarily, dendrimers of nucleic acids serve to vastly increase the amount of label that can be added to a single molecule, using a similar idea but different compositions. This technology is as described in U.S. Pat. No. 5,175,270 and Nilsen et al., J. Theor. Biol. 187:273 (1997), both of which are incorporated herein by reference.

[0022] U.S. Ser. Nos. 09/189,543; 08/944,850; 09/033, 462; 09/287,573; 09/151,877; 09/187,289 and 09/256,943; and PCT applications US98/09163 and US99/14387; US98/21193; US99/04473 and US98/05025, all of which are expressly incorporated by reference, describe novel compositions utilizing substrates with microsphere arrays, which allow for novel detection methods of nucleic acid hybridization.

[0023] The use of adapter-type sequences that allow the use of universal arrays has been described in limited contexts; see for example Chee et al., Nucl. Acid Res. 19:3301 (1991); Shoemaker et al., Nature Genetics 14:450 (1996); U.S. Pat. Nos. 5,494,810, 5,830,711, 6,027,889, 6,054,564, and 6,268,148; and EP 0 799 897 A1; WO 97/31256, all of which are expressly incorporated by reference.

[0024] Accordingly, it is an object of the present invention to provide methods for detecting nucleic acid reactions, and other target analytes, on arrays using adapter sequences.

#### SUMMARY OF THE INVENTION

[0025] In accordance with the above objects, the invention also provides a method of detecting a target nucleic acid. The method comprises contacting the target nucleic acid with an adapter sequence such that the target nucleic acid is joined to the adapter sequence to form a modified target nucleic acid. In addition, the method comprises contacting the modified target nucleic acid with an array comprising a substrate with a surface comprising discrete sites and a population of microspheres comprising at least a first subpopulation comprising a first capture probe, such that the first capture probe and the modified target nucleic acid form a complex, wherein the microspheres are distributed on the surface, and detecting the presence fo the target nucleic acid. In addition the method comprises adding at least one decoding binding ligand to the array such that the identity of the target nucleic acid is determined. Preferably the adapter nucleic acids include a sequence as set forth in Table Table I, Table II, Table III or Table IV.

[0026] In addition the invention provides a method of making an array. The method comprises forming a surface

comprising individual sites on a substrate, distributing microspheres on the surface such that the individual sites contain microspheres, wherein the microspheres comprise at least a first and a second subpopulation each comprising a capture probe, wherein the capture probe is complementary to an adapter sequence, the adapter sequence joined to a target nucleic acid, and an identifier binding ligand that will bind at least one decoder binding ligand such that the identification of the target nucleic acid is elucidated. Preferably the adapter nucleic acids include a sequence as set forth in Table I, Table II, Table III or Table IV.

[0027] In addition the invention provides a kit comprising at least one nucleic acid selected from the group consisting of the sequences set forth it Table I, Table II, Table III or Table IV. In one embodiment the invention provides a kit that includes a nucleic acid that includes a sequence as set forth in Table I, Table II, Table III or Table IV and at least a first universal priming sequence.

[0028] In addition the invention includes an array composition comprising a first population of microspheres comprising first and second subpopulations, wherein the first subpopulation includes a first nucleic acid selected from the sequences set forth in Table I, Table II, Table III or Table IV and the second subpopulation includes a second sequence selected from the sequences set forth in Table I, Table II, Table III or Table IV.

[0029] In addition the invention includes an array composition comprising a first sequence at a known location on a substrate, wherein the first sequence is selected from the sequences set forth in Table I, Table II, Table III or Table IV.

[0030] In addition the invention includes a method for making an array. The method includes distributing a population of microspheres on an substrate, wherein the population includes first and second subpopulations, wherein the first subpopulation includes a first sequence selected from the group consisting of the sequences set forth in Table I, Table II, Table III or Table IV and the second subpopulation includes a second sequence selected from the group consisting of the sequences set forth in Table I, Table III or Table IV.

[0031] In addition the method includes a method of immobilizing a target nucleic acid. The method includes hybridizing a first adapter probe with a first target nucleic acid, wherein the first adapter probe comprises a first domain that is complementary to the first target nucleic acid and a second domain, comprising a first sequence selected from the sequences set forth in Table I, Table II, Table III or Table IV to form a first hybridization complex. In addition the method includes contacting the first hybridization complex with a first capture probe immobilized on a first substrate, wherein the first capture probe is substantially complementary to the second domain of the first adapter probe.

[0032] In addition the invention includes a method of decoding an array composition comprising providing an array composition that includes a substrate with a surface comprising discrete sites and a population of microspheres comprising at least a first and a second subpopulation, wherein each subpopulation comprises a bioactive agent. The microspheres are distributed on the surface. The method further includes adding a plurality of decoding binding ligands to the array composition to identify the location of

at least a plurality of the bioactive agents wherein at least a first decoder binding ligand comprises a sequence selected from the group consisting of the sequences of Table I, Table II, Table III or Table IV.

[0033] A method of detecting a target nucleic acid sequence, said method comprising attaching a first adapter nucleic acid to a first target nucleic acid sequence to form a modified first target nucleic acid sequence, wherein the first adapter nucleic acid includes a sequence selected from the sequences set forth in Table I, Table II, Table III or Table IV. The method further includes contacting the modified first target nucleic acid sequence with an array comprising a substrate with a patterned surface comprising discrete sites and a population of microspheres comprising at least a first subpopulation comprising a first capture probe, such that the first capture probe and the modified first target nucleic acid sequence form a hybridization complex; wherein the microspheres are distributed on the surface and detecting the presence of the modified first target nucleic acid sequence.

#### DETAILED DESCRIPTION OF THE FIGURES

[0034] FIG. 1 depicts a method of selecting oligonucleotide sequences.

[0035] FIG. 2 depicts a scheme for selection of probes and decoder oligonucleotides.

[0036] FIG. 3 demonstrates hybridization intensity comparison of immobilized beads using non-purified oligonucleotides with HPLC purified oligonucleotides.

[0037] FIG. 4 depicts different oligonucleotide sequences immobilized onto silica beads at various salt concentration. Average intensity indicates hybridization intensity of beads in a BeadArray.

[0038] FIG. 5 depicts immobilization of oligonucleotides in increasing salt concentrations.

# DETAILED DESCRIPTION OF THE INVENTION

[0039] This invention is directed to the use of adapter sequences, and optionally capture extender probes, that allow the use of "universal" arrays. That is, a "universal" array is an array with a set of capture probes that will hybridize to adapter sequences, for use in any number of different reactions, including the binding of nucleic acid reactions and other target analytes comprising a nucleic acid adapter sequence that can hybridize to the array. In this way, a manufacturer of arrays can make one type of array that may be used in a variety of applications, thus reducing the manufacturing costs associated with the array. In addition, in the case of bead arrays, the decoding steps as outlined below can be simplified, as one set of decoding probes can be made.

[0040] In general, the use of adapter sequences can be described as follows for nucleic acid reactions. An adapter sequence can be added exogenously to a target nucleic acid sequence using any number of different techniques, including, but not limited to, amplification reactions as described in U.S. Ser. Nos. 09/425,633, filed Oct. 22, 1999; 09/513, 362, filed Feb. 25, 2000; 09/517,945, filed Mar. 3, 2000; 09/535,854, filed Mar. 27, 2000; 09/553,993, filed Apr. 20, 2000; 09/556,463, filed Apr. 21, 2000; 60/135,051, filed

May 20, 1999; 60/135,053, filed May 20, 1999; 60/135,123, filed May 20, 1999; 60/130,089, filed Apr. 20, 1999; 60/160, 917, filed Oct. 22, 1999; 60/160,927, filed Oct. 22, 1999; 60/161,148, filed Oct. 22, 1999; and 60/244,119, filed Oct. 26, 2000 all of which are hereby incorporated by reference. In addition, the adapter can be added to an extension probe. The adapter sequence can then be used to target to its complementary capture probe on the surface.

[0041] Alternatively, the adapter sequences can be added to other target analytes, to generate unique and reproducible arrays of target analytes in a similar manner. By adding the nucleic acid to the target analyte (for example to an antibody in an immunoassay), the target analytes may then be arrayed.

Accordingly, the present invention provides methods for the detection of target analytes, particularly nucleic acid target sequences, in a sample. As will be appreciated by those in the art, the sample solution may comprise any number of things, including, but not limited to, bodily fluids (including, but not limited to, blood, urine, serum, lymph, saliva, anal and vaginal secretions, perspiration and semen, of virtually any organism, with mammalian samples being preferred and human samples being particularly preferred); environmental samples (including, but not limited to, air, agricultural, water and soil samples); biological warfare agent samples; research samples; purified samples, such as purified genomic DNA, RNA, proteins, etc.; raw samples (bacteria, virus, genomic DNA, etc.; As will be appreciated by those in the art, virtually any experimental manipulation may have been done on the sample.

[0043] The present invention provides methods for the detection of target analytes, particularly nucleic acid target sequences, in a sample. By "target analyte" or "analyte" or grammatical equivalents herein is meant any molecule, compound or particle to be detected. As outlined below, target analytes preferably bind to binding ligands, as is more fully described below. As will be appreciated by those in the art, a large number of analytes may be detected using the present methods; basically, any target analyte for which a binding ligand, described below, may be made may be detected using the methods of the invention.

[0044] Suitable analytes include organic and inorganic molecules, including biomolecules. In a preferred embodiment, the analyte may be an environmental pollutant (including pesticides, insecticides, toxins, etc.); a chemical (including solvents, polymers, organic materials, etc.); therapeutic molecules (including therapeutic and abused drugs, antibiotics, etc.); biomolecules (including hormones, cytokines, proteins, lipids, carbohydrates, cellular membrane antigens and receptors (neural, hormonal, nutrient, and cell surface receptors) or their ligands, etc); whole cells (including procaryotic (such as pathogenic bacteria) and eukaryotic cells, including mammalian tumor cells); viruses (including retroviruses, herpesviruses, adenoviruses, lentiviruses, etc.); and spores; etc. Particularly preferred analytes are environmental pollutants; nucleic acids; proteins (including enzymes, antibodies, antigens, growth factors, cytokines, etc); therapeutic and abused drugs; cells; and viruses.

[0045] In a preferred embodiment, the target analyte is a protein. As will be appreciated by those in the art, there are a large number of possible proteinaceous target analytes that may be detected using the present invention. By "proteins"

or grammatical equivalents herein is meant proteins, oligopeptides and peptides, derivatives and analogs, including proteins containing non-naturally occurring amino acids and amino acid analogs, and peptidomimetic structures. The side chains may be in either the (R) or the (S) configuration. In a preferred embodiment, the amino acids are in the (S) or L-configuration. As discussed below, when the protein is used as a binding ligand, it may be desirable to utilize protein analogs to retard degradation by sample contaminants.

[0046] Suitable protein target analytes include, but are not limited to, (1) immunoglobulins, particularly IgEs, IgGs and IgMs, and particularly therapeutically or diagnostically relevant antibodies, including but not limited to, for example, antibodies to human albumin, apolipoproteins (including apolipoprotein E), human chorionic gonadotropin, cortisol,  $\alpha$ -fetoprotein, thyroxin, thyroid stimulating hormone (TSH), antithrombin, antibodies to pharmaceuticals (including antieptileptic drugs (phenytoin, primidone, carbariezepin, ethosuximide, valproic acid, and phenobarbitol), cardioactive drugs (digoxin, lidocaine, procainamide, and disopyramide), bronchodilators (theophylline), antibiotics (chloramphenicol, sulfonamides), antidepressants, immunosuppresants, abused drugs (amphetamine, methamphetamine, cannabinoids, cocaine and opiates) and antibodies to any number of viruses (including orthomyxoviruses, (e.g. influenza virus), paramyxoviruses (e.g respiratory syncytial virus, mumps virus, measles virus), adenoviruses, rhinoviruses, coronaviruses, reoviruses, togaviruses (e.g. rubella virus), parvoviruses, poxviruses (e.g. variola virus, vaccinia virus), enteroviruses (e.g. poliovirus, coxsackievirus), hepatitis viruses (including A, B and C), herpesviruses (e.g. Herpes simplex virus, varicella-zoster virus, cytomegalovirus, Epstein-Barr virus), rotaviruses, Norwalk viruses, hantavirus, arenavirus, rhabdovirus (e.g. rabies virus), retroviruses (including HIV, HTLV-I and -II), papovaviruses (e.g. papillomavirus), polyomaviruses, and picornaviruses, and the like), and bacteria (including a wide variety of pathogenic and non-pathogenic prokaryotes of interest including Bacillus; Vibrio, e.g. V. cholerae; Escherichia, e.g. Enterotoxigenic E. coli, Shigella, e.g. S. dysenteriae; Salmonella, e.g. S. typhi; Mycobacterium e.g. M. tuberculosis, M. leprae; Clostridium, e.g. C. botulinum, C. tetani, C. difficile, C.peffringens; Cornyebacterium, e.g. C. diphtheriae; Streptococcus, S. pyogenes, S. pneumoniae; Staphylococcus, e.g. S. aureus; Haemophilus, e.g. H. influenzae; Neisseria, e.g. N. meningitidis, N. gonorrhoeae; Yersinia, e.g. G. lambliaY. pestis, Pseudomonas, e.g. P. aeruginosa, P. putida; Chlamydia, e.g. C. trachomatis; Bordetella, e.g. B. pertussis; Treponema, e.g. T. palladium; and the like); (2) enzymes (and other proteins), including but not limited to, enzymes used as indicators of or treatment for heart disease, including creatine kinase, lactate dehydrogenase, aspartate amino transferase, troponin T, myoglobin, fibrinogen, cholesterol, triglycerides, thrombin, tissue plasminogen activator (tPA); pancreatic disease indicators including amylase, lipase, chymotrypsin and trypsin; liver function enzymes and proteins including cholinesterase, bilirubin, and alkaline phosphotase; aldolase, prostatic acid phosphatase, terminal deoxynucleotidyl transferase, and bacterial and viral enzymes such as HIV protease; (3) hormones and cytokines (many of which serve as ligands for cellular receptors) such as erythropoietin (EPO), thrombopoietin (TPO), the interleukins (including IL-1 through IL-17), insulin, insulin-like growth

factors (including IGF-1 and -2), epidermal growth factor (EGF), transforming growth factors (including TGF- $\alpha$  and TGF- $\beta$ ), human growth hormone, transferrin, epidermal growth factor (EGF), low density lipoprotein, high density lipoprotein, leptin, VEGF, PDGF, ciliary neurotrophic factor, prolactin, adrenocorticotropic hormone (ACTH), calcitonin, human chorionic gonadotropin, cotrisol, estradiol, follicle stimulating hormone (FSH), thyroid-stimulating hormone (TSH), leutinzing hormone (LH), progeterone, testosterone, ; and (4) other proteins (including  $\alpha$ -fetoprotein, carcinoembryonic antigen CEA.

[0047] In addition, any of the biomolecules for which antibodies may be detected may be detected directly as well; that is, detection of virus or bacterial cells, therapeutic and abused drugs, etc., may be done directly.

[0048] Suitable target analytes include carbohydrates, including but not limited to, markers for breast cancer (CA15-3, CA 549, CA 27.29), mucin-like carcinoma associated antigen (MCA), ovarian cancer (CA125), pancreatic cancer (DE-PAN-2), and colorectal and pancreatic cancer (CA 19, CA 50, CA242).

[0049] In a preferred embodiment, the target analyte (and various adapters and other probes of the invention), comprise nucleic acids. By "nucleic acid" or "oligonucleotide" or grammatical equivalents herein means at least two nucleotides covalently linked together. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, as outlined below, nucleic acid analogs are included that may have alternate backbones, comprising, for example, phosphoramide (Beaucage et al., Tetrahedron 49(10):1925 (1993) and references therein; Letsinger, J. Org. Chem. 35:3800 (1970); Sprinzl et al., Eur. J. Biochem. 81:579 (1977); Letsinger et al., Nucl. Acids Res. 14:3487 (1986); Sawai et al, Chem. Lett. 805 (1984), Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); and Pauwels et al., Chemica Scripta 26:141 91986)), phosphorothioate (Mag et al., Nucleic Acids Res. 19:1437 (1991); and U.S. Pat. No. 5,644,048), phosphorodithioate (Briu et al., J. Am. Chem. Soc. 111:2321 (1989), O-methylphophoroamidite linkages (see Eckstein, Oligonucleotides and Analogues: A Practical Approach, Oxford University Press), and peptide nucleic acid backbones and linkages (see Egholm, J. Am. Chem. Soc. 114:1895 (1992); Meier et al., Chem. Int. Ed. Engl. 31:1008 (1992); Nielsen, Nature, 365:566 (1993); Carlsson et al., Nature 380:207 (1996), all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy et al., Proc. Natl. Acad. Sci. USA 92:6097 (1995); non-ionic backbones (U.S. Pat. Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowshi et al., Angew. Chem. Intl. Ed. English 30:423 (1991); Letsinger et al., J. Am. Chem. Soc. 110:4470 (1988); Letsinger et al., Nucleoside & Nucleotide 13:1597 (1994); Chapters 2 and 3, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y. S. Sanghui and P. Dan Cook; Mesmaeker et al., Bioorganic & Medicinal Chem. Left. 4:395 (1994); Jeffs et al., J. Biomolecular NMR 34:17 (1994); Tetrahedron Left. 37:743 (1996)) and non-ribose backbones, including those described in U.S. Pat. Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y. S. Sanghui and P. Dan Cook. Nucleic acids containing one or more carbocyclic sugars are also included within the definition of nucleic acids (see Jenkins et al., Chem. Soc. Rev. (1995) pp169-176). Several nucleic acid analogs are described in Rawls, C & E News Jun. 2,1997 page 35. All of these references are hereby expressly incorporated by reference. These modifications of the ribose-phosphate backbone may be done to facilitate the addition of labels, alter the hybridization properties of the nucleic acids, or to increase the stability and half-life of such molecules in physiological environments.

[0050] As will be appreciated by those in the art, all of these nucleic acid analogs may find use in the present invention. In addition, mixtures of naturally occurring nucleic acids and analogs can be made. Alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

[0051] Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (Tm) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C. drop in Tm for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. This allows for better detection of mismatches. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration.

[0052] The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both Id double stranded or single stranded sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA or a hybrid, where the nucleic acid contains any combination of deoxyribo- and ribo-nucleotides, and any combination of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xathanine hypoxathanine, isocytosine, isoguanine, etc. A preferred embodiment utilizes isocytosine and isoguanine in nucleic acids designed to be complementary to other probes, rather than target sequences, as this reduces non-specific hybridization, as is generally described in U.S. Pat. No. 5,681,702. As used herein, the term "nucleoside" includes nucleotides as well as nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occuring analog structures. Thus for example the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

[0053] In general, probes of the present invention (including adapter sequences and capture probes, described below) are designed to be complementary to a target sequence (either the target sequence of the sample or to other probe sequences, for example adapter sequences) such that hybridization of the target and the probes of the present invention occurs. This complementarity need not be perfect; there may be any number of base pair mismatches that will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary"

herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under the selected reaction conditions.

[0054] When nucleic acids are to be detected, they are referred to herein as "target nucleic acids" or "target sequences". The term "target sequence" or "target nucleic acid" or grammatical equivalents herein means a nucleic acid sequence on a single strand of nucleic acid. The target sequence may be a portion of a gene, a regulatory sequence, genomic DNA, cDNA, RNA including mRNA and rRNA, or others. As is outlined herein, the target sequence may be a target sequence from a sample, or a derivative target such as a product of a reaction such as a detection sequence from an Invader™ reaction, a ligated probe from an OLA reaction, an extended probe from an SBE reaction, etc. It may be any length, with the understanding that longer sequences are more specific. As will be appreciated by those in the art, the complementary target sequence may take many forms. For example, it may be contained within a larger nucleic acid sequence, i.e. all or part of a gene or mRNA, a restriction fragment of a plasmid or genomic DNA, among others. As is outlined more fully below, probes are made to hybridize to target sequences to determine the presence or absence of the target sequence in a sample. Generally speaking, this term will be understood by those skilled in the art. The target sequence may also be comprised of different target domains; for example, a first target domain of the sample target sequence may hybridize to a capture probe, a second target domain may hybridize to a portion of a label probe, etc. The target domains may be adjacent or separated as indicated. Unless specified, the terms "first" and "second" are not meant to confer an orientation of the sequences with respect to the 5'-3' orientation of the target sequence. For example, assuming a 5'-3' orientation of the complementary target sequence, the first target domain may be located either 5' to the second domain, or 3' to the second domain. In addition, as will be appreciated by those in the art, the probes on the surface of the array (e.g. attached to the microspheres) may be attached in either orientation, either such that they have a free 3' end or a free 5' end.

[0055] As is more fully outlined below, the target sequence may comprise a position for which sequence information is desired, generally referred to herein as the "detection position" or "detection locus". In a preferred embodiment, the detection position is a single nucleotide, although in some embodiments, rt may comprise a plurality of nucleotides, either contiguous with each other or separated by one or more nucleotides. By "plurality" as used herein is meant at least two. As used herein, the base which basepairs with a detection position base in a hybrid is termed a "readout position" or an "interrogation position".

[0056] In some embodiments, as is outlined herein, the target sequence may not be the sample target sequence but instead is a product of a reaction herein, sometimes referred to herein as a "secondary" or "derivative" target sequence. Thus, for example, in SBE, the extended primer may serve as the target sequence; similarly, in invasive cleavage variations, the cleaved detection sequence may serve as the target sequence.

[0057] If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation,

etc., with purification and/or amplification as needed, as will be appreciated by those in the art.

[0058] Once prepared, the target sequence can be used in a variety of reactions for a variety of reasons. For example, in a preferred embodiment, genotyping reactions are done. Similarly, these reactions can also be used to detect the presence or absence of a target sequence. Sequencing or amplification reactions are also preferred. In addition, in any reaction, quantitation of the amount of a target sequence may be done.

[0059] Furthermore, as outlined below for each reaction, many of these techniques may be used in a solution based assay, wherein the reaction is done in solution and a reaction product is bound to the array for subsequent detection, or in solid phase assays, where the reaction occurs on the surface and is detected.

[0060] In general, the present invention provides pairs of capture probes (nucleic acids that are attached to addresses on arrays) and adapter sequences (sequences that are either perfectly or substantially complementary to the capture probe sequences) that can be used in a wide variety of ways, to immobilize target nucleic acids (either primary targets, such as genomic DNA, mRNA or cDNA, or secondary targets such as amplicons from a nucleic acid amplification or extension reaction, as outlined herein) to the addresses of the array. Thus, all the sequences in the Tables include their complements, and either sequence can be used as a capture probe (e.g. spotted onto a surface or attached to a microsphere of an array) or as the adapter sequence that binds to the capture probe.

[0061] Accordingly, by "adapter sequences" or "adapters" or grammatical equivalents is meant a nucleic acid segment generally non-native or exogenous to a target molecule that is used to immobilize the target molecule to a solid support via binding to a capture probe sequence. In a preferred embodiment the adapter sequences and capture probes are selected from the sequences set forth in Table I, Table II, Table III or Table IV.

[0062] Table I includes the sequence of the preferred 4000 sequences labeled "Decoder (5'-3')", and inherent in this table are the complementary sequences as well. In addition, the invention includes oligonucleotides that are complementary to those depicted in Table 1.

[0063] Table II includes the sequence of the preferred adapter/capture probe sequences and their complementary sequence. Table 2 depicts a preferred subset of 3172 decoder oligonucleotides and their complementary probe oligonucleotides. Accordingly, the invention provides compositions comprising a sequence as outlined in Table 2. In addition, the invention provides a composition comprising a complementary binding pair as outlined in Table 2.

[0064] Table 3 includes a preferred subset of 768 decoder oligonucleotides and complementary probe sequences. In some embodiments it may be desirable to include a uniform base at a terminus of the oligonucleotide, such as a T at the 5' end as depicted in Table 4. The inclusion of this uniform or constant base facilitates uniform labeling of the oligonucleotides.

[0065] These sequences are used as decoder probes, capture probes or adapter sequences as outlined in U.S. Ser. No.

09/344,526 and PCT/US99/14387, and U.S. Ser. Nos. 60/160,917 and 09/5656,463 all of which are expressly incorporated by reference in their entirety.

[0066] As will be appreciated by those in the art, the length of the capture probe/adapter sequences will vary, depending on the desired "strength" of binding and the number of different adapters desired. In a preferred embodiment, adapter sequences range from about 5 to about 500 basepairs in length, with from about 8 to about 100 being preferred, and from about 10 to about 50 being particularly preferred.

[0067] As will be appreciated by those in the art, it is desirable to have adapter sequences that do not have significant homology to naturally occurring target sequences, to avoid non-specific or erroneous binding of target sequences to the capture probes. Accordingly, preferred embodiments utilize some method to select useful adapter sequences. In a preferred embodiment the method is outlined in FIG. 1. Briefly, random 24-mer (or could be any desired length as outlined herein), sequences were assembled and subjected to certain defined screening procedures including such steps as requiring that the Tm of each of the sequence be within a pre-defined range. In addition the GC content must be balanced with the AT content and the self-complementarity must be minimized. In addition GC runs should be minimized, that is, runs of Gs or Cs should be reduced. In addition, decoder (adapter) to decoder (adapter) complementarity should be reduced so that the adapters do not hybridize with each other. Finally, the sequences are screened against a specified genomic database. In a preferred embodiment the adapters comprise at least one sequence selected from the sequences in Table I, Table II, Table III or Table IV.

[0068] In a preferred embodiment, the adapter sequences are chosen on the basis of a decoding step. As is more fully outlined below, a decoding step is used to decode random bead arrays. In this embodiment, a set of candidate capture probes is chosen; this may be done in a variety of ways. In a preferred embodiment, the sequences are generated randomly, each of a sufficient length to ensure a low probability of occurring naturally. In some embodiments, for example when the array will be used with a particular organism's genome (e.g. the human genome, the Drosophila genome, etc. ), the sequences are compared to the genome as a first filter, for example to remove sequences that would cross hybridize. Additionally, further filtering may be done using well-known methods, such as known methods for selecting good PCR primers. These techniques generally include steps that remove sequences that may have a propensity to form secondary structures or otherwise to cross-hybridize. Additionally, sequences that have extremes of melting temperatures can be optionally discarded, depending on the planned assay conditions.

[0069] Once a set of candidate capture probes is obtained, an array comprising the capture probes is made, and a matching set of decoding probes comprising the adapter sequences (e.g. the complements of the capture probes), as more fully outlined below, is made. Decoding then proceeds. Probes that do not hybridize well, for whatever reason, will not decode well, generally due to weak signals, and are generally discarded. Probes that cross-hybridize will also not decode well, as they will give ambiguous or mixed

decoding signals. Only probes that hybridize sufficiently strongly and specifically will decode. Thus, by setting suitable thresholds for signal strength and signal purity, adapter sequences that perform according to specified criteria are identified. Additionally, by setting a range on signal strength, capture probe/adapter sequence pairs that perform similarly (but hybridize specifically) are identified. In a preferred embodiment, decoding reactions are repeated, under a variety of conditions, to test the robustness of the sequence pair.

[0070] Once identified, the adapter sequences are added to target sequences in a variety of ways, as will be appreciated by those in the art. In a preferred embodiment, nucleic acid amplification reactions are done, as is generally outlined in "Detection of Nucleic Acid Amplification Reactions Using Bead Arrays" and "Sequence Determination of Nucleic Acids using Arrays with Microspheres", both of which were filed on Oct. 22, 1999, (U.S. Ser. Nos. 60/161,148 and 09/425,633, respectively), both of which are hereby incorporated by reference in their entirety. These may be either target amplification or signal amplification. In general, the techniques can be described as follows. Most amplification techniques require one or more primers hybridizing to all or part the target sequence (e.g. that hybridize to a target domain). The adapter sequences can be added to one or more of the primers (depending on the configuration/orientation of the system and need) and the amplification reactions are run. Thus, for example, PCR primers comprising at least one adapter sequence (and preferably one on each PCR primer) may be used; one or both of the ligation probes of an OLA or LCR reaction may comprise an adapter sequence; the sequencing primers for pyrosequencing, single-base extension, reversible chain termination, etc., reactions may comprise an adapter sequence; either the invader probe or the signalling probe of invasive cleavage reactions can comprise an adapter sequence; etc. Similarly, for signal detection techniques, the probes may comprise adapter sequences, with preferred methods utilizing removal of the unreacted probes. In addition, primers may include universal priming sequences. That is, the adapters may additionally contain universal priming sequences for universal amplification of products of any of the reactions described herein. Universal priming sequences are further outlined in 09/779376, filed Feb. 7, 2001; 09/779202, filed Feb. 7, 2001; 09/915231, filed Jul. 24, 2001; 60/180810, filed Feb. 7, 2000; and 60/297609, filed Jun. 11, 2001; and 60/311194 filed Aug. 9, 2001, all of which are expressly incorporated herein by reference.

[0071] In an alternative embodiment, non-nucleic acid reactions are used to add adapter sequences to the nucleic acid targets. For example, for the direct detection of nonamplified target sequences (e.g. genomic DNA samples, etc.) on universal arrays, non-amplification methods are required. In this embodiment, binding partner pairs or chemical methods may be used. For example, one member of a binding partner pair may be attached to the adapter sequence and the other member attached to the target sequence. For example, the binding partner be a hapten or antigen, which will bind its binding partner. For example, suitable binding partner pairs include, but are not limited to: antigens (such as proteins (including peptides)) and antibodies (including fragments thereof (FAbs, etc.)); proteins and small molecules, including biotin/streptavidin and digoxygenin and antibodies; enzymes and substrates or inhibitors; other protein-protein interacting pairs; receptorligands; and carbohydrates and their binding partners, are also suitable binding pairs. Nucleic acid-nucleic acid binding proteins pairs are also useful. In general, the smaller of the pair is attached to the NTP (or the probe) for incorporation into the extension primer. Preferred binding partner pairs include, but are not limited to, biotin (or imino-biotin) and streptavidin, digeoxinin and Abs, and Prolinx<sup>TM</sup> reagents.

[0072] In a preferred embodiment, chemical attachment methods are used. In this embodiment, chemical functional groups on each of the target sequences and adapter sequences are used. As is known in the art, this may be accomplished in a variety of ways. Preferred functional groups for attachment are amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the two sequences are joined together; for example, amino groups on each nucleic acid may be attached, for example using linkers as are known in the art; for example, homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200, incorporated herein by reference).

[0073] In a preferred embodiment, aptamers are used in the system. Aptamers are nucleic acids that can be made to bind to virtually any target analyte; see Bock et al., Nature 355:564 (1992); Femulok et al., Current Op. Chem. Biol. 2:230 (1998); and U.S. Pat. Nos. 5,270,163, 5,475,096, 5,567,588, 5,595,877, 5,637,459, 5,683,867,5,705,337, and related patents, hereby incorporated by reference.

[0074] In a preferred embodiment, an array comprising capture probes that hybridize to adapter sequences is made, as outlined herein. In one embodiment aptamers, comprising adapter sequences, can be added. As will be appreciated by those in the art, the aptamers may be preassociated with their binding partners, e.g. target analytes, prior to introduction to the array, or not. In addition, the association between the adapter sequences on the aptamers and the capture probes can be made covalent, for example through the use of reactive groups (e.g. psoralen) and appropriate activation.

[0075] In addition, the present invention is directed to the use of adapter sequences to assemble arrays comprising other target analytes.

[0076] The adapter sequences may be chosen as outlined above. Preferably the adapters are selected from the sequences set forth in Table I, Table II, Table III or Table IV. These adapter sequences can then be added to the target analytes using a variety of techniques. In general, as described above, non-covalent attachment using binding partner pairs may be done, or covalent attachment using chemical moieties (including linkers).

[0077] Advantages of using adapters include but are not limited to, for example, the ability to create universal arrays. That is, a single array is utilized with each capture probe designed to hybridize with a specific adapter. The adapters are joined to any number of target analytes, such as nucleic acids, as is described herein. Thus, the same array is used for vastly different target analytes. Furthermore, hybridization of adapters with capture probes results in non-covalent attachment of the target nucleic acid to the address of the array (e.g. a microsphere in some embodiments). As such,

the target nucleic/adapter hybrid is easily removed, and the microsphere/capture probe can be re-used. In addition, the construction of kits is greatly facilitated by the use of adapters. For example, arrays or microspheres can be prepared that comprise the capture probe; the adapters can be packaged along with the microspheres for attachment to any target analyte of interest. Thus, one need only attach the adapter to the target analyte and disperse on the array for the construction of an array of target analytes.

[0078] Accordingly the present invention provides kits comprising adapters. Preferably the kits include at least 1 nucleic acid sequence as set forth in Table 1. More preferably the kits include at least 10-25 nucleic acids, with at least 50 nucleic acids more preferred. Even more preferable are kits that include at least 100 nucleic acids with more than 1000 even more preferred and more than 2000 even more preferred.

[0079] It should also be noted that the sequences defined herein can also be used in "sandwich" assay formats, wherein a capture extender probe comprising a first domain that will hybridize to the capture probe and a second domain that has a target specific domain is used. The capture extender probe hybridizes both to the target sequence and the capture probe, thereby immobilizing the target sequence on the array.

[0080] Once the adapter sequences are associated with the target analyte, including target nucleic acids, the compositions are added to an array comprising addresses comprising capture probes. In one embodiment a plurality of hybrid adapter sequence/target analytes are pooled prior to addition to an array. All of the methods and compositions herein are drawn to compositions and methods for detecting the presence of target analytes, particularly nucleic acids, using adapter arrays.

[0081] Accordingly, the present invention provides array compositions comprising at least a first substrate with a surface comprising individual sites. The present system finds particular utility in array formats, i.e. wherein there is a matrix of capture probes (herein generally referred to "pads", "addresses" or "micro-locations"). By "array" or "biochip" herein is meant a plurality of nucleic acids in an array format; the size of the array will depend on the composition and end use of the array. Nucleic acids arrays are known in the art, and can be classified in a number of ways; both ordered arrays (e.g. the ability to resolve chemistries at discrete sites), and random arrays are included. Ordered arrays include, but are not limited to, those made using photolithography techniques (Affymetrix Gene-Chip™), spotting techniques (Synteni and others), printing techniques (Hewlett Packard and Rosetta), three dimensional "gel pad" arrays, etc. In one embodiment the ordered arrays include arrays that contain nucleic acids at known locations. That is, the adapters or capture probes described herein are immobilized at known locations on a substrate. By "known" locations is meant a site that is known or has been known.

[0082] In addition, adapters find use "liquid arrays". By "liquid arrays" is meant an array in solution for analysis, for example, by flow cytometry.

[0083] A preferred embodiment utilizes microspheres on a variety of substrates including fiber optic bundles, as are

outlined in PCTs US98/21193, PCT US99/14387 and PCT US98/05025; WO98/50782; and U.S. Ser. Nos. 09/287,573, 09/151,877, 09/256,943, 09/316,154, 60/119,323, 09/315,584; all of which are expressly incorporated by reference. While much of the discussion below is directed to the use of microsphere arrays on fiber optic bundles, any array format of nucleic acids on solid supports may be utilized.

[0084] Arrays containing from about 2 different bioactive agents (e.g. different beads, when beads are used) to many millions can be made, with very large arrays being possible. Generally, the array will comprise from two to as many as a billion or more, depending on the size of the beads and the substrate, as well as the end use of the array, thus very high density, high density, moderate density, low density and very low density arrays may be made. Preferred ranges for very high density arrays are from about 10,000,000 to about 2,000,000,000, with from about 100,000,000 to about 1,000, 000,000 being preferred (all numbers being in square cm). High density arrays range about 100,000 to about 10,000, 000, with from about 1,000,000 to about 5,000,000 being particularly preferred. Moderate density arrays range from about 10,000 to about 100,000 being particularly preferred, and from about 20,000 to about 50,000 being especially preferred. Low density arrays are generally less than 10,000, with from about 1,000 to about 5,000 being preferred. Very low density arrays are less than 1,000, with from about 10 to about 1000 being preferred, and from about 100 to about 500 being particularly preferred. In some embodiments, the compositions of the invention may not be in array format; that is, for some embodiments, compositions comprising a single bioactive agent may be made as well. In addition, in some arrays, multiple substrates may be used, either of different or identical compositions. Thus for example, large arrays may comprise a plurality of smaller substrates.

[0085] In addition, one advantage of the present compositions is that particularly through the use of fiber optic technology, extremely high density arrays can be made. Thus for example, because beads of 200  $\mu$ m or less (with beads of 200 nm possible) can be used, and very small fibers are known, it is possible to have as many as 40,000 or more (in some instances, 1 million) different elements (e.g. fibers and beads) in a 1 mm<sup>2</sup> fiber optic bundle, with densities of greater than 25,000,000 individual beads and fibers (again, in some instances as many as 50-100 million) per 0.5 cm<sup>2</sup> obtainable (4 million per square cm for 5  $\mu$  center-to-center and 100 million per square cm for 1  $\mu$  center-to-center).

[0086] By "substrate" or "solid support" or other grammatical equivalents herein is meant any material that can be modified to contain discrete individual sites appropriate for the attachment or association of beads and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates is very large. Possible substrates include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, optical fiber bundles, and a variety of other polymers. In general, the substrates allow optical detection and do not themselves appreciably fluoresce.

[0087] Generally the substrate is flat (planar), although as will be appreciated by those in the art, other configurations of substrates may be used as well; for example, three dimensional configurations can be used, for example by embedding the beads in a porous block of plastic that allows sample access to the beads and using a confocal microscope for detection. Similarly, the beads may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Preferred substrates include optical fiber bundles as discussed below, and flat planar substrates such as glass, polystyrene and other plastics and acrylics.

[0088] In a preferred embodiment, the substrate is an optical fiber bundle or array, as is generally described in U.S. Ser. Nos. 08/944,850 and 08/519,062, PCT US98/05025, and PCT US98/09163, all of which are expressly incorporated herein by reference. Preferred embodiments utilize preformed unitary fiber optic arrays. By "preformed unitary fiber optic arrays. By "preformed unitary fiber optic array" herein is meant an array of discrete individual fiber optic strands that are co-axially disposed and joined along their lengths. The fiber strands are generally individually clad. However, one thing that distinguished a preformed unitary array from other fiber optic formats is that the fibers are not individually physically manipulatable; that is, one strand generally cannot be physically separated at any point along its length from another fiber strand.

[0089] At least one surface of the substrate is modified to contain discrete, individual sites for later association of microspheres. These sites may comprise physically altered sites, i.e. physical configurations such as wells or small depressions in the substrate that can retain the beads, such that a microsphere can rest in the well, or the use of other forces (magnetic or compressive), or chemically altered or active sites, such as chemically functionalized sites, electrostatically altered sites, hydrophobically/ hydrophilically functionalized sites, spots of adhesive, etc.

[0090] The sites may be a pattern, i.e. a regular design or configuration, or randomly distributed. A preferred embodiment utilizes a regular pattern of sites such that the sites may be addressed in the X-Y coordinate plane. "Pattern" in this sense includes a repeating unit cell, preferably one that allows a high density of beads on the substrate. However, it should be noted that these sites may not be discrete sites. That is, it is possible to use a uniform surface of adhesive or chemical functionalities, for example, that allows the attachment of beads at any position. That is, the surface of the substrate is modified to allow attachment of the microspheres at individual sites, whether or not those sites are contiguous or non-contiguous with other sites. Thus, the surface of the substrate may be modified such that discrete sites are formed that can only have a single associated bead, or alternatively, the surface of the substrate is modified and beads may go down anywhere, but they end up at discrete

[0091] In a preferred embodiment, the surface of the substrate is modified to contain wells, i.e. depressions in the surface of the substrate. This may be done as is generally known in the art using a variety of techniques, including, but not limited to, photolithography, stamping techniques, molding techniques and microetching techniques. As will be appreciated by those in the art, the technique used will depend on the composition and shape of the substrate.

[0092] In a preferred embodiment, physical alterations are made in a surface of the substrate to produce the sites. In a

preferred embodiment, the substrate is a fiber optic bundle and the surface of the substrate is a terminal end of the fiber bundle, as is generally described in 08/818,199 and 09/151, 877, both of which are hereby expressly incorporated by reference. In this embodiment, wells are made in a terminal or distal end of a fiber optic bundle comprising individual fibers. In this embodiment, the cores of the individual fibers are etched, with respect to the cladding, such that small wells or depressions are formed at one end of the fibers. The required depth of the wells will depend on the size of the beads to be added to the wells.

[0093] Generally in this embodiment, the microspheres are non-covalently associated in the wells, although the wells may additionally be chemically functionalized as is generally described below, cross-linking agents may be used, or a physical barrier may be used, i.e. a film or membrane over the beads.

[0094] In a preferred embodiment, the surface of the substrate is modified to contain chemically modified sites, that can be used to attach, either covalently or non-covalently, the microspheres of the invention to the discrete sites or locations on the substrate. "Chemically modified sites" in this context includes, but is not limited to, the addition of a pattern of chemical functional groups including amino groups, carboxy groups, oxo groups and thiol groups, that can be used to covalently attach microspheres, which generally also contain corresponding reactive functional groups; the addition of a pattern of adhesive that can be used to bind the microspheres (either by prior chemical functionalization for the addition of the adhesive or direct addition of the adhesive); the addition of a pattern of charged groups (similar to the chemical functionalities) for the electrostatic attachment of the microspheres, i.e. when the microspheres comprise charged groups opposite to the sites; the addition of a pattern of chemical functional groups that renders the sites differentially hydrophobic or hydrophilic, such that the addition of similarly hydrophobic or hydrophilic microspheres under suitable experimental conditions will result in association of the microspheres to the sites on the basis of hydroaffinity. For example, the use of hydrophobic sites with hydrophobic beads, in an aqueous system, drives the association of the beads preferentially onto the sites. As outlined above, "pattern" in this sense includes the use of a uniform treatment of the surface to allow attachment of the beads at discrete sites, as well as treatment of the surface resulting in discrete sites. As will be appreciated by those in the art, this may be accomplished in a variety of ways.

[0095] In a preferred embodiment, the compositions of the invention further comprise a population of microspheres. By "population" herein is meant a plurality of beads as outlined above for arrays. Within the population are separate subpopulations, which can be a single microsphere or multiple identical microspheres. That is, in some embodiments, as is more fully outlined below, the array may contain only a single bead for each capture probe; preferred embodiments utilize a plurality of beads of each type.

[0096] By "microspheres" or "beads" or "particles" or grammatical equivalents herein is meant small discrete particles. The composition of the beads will vary, depending on the class of capture probe and the method of synthesis. Suitable bead compositions include those used in peptide, nucleic acid and organic moiety synthesis, including, but not

limited to, plastics, ceramics, glass, polystyrene, methylstyrene, acrylic polymers, paramagnetic materials, thoria sol, carbon graphite, titanium dioxide, latex or cross-linked dextrans such as Sepharose, cellulose, nylon, cross-linked micelles and Teflon may all be used. "Microsphere Detection Guide" from Bangs Laboratories, Fishers IN is a helpful guide.

[0097] The beads need not be spherical; irregular particles may be used. In addition, the beads may be porous, thus increasing the surface area of the bead available for either capture probe attachment or tag attachment. The bead sizes range from nanometers, i.e. 100 nm, to millimeters, i.e. 1 mm, with beads from about 0.2 micron to about 200 microns being preferred, and from about 0.5 to about 5 micron being particularly preferred, although in some embodiments smaller beads may be used.

[0098] It should be noted that a key component of this embodiment of the invention is the use of a substrate/bead pairing that allows the association or attachment of the beads at discrete sites on the surface of the substrate, such that the beads do not move during the course of the assay.

[0099] Each microsphere comprises a capture probe, although as will be appreciated by those in the art, there may be some microspheres which do not contain a capture probe, depending on the synthetic methods. Alternatively, some have more than one capture probe.

[0100] Attachment of the nucleic acids may be done in a variety of ways, as will be appreciated by those in the art, including, but not limited to, chemical or affinity capture (for example, including the incorporation of derivatized nucleotides such as AminoLink or biotinylated nucleotides that can then be used to attach the nucleic acid to a surface, as well as affinity capture by hybridization), cross-linking, and electrostatic attachment, etc. In a preferred embodiment, affinity capture is used to attach the nucleic acids to the beads. For example, nucleic acids can be derivatized, for example with one member of a binding pair, and the beads derivatized with the other member of a binding pair. Suitable binding pairs are as described herein for IBUDBL pairs. For example, the nucleic acids may be biotinylated (for example using enzymatic incorporate of biotinylated nucleotides, for by photoactivated cross-linking of biotin). Biotinylated nucleic acids can then be captured on streptavidin-coated beads, as is known in the art. Similarly, other haptenreceptor combinations can be used, such as digoxigenin and anti-digoxigenin antibodies. Alternatively, chemical groups can be added in the form of derivatized nucleotides, that can them be used to add the nucleic acid to the surface.

[0101] Preferred attachments are covalent, although even relatively weak interactions (i.e. non-covalent) can be sufficient to attach a nucleic acid to a surface, if there are multiple sites of attachment per each nucleic acid. Thus, for example, electrostatic interactions can be used for attachment, for example by having beads carrying the opposite charge to the bioactive agent.

[0102] Similarly, affinity capture utilizing hybridization can be used to attach nucleic acids to beads. For example, as is known in the art, polyA+RNA is routinely captured by hybridization to oligo-dT beads; this may include oligo-dT capture followed by a cross-linking step, such as psoralen crosslinking). If the nucleic acids of interest do not contain

a polyA tract, one can be attached by polymerization with terminal transferase, or via ligation of an oligoA linker, as is known in the art.

[0103] Alternatively, chemical crosslinking may be done, for example by photoactivated crosslinking of thymidine to reactive groups, as is known in the art.

[0104] In a preferred embodiment, each bead comprises a single type of capture probe, although a plurality of individual capture probes are preferably attached to each bead. Similarly, preferred embodiments utilize more than one microsphere containing a unique capture probe; that is, there is redundancy built into the system by the use of subpopulations of microspheres, each microsphere in the subpopulation containing the same capture probe.

[0105] In an alternative embodiment, each bead comprises a plurality of different capture probes.

[0106] As will be appreciated by those in the art, the capture probes may either be synthesized directly on the beads, or they may be made and then attached after synthesis. In a preferred embodiment, linkers are used to attach the capture probes to the beads, to allow both good attachment, sufficient flexibility to allow good interaction with the target molecule, and to avoid undesirable binding reactions.

[0107] In a preferred embodiment, the capture probes are synthesized directly on the beads. As is known in the art, many classes of chemical compounds are currently synthesized on solid supports, such as peptides, organic moieties, and nucleic acids. It is a relatively straightforward matter to adjust the current synthetic techniques to use beads.

[0108] In a preferred embodiment, the capture probes are synthesized first, and then covalently attached to the beads. As will be appreciated by those in the art, this will be done depending on the composition of the capture probes and the beads. The functionalization of solid support surfaces such as certain polymers with chemically reactive groups such as thiols, amines, carboxyls, etc. is generally known in the art. Accordingly, "blank" microspheres may be used that have surface chemistries that facilitate the attachment of the desired functionality by the user. Some examples of these surface chemistries for blank microspheres include, but are not limited to, amino groups including aliphatic and aromatic amines, carboxylic acids, aldehydes, amides, chloromethyl groups, hydrazide, hydroxyl groups, sulfonates and sulfates.

[0109] In a preferred embodiment the attachment of nucleic acids to substrates includes contacting the oligonucleotide and the solid support in the presence of high salt concentrations. As is appreciated by those skilled in the art, salt includes, but is not limited to sodium chloride, potassium chloride, calcium chloride, magnesium chloride, lithium chloride, rubidium chloride, cesium chloride, barium chloride and the like. In a preferred embodiment, salt as used in the invention includes sodium chloride.

[0110] By high salt concentrations is meant salt that is more concentrated than about 0.1 M salt. In a preferred embodiment, by high salt concentrations is meant greater than about 0.2 M salt. In a particularly preferred embodiment, high salt concentrations include from about 0.5 to 3 M salt, with about 1 M to 2 M being most preferred.

[0111] By solid support or other grammatical equivalents herein is meant any material that can be modified to contain oligonucleotides. As will be appreciated by those in the art, the number of possible solid supports is very large. Possible solid supports include, but are not limited to beads, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, optical fiber bundles, and a variety of other polymers.

[0112] Once formed, the support containing the oligonucleotides finds use in a variety of systems including decoding arrays as described in more detail in U.S. Ser. No. 09/344,526, and U.S. Ser. No. 09/574,117, both of which are expressly incorporated herein by reference. In addition, the support containing the oligonucleotides finds use in microfluidic systems as described in U.S. Ser. No. 09/306,369 which is expressly incorporated herein by reference. In addition, the support containing the oligonucleotides finds use in composite array systems as described in U.S. Ser. No. 09/606,369, which is expressly incorporated herein by reference. In addition the support containing the oligonucleotides finds use in a variety of assays as outlined in more detail in U.S. Ser. Nos. 09/513,362, 09/517,945, 09/535,854, 60/160,917, 60/180,810, 60/182,955, and 09/566,463, all of which are expressly incorporated herein by reference in their entirety. In addition, the support containing the oligonucleotides finds use in array based sensors as described in more detail in 09/287,573, 09/260,963, 09/450,829, 09/151,877, 09/187,289 and 08/519,062, all of which are expressly incorporated herein by reference in their entirety.

[0113] Accordingly the invention provides a method of attaching oligonucleotides to a solid support. The method includes contacting the oligonucleotides with the support in the presence of high salt as described herein. Once attached, as discussed in the examples, the attached oligonucleotides readily hybridize to targets, probes and the like. Attachment of crude oligonucleotides in the presence of high salt is as efficient as attaching purified oligonucleotides. Thus, the invention also contemplates a method of attachment of oligonucleotides to a solid support without prior purification of the oligonucleotides. Again, the method includes contacting the crude oligonucleotides with a solid support in the presence of high salt as described herein.

[0114] The capture probes are designed to be substantially complementary to the adapter sequences, to allow for a minimum of cross reactivity.

[0115] When microsphere arrays are used, an encoding/decoding system must be used. That is, since the beads are generally put onto the substrate randomly, there are several ways to correlate the functionality on the bead with its location, including the incorporation of unique optical signatures, generally fluorescent dyes, that could be used to identify the chemical functionality on any particular bead. This allows the synthesis of the candidate agents (i.e. compounds such as nucleic acids and antibodies) to be divorced from their placement on an array, i.e. the candidate agents may be synthesized on the beads, and then the beads are randomly distributed on a patterned surface. Since the

beads are first coded with an optical signature, this means that the array can later be "decoded", i.e. after the array is made, a correlation of the location of an individual site on the array with the bead or candidate agent at that particular site can be made. This means that the beads may be randomly distributed on the array, a fast and inexpensive process as compared to either the in situ synthesis or spotting techniques of the prior art.

[0116] However, the drawback to these methods is that for a large array, the system requires a large number of different optical signatures, which may be difficult or time-consuming to utilize. Accordingly, the present invention provides several improvements over these methods, generally directed to methods of coding and decoding the arrays. That is, as will be appreciated by those in the art, the placement of the capture probes is generally random, and thus a coding/ decoding system is required to identify the probe at each location in the array. This may be done in a variety of ways, as is more fully outlined below, and generally includes: a) the use a decoding binding ligand (DBL), generally directly labeled, that binds to either the capture probe or to identifier binding ligands (IBLs) attached to the beads; b) positional decoding, for example by either targeting the placement of beads (for example by using photoactivatible or photocleavable moieties to allow the selective addition of beads to particular locations), or by using either sub-bundles or selective loading of the sites, as are more fully outlined below; c) selective decoding, wherein only those beads that bind to a target are decoded; or d) combinations of any of these. In some cases, as is more fully outlined below, this decoding may occur for all the beads, or only for those that bind a particular target sequence. Similarly, this may occur either prior to or after addition of a target sequence. In addition, as outlined herein, the target sequences detected may be either a primary target sequence (e.g. a patient sample), or a reaction product from one of the methods described herein (e.g. an extended SBE probe, a ligated probe, a cleaved signal probe, etc.).

[0117] Once the identity (i.e. the actual agent) and location of each microsphere in the array has been fixed, the array is exposed to samples containing the target sequences, although as outlined below, this can be done prior to or during the analysis as well. The target sequences can hybridize (either directly or indirectly) to the capture probes as is more fully outlined below, and results in a change in the optical signal of a particular bead.

[0118] In the present invention, "decoding" may not rely on the use of optical signatures, but rather on the use of decoding binding ligands that are added during a decoding step. The decoding binding ligands will bind either to a distinct identifier binding ligand partner that is placed on the beads, or to the capture probe itself. In this embodiment the decoding binding ligand either is complementary to the capture probe. In this embodiment the decoding binding ligand has the sequence of the adapter that also binds to the capture probe. In a preferred embodiment the decoder binding ligand is a nucleic acid that has the sequence of at least one of the nucleic acids set forth in Table 1.

[0119] The decoding binding ligands are either directly or indirectly labeled, and thus decoding occurs by detecting the presence of the label. By using pools of decoding binding ligands in a sequential fashion, it is possible to greatly minimize the number of required decoding steps.

[0120] In some embodiments, the microspheres may additionally comprise identifier binding ligands for use in certain decoding systems. By "identifier binding ligands" or "IBLs" herein is meant a compound that will specifically bind a corresponding decoder binding ligand (DBL) to facilitate the elucidation of the identity of the capture probe attached to the bead. That is, the IBL and the corresponding DBL form a binding partner pair. By "specifically bind" herein is meant that the IBL binds its DBL with specificity sufficient to differentiate between the corresponding DBL and other DBLs (that is, DBLs for other IBLs), or other components or contaminants of the system. The binding should be sufficient to remain bound under the conditions of the decoding step, including wash steps to remove non-specific binding. In some embodiments, for example when the IBLs and corresponding DBLs are proteins or nucleic acids, the dissociation constants of the IBL to its DBL will be less than about  $10^{-4}$ - $10^{-6}$  M<sup>-1</sup>, with less than about  $10^{-5}$  to  $10^{-9}$  M<sup>-1</sup> being preferred and less than about  $10^{-7}$ - $10^{-9}$  M<sup>-1</sup> being particularly preferred.

[0121] IBL-DBL binding pairs are known or can be readily found using known techniques. For example, when the IBL is a protein, the DBLs include proteins (particularly including antibodies or fragments thereof (FAbs, etc.)) or small molecules, or vice versa (the IBL is an antibody and the DBL is a protein). Metal ion-metal ion ligands or chelators pairs are also useful. Antigen-antibody pairs, enzymes and substrates or inhibitors, other protein-protein interacting pairs, receptor-ligands, complementary nucleic acids, and carbohydrates and their binding partners are also suitable binding pairs. Nucleic acid—nucleic acid binding proteins pairs are also useful. Similarly, as is generally described in U.S. Pat. Nos. 5,270,163, 5,475,096, 5,567,588, 5,595,877, 5,637,459, 5,683,867, 5,705,337, and related patents, hereby incorporated by reference, nucleic acid "aptamers" can be developed for binding to virtually any target; such an aptamer-target pair can be used as the IBL-DBL pair. Similarly, there is a wide body of literature relating to the development of binding pairs based on combinatorial chemistry methods.

[0122] In a preferred embodiment, the IBL is a molecule whose color or luminescence properties change in the presence of a selectively-binding DBL. For example, the IBL may be a fluorescent pH indicator whose emission intensity changes with pH. Similarly, the IBL may be a fluorescent ion indicator, whose emission properties change with ion concentration.

[0123] Alternatively, the IBL is a molecule whose color or luminescence properties change in the presence of various solvents. For example, the IBL may be a fluorescent molecule such as an ethidium salt whose fluorescence intensity increases in hydrophobic environments. Similarly, the IBL may be a derivative of fluorescein whose color changes between aqueous and nonpolar solvents.

[0124] In one embodiment, the DBL may be attached to a bead, i.e. a "decoder bead", that may carry a label such as a fluorophore.

[0125] In a preferred embodiment, the IBL-DBL pair comprise substantially complementary single-stranded nucleic acids. In this embodiment, the binding ligands can be referred to as "identifier probes" and "decoder probes". Generally, the identifier and decoder probes range from

about 4 basepairs in length to about 1000, with from about 6 to about 100 being preferred, and from about 8 to about 40 being particularly preferred. What is important is that the probes are long enough to be specific, i.e. to distinguish between different IBL-DBL pairs, yet short enough to allow both a) dissociation, if necessary, under suitable experimental conditions, and b) efficient hybridization.

[0126] In a preferred embodiment, as is more fully outlined below, the IBLs do not bind to DBLs. Rather, the IBLs are used as identifier moieties ("IMs") that are identified directly, for example through the use of mass spectroscopy.

[0127] Alternatively, in a preferred embodiment, the IBL and the capture probe are the same moiety; thus, for example, as outlined herein, particularly when no optical signatures are used, the capture probe can serve as both the identifier and the agent. For example, in the case of nucleic acids, the bead-bound probe (which serves as the capture probe) can also bind decoder probes, to identify the sequence of the probe on the bead. Thus, in this embodiment, the DBLs bind to the capture probes.

[0128] In one embodiment, the microspheres may contain an optical signature. That is, as outlined in U.S. Ser. Nos. 08/818,199 and 09/151,877, previous work had each subpopulation of microspheres comprising a unique optical signature or optical tag that is used to identify the unique capture probe of that subpopulation of microspheres; that is, decoding utilizes optical properties of the beads such that a bead comprising the unique optical signature may be distinguished from beads at other locations with different optical signatures. Thus the previous work assigned each capture probe a unique optical signature such that any microspheres comprising that capture probe are identifiable on the basis of the signature. These optical signatures comprised dyes, usually chromophores or fluorophores, that were entrapped or attached to the beads themselves. Diversity of optical signatures utilized different fluorochromes, different ratios of mixtures of fluorochromes, and different concentrations (intensities) of fluorochromes.

[0129] In a preferred embodiment, the present invention does not rely solely on the use of optical properties to decode the arrays. However, as will be appreciated by those in the art, it is possible in some embodiments to utilize optical signatures as an additional coding method, in conjunction with the present system. Thus, for example, as is more fully outlined below, the size of the array may be effectively increased while using a single set of decoding moieties in several ways, one of which is the use of optical signatures one some beads. Thus, for example, using one "set" of decoding molecules, the use of two populations of beads, one with an optical signature and one without, allows the effective doubling of the array size. The use of multiple optical signatures similarly increases the possible size of the array.

[0130] In a preferred embodiment, each subpopulation of beads comprises a plurality of different IBLs. By using a plurality of different IBLs to encode each capture probe, the number of possible unique codes is substantially increased. That is, by using one unique IBL per capture probe the size of the array will be the number of unique IBLs (assuming no "reuse" occurs, as outlined below). However, by using a plurality of different IBLs per bead, n, the size of the array can be increased to 2<sup>n</sup>, when the presence or absence of each

IBL is used as the indicator. For example, the assignment of 10 IBLs per bead generates a bit binary code, where each bit can be designated as "1" (IBL is present) or "0" (IBL is absent). A 10 bit binary code has 2<sup>10</sup> possible variants However, as is more fully discussed below, the size of the array may be further increased if another parameter is included such as concentration or intensity; thus for example, if two different concentrations of the IBL are used, then the array size increases as 3<sup>n</sup>. Thus, in this embodiment, each individual capture probe in the array is assigned a combination of IBLs, which can be added to the beads prior to the addition of the capture probe, after, or during the synthesis of the capture probe, i.e. simultaneous addition of IBLs and capture probe components.

[0131] Alternatively, the combination of different IBLs can be used to elucidate the sequence of the nucleic acid. Thus, for example, using two different IBLs (IBL1 and IBL2), the first position of a nucleic acid can be elucidated: for example, adenosine can be represented by the presence of both IBL1 and IBL2; thymidine can be represented by the presence of IBL1 but not IBL2, cytosine can be represented by the presence of IBL2 but not IBL1, and guanosine can be represented by the absence of both. The second position of the nucleic acid can be done in a similar manner using IBL3 and IBL4; thus, the presence of IBL1, IBL2, IBL3 and IBL4 gives a sequence of AA; IBL1, IBL2, and IBL3 shows the sequence AT; IBL1, IBL3 and IBL4 gives the sequence TA, etc. The third position utilizes IBL5 and IBL6, etc. In this way, the use of 20 different identifiers can yield a unique code for every possible 10-mer.

[0132] In this way, a sort of "bar code" for each sequence can be constructed; the presence or absence of each distinct IBL will allow the identification of each capture probe.

[0133] In addition, the use of different concentrations or densities of IBLs allows a "reuse" of sorts. If, for example, the bead comprising a first agent has a 1× concentration of IBL, and a second bead comprising a second agent has a 1× concentration of IBL, using saturating concentrations of the corresponding labelled DBL allows the user to distinguish between the two beads.

[0134] Once the microspheres comprising the capture probes are generated, they are added to the substrate to form an array. It should be noted that while most of the methods described herein add the beads to the substrate prior to the assay, the order of making, using and decoding the array can vary. For example, the array can be made, decoded, and then the assay done. Alternatively, the array can be made, used in an assay, and then decoded; this may find particular use when only a few beads need be decoded. Alternatively, the beads can be added to the assay mixture, i.e. the sample containing the target sequences, prior to the addition of the beads to the substrate; after addition and assay, the array may be decoded. This is particularly preferred when the sample comprising the beads is agitated or mixed; this can increase the amount of target sequence bound to the beads per unit time, and thus (in the case of nucleic acid assays) increase the hybridization kinetics. This may find particular use in cases where the concentration of target sequence in the sample is low; generally, for low concentrations, long binding times must be used.

[0135] In general, the methods of making the arrays and of decoding the arrays is done to maximize the number of

different candidate agents that can be uniquely encoded. The compositions of the invention may be made in a variety of ways. In general, the arrays are made by adding a solution or slurry comprising the beads to a surface containing the sites for attachment of the beads. This may be done in a variety of buffers, including aqueous and organic solvents, and mixtures. The solvent can evaporate, and excess beads are removed.

[0136] In a preferred embodiment, when non-covalent methods are used to associate the beads with the array, a novel method of loading the beads onto the array is used. This method comprises exposing the array to a solution of particles (including microspheres and cells) and then applying energy, e.g. agitating or vibrating the mixture. This results in an array comprising more tightly associated particles, as the agitation is done with sufficient energy to cause weakly-associated beads to fall off (or out, in the case of wells). These sites are then available to bind a different bead. In this way, beads that exhibit a high affinity for the sites are selected. Arrays made in this way have two main advantages as compared to a more static loading: first of all, a higher percentage of the sites can be filled easily, and secondly, the arrays thus loaded show a substantial decrease in bead loss during assays. Thus, in a preferred embodiment, these methods are used to generate arrays that have at least about 50% of the sites filled, with at least about 75% being preferred, and at least about 90% being particularly preferred. Similarly, arrays generated in this manner preferably lose less than about 20% of the beads during an assay, with less than about 10% being preferred and less than about 5% being particularly preferred.

[0137] In this embodiment, the substrate comprising the surface with the discrete sites is immersed into a solution comprising the particles (beads, cells, etc.). The surface may comprise wells, as is described herein, or other types of sites on a patterned surface such that there is a differential affinity for the sites. This differnetial affinity results in a competitive process, such that particles that will associate more tightly are selected. Preferably, the entire surface to be "loaded" with beads is in fluid contact with the solution. This solution is generally a slurry ranging from about 10,000:1 beads:solution (vol:vol) to 1:1. Generally, the solution can comprise any number of reagents, including aqueous buffers, organic solvents, salts, other reagent components, etc. In addition, the solution preferably comprises an excess of beads; that is, there are more beads than sites on the array. Preferred embodiments utilize two-fold to billion-fold excess of beads.

[0138] The immersion can mimic the assay conditions; for example, if the array is to be "dipped" from above into a microtiter plate comprising samples, this configuration can be repeated for the loading, thus minimizing the beads that are likely to fall out due to gravity.

[0139] Once the surface has been immersed, the substrate, the solution, or both are subjected to a competitive process, whereby the particles with lower affinity can be disassociated from the substrate and replaced by particles exhibiting a higher affinity to the site. This competitive process is done by the introduction of energy, in the form of heat, sonication, stirring or mixing, vibrating or agitating the solution or substrate, or both.

[0140] A preferred embodiment utilizes agitation or vibration. In general, the amount of manipulation of the substrate

is minimized to prevent damage to the array; thus, preferred embodiments utilize the agitation of the solution rather than the array, although either will work. As will be appreciated by those in the art, this agitation can take on any number of forms, with a preferred embodiment utilizing microtiter plates comprising bead solutions being agitated using microtiter plate shakers.

[0141] The agitation proceeds for a period of time sufficient to load the array to a desired fill. Depending on the size and concentration of the beads and the size of the array, this time may range from about 1 second to days, with from about 1 minute to about 24 hours being preferred.

[0142] It should be noted that not all sites of an array may comprise a bead; that is, there may be some sites on the substrate surface which are empty. In addition, there may be some sites that contain more than one bead, although this is not preferred.

[0143] In some embodiments, for example when chemical attachment is done, it is possible to attach the beads in a non-random or ordered way. For example, using photoactivatible attachment linkers or photoactivatible adhesives or masks, selected sites on the array may be sequentially rendered suitable for attachment, such that defined populations of beads are laid down.

[0144] The arrays of the present invention are constructed such that information about the identity of the capture probe is built into the array, such that the random deposition of the beads in the fiber wells can be "decoded" to allow identification of the capture probe at all positions. This may be done in a variety of ways, and either before, during or after the use of the array to detect target molecules.

[0145] Thus, after the array is made, it is "decoded" in order to identify the location of one or more of the capture probes, i.e. each subpopulation of beads, on the substrate surface.

[0146] In a preferred embodiment, pyrosequencing techniques are used to decode the array, as is generally described in "Nucleic Acid Sequencing using Microsphere Arrays", filed Oct. 22, 1999 (no U.S. Ser. No. received yet), hereby incorporated by reference.

[0147] In a preferred embodiment, a selective decoding system is used. In this case, only those microspheres exhibiting a change in the optical signal as a result of the binding of a target sequence are decoded. This is commonly done when the number of "hits", i.e. the number of sites to decode, is generally low. That is, the array is first scanned under experimental conditions in the absence of the target sequences. The sample containing the target sequences is added, and only those locations exhibiting a change in the optical signal are decoded. For example, the beads at either the positive or negative signal locations may be either selectively tagged or released from the array (for example through the use of photocleavable linkers), and subsequently sorted or enriched in a fluorescence-activated cell sorter (FACS). That is, either all the negative beads are released, and then the positive beads are either released or analyzed in situ, or alternatively all the positives are released and analyzed. Alternatively, the labels may comprise halogenated aromatic compounds, and detection of the label is done using for example gas chromatography, chemical tags, isotopic tags mass spectral tags.

[0148] As will be appreciated by those in the art, this may also be done in systems where the array is not decoded; i.e. there need not ever be a correlation of bead composition with location. In this embodiment, the beads are loaded on the array, and the assay is run. The "positives", i.e. those beads displaying a change in the optical signal as is more fully outlined below, are then "marked" to distinguish or separate them from the "negative" beads. This can be done in several ways, preferably using fiber optic arrays. In a preferred embodiment, each bead contains a fluorescent dye. After the assay and the identification of the "positives" or "active beads", light is shown down either only the positive fibers or only the negative fibers, generally in the presence of a light-activated reagent (typically dissolved oxygen). In the former case, all the active beads are photobleached. Thus, upon non-selective release of all the beads with subsequent sorting, for example using a fluorescence activated cell sorter (FACS) machine, the non-fluorescent active beads can be sorted from the fluorescent negative beads. Alternatively, when light is shown down the negative fibers, all the negatives are non-fluorescent and the the postives are fluorescent, and sorting can proceed. The characterization of the attached capture probe may be done directly, for example using mass spectroscopy.

[0149] Alternatively, the identification may occur through the use of identifier moieties ("IMs"), which are similar to IBLs but need not necessarily bind to DBLs. That is, rather than elucidate the structure of the capture probe directly, the composition of the IMs may serve as the identifier. Thus, for example, a specific combination of IMs can serve to code the bead, and be used to identify the agent on the bead upon release from the bead followed by subsequent analysis, for example using a gas chromatograph or mass spectroscope.

[0150] Alternatively, rather than having each bead contain a fluorescent dye, each bead comprises a non-fluorescent precursor to a fluorescent dye. For example, using photocleavable protecting groups, such as certain ortho-nitrobenzyl groups, on a fluorescent molecule, photoactivation of the fluorochrome can be done. After the assay, light is shown down again either the "positive" or the "negative" fibers, to distinguish these populations. The illuminated precursors are then chemically converted to a fluorescent dye. All the beads are then released from the array, with sorting, to form populations of fluorescent and non-fluorescent beads (either the positives and the negatives or vice versa).

[0151] In an alternate preferred embodiment, the sites of attachment of the beads (for example the wells) include a photopolymerizable reagent, or the photopolymerizable agent is added to the assembled array. After the test assay is run, light is shown down again either the "positive" or the "negative" fibers, to distinguish these populations. As a result of the irradiation, either all the positives or all the negatives are polymerized and trapped or bound to the sites, while the other population of beads can be released from the array.

[0152] In a preferred embodiment, the location of every capture probe is determined using decoder binding ligands (DBLs). As outlined above, DBLs are binding ligands that will either bind to identifier binding ligands, if present, or to the capture probes themselves, preferably when the capture probe is a nucleic acid or protein.

[0153] In a preferred embodiment, as outlined above, the DBL binds to the IBL.

[0154] In a preferred embodiment, the capture probes are single-stranded nucleic acids and the DBL is a substantially complementary single-stranded nucleic acid that binds (hybridizes) to the capture probe, termed a decoder probe herein. A decoder probe that is substantially complementary to each candidate probe is made and used to decode the array. In this embodiment, the candidate probes and the decoder probes should be of sufficient length (and the decoding step run under suitable conditions) to allow specificity; i.e. each candidate probe binds to its corresponding decoder probe with sufficient specificity to allow the distinction of each candidate probe.

[0155] In a preferred embodiment, the DBLs are either directly or indirectly labeled. In a preferred embodiment, the DBL is directly labeled, that is, the DBL comprises a label. In an alternate embodiment, the DBL is indirectly labeled; that is, a labeling binding ligand (LBL) that will bind to the DBL is used. In this embodiment, the labeling binding ligand-DBL pair can be as described above for IBL-DBL pairs.

[0156] Accordingly, the identification of the location of the individual beads (or subpopulations of beads) is done using one or more decoding steps comprising a binding between the labeled DBL and either the IBL or the capture probe (i.e. a hybridization between the candidate probe and the decoder probe when the capture probe is a nucleic acid). After decoding, the DBLs can be removed and the array can be used; however, in some circumstances, for example when the DBL binds to an IBL and not to the capture probe, the removal of the DBL is not required (although it may be desirable in some circumstances). In addition, as outlined herein, decoding may be done either before the array is used to in an assay, during the assay, or after the assay.

[0157] In one embodiment, a single decoding step is done. In this embodiment, each DBL is labeled with a unique label, such that the the number of unique tags is equal to or greater than the number of capture probes (although in some cases, "reuse" of the unique labels can be done, as described herein; similarly, minor variants of candidate probes can share the same decoder, if the variants are encoded in another dimension, i.e. in the bead size or label). For each capture probe or IBL, a DBL is made that will specifically bind to it and contains a unique tag, for example one or more fluorochromes. Thus, the identity of each DBL, both its composition (i.e. its sequence when it is a nucleic acid) and its label, is known. Then, by adding the DBLs to the array containing the capture probes under conditions which allow the formation of complexes (termed hybridization complexes when the components are nucleic acids) between the DBLs and either the capture probes or the IBLs, the location of each DBL can be elucidated. This allows the identification of the location of each capture probe; the random array has been decoded. The DBLs can then be removed, if necessary, and the target sample applied.

[0158] In a preferred embodiment, the number of unique labels is less than the number of unique capture probes, and thus a sequential series of decoding steps are used. In this embodiment, decoder probes are divided into n sets for decoding. The number of sets corresponds to the number of unique tags. Each decoder probe is labeled in n separate reactions with n distinct tags. All the decoder probes share the same n tags. The decoder probes are pooled so that each

pool contains only one of the n tag versions of each decoder, and no two decoder probes have the same sequence of tags across all the pools. The number of pools required for this to be true is determined by the number of decoder probes and the n. Hybridization of each pool to the array generates a signal at every address. The sequential hybridization of each pool in turn will generate a unique, sequence-specific code for each candidate probe. This identifies the candidate probe at each address in the array. For example, if four tags are used, then 4×n sequential hybridizations can ideally distinguish 4<sup>n</sup> sequences, although in some cases more steps may be required. After the hybridization of each pool, the hybrids are denatured and the decoder probes removed, so that the probes are rendered single-stranded for the next hybridization (although it is also possible to hybridize limiting amounts of target so that the available probe is not saturated. Sequential hybridizations can be carried out and analyzed by subtracting pre-existing signal from the previous hybridiza-

[0159] An example is illustrative. Assuming an array of 16 probe nucleic acids (numbers 1-16), and four unique tags (four different fluors, for example; labels A-D). Decoder probes 1-16 are made that correspond to the probes on the beads. The first step is to label decoder probes 1-4 with tag A, decoder probes 5-8 with tag B, decoder probes 9-12 with tag C, and decoder probes 13-16 with tag D. The probes are mixed and the pool is contacted with the array containing the beads with the attached candidate probes. The location of each tag (and thus each decoder and candidate probe pair) is then determined. The first set of decoder probes are then removed. A second set is added, but this time, decoder probes 1, 5, 9 and 13 are labeled with tag A, decoder probes 2, 6, 10 and 14 are labeled with tag B, decoder probes 3, 7, 11 and 15 are labeled with tag C, and decoder probes 4, 8, 12 and 16 are labeled with tag D. Thus, those beads that contained tag A in both decoding steps contain candidate probe 1; tag A in the first decoding step and tag B in the second decoding step contain candidate probe 2; tag A in the first decoding step and tag C in the second step contain candidate probe 3; etc. In one embodiment, the decoder probes are labeled in situ; that is, they need not be labeled prior to the decoding reaction. In this embodiment, the incoming decoder probe is shorter than the candidate probe, creating a 5"overhang" on the decoding probe. The addition of labeled ddNTPs (each labeled with a unique tag) and a polymerase will allow the addition of the tags in a sequence specific manner, thus creating a sequence-specific pattern of signals. Similarly, other modifications can be done, including ligation, etc.

[0160] In addition, since the size of the array will be set by the number of unique decoding binding ligands, it is possible to "reuse" a set of unique DBLs to allow for a greater number of test sites. This may be done in several ways; for example, by using some subpopulations that comprise optical signatures. Similarly, the use of a positional coding scheme within an array; different sub-bundles may reuse the set of DBLs. Similarly, one embodiment utilizes bead size as a coding modality, thus allowing the reuse of the set of unique DBLs for each bead size. Alternatively, sequential partial loading of arrays with beads can also allow the reuse of DBLs. Furthermore, "code sharing" can occur as well.

[0161] In a preferred embodiment, the DBLs may be reused by having some subpopulations of beads comprise

optical signatures. In a preferred embodiment, the optical signature is generally a mixture of reporter dyes, preferably flourescent. By varying both the composition of the mixture (i.e. the ratio of one dye to another) and the concentration of the dye (leading to differences in signal intensity), matrices of unique optical signatures may be generated. This may be done by covalently attaching the dyes to the surface of the beads, or alternatively, by entrapping the dye within the bead.

[0162] In a preferred embodiment, the encoding can be accomplished in a ratio of at least two dyes, although more encoding dimensions may be added in the size of the beads, for example. In addition, the labels are distinguishable from one another; thus two different labels may comprise different molecules (i.e. two different fluors) or, alternatively, one label at two different concentrations or intensity.

[0163] In a preferred embodiment, the dyes are covalently attached to the surface of the beads. This may be done as is generally outlined for the attachment of the capture probes, using functional groups on the surface of the beads. As will be appreciated by those in the art, these attachments are done to minimize the effect on the dye.

[0164] In a preferred embodiment, the dyes are non-covalently associated with the beads, generally by entrapping the dyes in the pores of the beads.

[0165] Additionally, encoding in the ratios of the two or more dyes, rather than single dye concentrations, is preferred since it provides insensitivity to the intensity of light used to interrogate the reporter dye's signature and detector sensitivity.

[0166] In a preferred embodiment, a spatial or positional coding system is done. In this embodiment, there are subbundles or subarrays (i.e. portions of the total array) that are utilized. By analogy with the telephone system, each subarray is an "area code", that can have the same tags (i.e. telephone numbers) of other subarrays, that are separated by virtue of the location of the subarray. Thus, for example, the same unique tags can be reused from bundle to bundle. Thus, the use of 50 unique tags in combination with 100 different subarrays can form an array of 5000 different capture probes. In this embodiment, it becomes important to be able to identify one bundle from another; in general, this is done either manually or through the use of marker beads, i.e. beads containing unique tags for each subarray.

[0167] In alternative embodiments, additional encoding parameters can be added, such as microsphere size. For example, the use of different size beads may also allow the reuse of sets of DBLs; that is, it is possible to use microspheres of different sizes to expand the encoding dimensions of the microspheres. Optical fiber arrays can be fabricated containing pixels with different fiber diameters or crosssections; alternatively, two or more fiber optic bundles, each with different cross-sections of the individual fibers, can be added together to form a larger bundle; or, fiber optic bundles with fiber of the same size cross-sections can be used, but just with different sized beads. With different diameters, the largest wells can be filled with the largest microspheres and then moving onto progressively smaller microspheres in the smaller wells until all size wells are then filled. In this manner, the same dye ratio could be used to encode microspheres of different sizes thereby expanding

the number of different oligonucleotide sequences or chemical functionalities present in the array. Although outlined for fiber optic substrates, this as well as the other methods outlined herein can be used with other substrates and with other attachment modalities as well.

[0168] In a preferred embodiment, the coding and decoding is accomplished by sequential loading of the microspheres into the array. As outlined above for spatial coding, in this embodiment, the optical signatures can be "reused". In this embodiment, the library of microspheres each comprising a different capture probe (or the subpopulations each comprise a different capture probe), is divided into a plurality of sublibraries; for example, depending on the size of the desired array and the number of unique tags, 10 sublibraries each comprising roughly 10% of the total library may be made, with each sublibrary comprising roughly the same unique tags. Then, the first sublibrary is added to the fiber optic bundle comprising the wells, and the location of each capture probe is determined, generally through the use of DBLs. The second sublibrary is then added, and the location of each capture probe is again determined. The signal in this case will comprise the signal from the "first" DBL and the "second" DBL; by comparing the two matrices the location of each bead in each sublibrary can be determined. Similarly, adding the third, fourth, etc. sublibraries sequentially will allow the array to be filled.

[0169] In a preferred embodiment, codes can be "shared" in several ways. In a first embodiment, a single code (i.e. IBL/DBL pair) can be assigned to two or more agents if the target sequences different sufficiently in their binding strengths. For example, two nucleic acid probes used in an mRNA a quantitation assay can share the same code if the ranges of their hybridization signal intensities do not overlap. This can occur, for example, when one of the target sequences is always present at a much higher concentration than the other. Alternatively, the two target sequences might always be present at a similar concentration, but differ in hybridization efficiency.

[0170] Alternatively, a single code can be assigned to multiple agents if the agents are functionally equivalent. For example, if a set of oligonucleotide probes are designed with the common purpose of detecting the presence of a particular gene, then the probes are functionally equivalent, even though they may differ in sequence. Similarly, an array of this type could be used to detect homologs of known genes. In this embodiment, each gene is represented by a heterologous set of probes, hybridizing to different regions of the gene (and therefore differing in sequence). The set of probes share a common code. If a homolog is present, it might hybridize to some but not all of the probes. The level of homology might be indicated by the fraction of probes hybridizing, as well as the average hybridization intensity. Similarly, multiple antibodies to the same protein could all share the same code.

[0171] In a preferred embodiment, decoding of self-assembled random arrays is done on the bases of pH titration. In this embodiment, in addition to capture probes, the beads comprise optical signatures, wherein the optical signatures are generated by the use of pH-responsive dyes (sometimes referred to herein as "ph dyes") such as fluorophores. This embodiment is similar to that outlined in PCT US98/05025 and U.S. Ser. No. 09/151,877, both of which are expressly

incorporated by reference, except that the dyes used in the present ivention exhibits changes in fluorescence intensity (or other properties) when the solution pH is adjusted from below the pKa to above the pKa (or vice versa). In a preferred embodiment, a set of pH dyes are used, each with a different pKa, preferably separated by at least 0.5 pH units. Preferred embodiments utilize a pH dye set of pka's of 2.0, 2.5, 3.0, 3.5, 4.0, 4.5, 5.0, 5.5, 6.0, 6.5, 7.0, 7.5, 8.0, 8.5, 9.0, 9.5, 10.0, 10.5, 11, and 11.5. Each bead can contain any subset of the pH dyes, and in this way a unique code for the capture probe is generated. Thus, the decoding of an array is achieved by titrating the array from pH 1 to pH 13, and measuring the fluorescence signal from each bead as a function of solution pH.

[0172] Thus, the present invention provides array compositions comprising a substrate with a surface comprising discrete sites. A population of microspheres is distributed on the sites, and the population comprises at least a first and a second subpopulation. Each subpopulation comprises a capture probe, and, in addition, at least one optical dye with a given pKa. The pKas of the different optical dyes are different.

[0173] In a preferred embodiment, "random" decoding probes can be made. By sequential hybridizations or the use of multiple labels, as is outlined above, a unique hybridization pattern can be generated for each sensor element. This allows all the beads representing a given clone to be identified as belonging to the same group. In general, this is done by using random or partially degenerate decoding probes, that bind in a sequence-dependent but not highly sequencespecific manner. The process can be repeated a number of times, each time using a different labeling entity, to generate a different pattern of singals based on quasi-specific interactions. In this way, a unique optical signature is eventually built up for each sensor element. By applying pattern recognition or clustering algorithms to the optical signatures, the beads can be grouped into sets that share the same signature (i.e. carry the same probes).

[0174] In order to identify the actual sequence of the clone itself, additional procedures are required; for example, direct sequencing can be done, or an ordered array containing the clones, such as a spotted cDNA array, to generate a "key" that links a hybridization pattern to a specific clone.

[0175] Alternatively, clone arrays can be decoded using binary decoding with vector tags. For example, partially randomized oligos are cloned into a nucleic acid vector (e.g. plasmid, phage, etc.). Each oligonucleotide sequence consists of a subset of a limited set of sequences. For example, if the limites set comprises 10 sequences, each oligonucleotide may have some subset (or all of the 10) sequences. Thus each of the 10 sequences can be present or absent in the oligonucleotide. Therefore, there are 210 or 1,024 possible combinations. The sequences may overlap, and minor variants can also be represented (e.g. A, C, T and G substitutions) to increase the number of possible combinations. A nucleic acid library is cloned into a vector containing the random code sequences. Alternatively, other methods such as PCR can be used to add the tags. In this way it is possible to use a small number of oligo decoding probes to decode an array of clones.

[0176] As will be appreciated by those in the art, the systems of the invention may take on a large number of

different configurations, as is generally depicted in the Figures. In general, there are three types of systems that can be used: (1) "non-sandwich" systems (also referred to herein as "direct" detection) in which the target sequence itself is labeled with detectable labels (again, either because the primers comprise labels or due to the incorporation of labels into the newly synthesized strand); (2) systems in which label probes directly bind to the target analytes; and (3) systems in which label probes are indirectly bound to the target sequences, for example through the use of amplifier probes.

[0177] Detection of the reactions of the invention, including the direct detection of products and indirect detection utilizing label probes (i.e. sandwich assays), is preferably done by detecting assay complexes comprising detectable labels, which can be attached to the assay complex in a variety of ways.

[0178] In a preferred embodiment, an array of different and usually artificial capture probes are made; that is, the capture probes do not have complementarity to known target sequences. The adapter sequences can then be added to any target sequences, or soluble capture extender probes are made; this allows the manufacture of only one kind of array, with the user able to customize the array through the use of adapter sequences or capture extender probes. This then allows the generation of customized soluble probes, which as will be appreciated by those in the art is generally simpler and less costly.

[0179] When capture extender probes are used, in one embodiment, microsphere arrays containing a single type of capture probe are made; in this embodiment, the capture extender probes are added to the beads prior to loading on the array. The capture extender probes may be additionally fixed or crosslinked, as necessary.

[0180] Accordingly, the present invention provides compositions and methods for detecting the presence or absence of target analytes, including nucleic acid sequences, in a sample. As will be appreciated by those in the art, the sample solution may comprise any number of things, including, but not limited to, bodily fluids (including, but not limited to, blood, urine, serum, lymph, saliva, anal and vaginal secretions, perspiration and semen, of virtually any organism, with mammalian samples being preferred and human samples being particularly preferred); environmental samples (including, but not limited to, air, agricultural, water and soil samples); biological warfare agent samples; research samples (i.e. in the case of nucleic acids, the sample may be the products of an amplification reaction, including both target and signal amplification); purified samples, such as purified genomic DNA, RNA, proteins, etc.; raw samples (bacteria, virus, genomic DNA, etc.; As will be appreciated by those in the art, virtually any experimental manipulation may have been done on the sample.

[0181] The present invention provides compositions and methods for detecting the presence or absence of target nucleic acid sequences in a sample.

[0182] In a preferred embodiment, several levels of redundancy are built into the arrays of the invention. Building redundancy into an array gives several significant advantages, including the ability to make quantitative estimates of confidence about the data and signficant increases in sensi-

tivity. Thus, preferred embodiments utilize array redundancy. As will be appreciated by those in the art, there are at least two types of redundancy that can be built into an array: the use of multiple identical sensor elements (termed herein "sensor redundancy"), and the use of multiple sensor elements directed to the same target analyte, but comprising different chemical functionalities (termed herein "target redundancy"). For example, for the detection of nucleic acids, sensor redundancy utilizes of a plurality of sensor elements such as beads comprising identical binding ligands such as probes. Target redundancy utilizes sensor elements with different probes to the same target: one probe may span the first 25 bases of the target, a second probe may span the second 25 bases of the target, etc. By building in either or both of these types of redundancy into an array, significant benefits are obtained. For example, a variety of statistical mathematical analyses may be done.

[0183] In addition, while this is generally described herein for bead arrays, as will be appreciated by those in the art, this techniques can be used for any type of arrays designed to detect target analytes. Furthermore, while these techniques are generally described for nucleic acid systems, these techniques are useful in the detection of other binding ligand/target analyte systems as well.

[0184] In a preferred embodiment, sensor redundancy is used. In this embodiment, a plurality of sensor elements, e.g. beads, comprising identical bioactive agents are used. That is, each subpopulation comprises a plurality of beads comprising identical bioactive agents (e.g. binding ligands). By using a number of identical sensor elements for a given array, the optical signal from each sensor element can be combined and any number of statistical analyses run, as outlined below. This can be done for a variety of reasons. For example, in time varying measurements, redundancy can significantly reduce the noise in the system. For non-time based measurements, redundancy can significantly increase the confidence of the data.

[0185] In a preferred embodiment, a plurality of identical sensor elements are used. As will be appreciated by those in the art, the number of identical sensor elements will vary with the application and use of the sensor array. In general, anywhere from 2 to thousands may be used, with from 2 to 100 being preferred, 2 to 50 being particularly preferred and from 5 to 20 being especially preferred. In general, preliminary results indicate that roughly 10 beads gives a sufficient advantage, although for some applications, more identical sensor elements can be used.

[0186] Once obtained, the optical response signals from a plurality of sensor beads within each bead subpopulation can be manipulated and analyzed in a wide variety of ways, including baseline adjustment, averaging, standard deviation analysis, distribution and cluster analysis, confidence interval analysis, mean testing, etc.

[0187] In a preferred embodiment, the first manipulation of the optical response signals is an optional baseline adjustment. In a typical procedure, the standardized optical responses are adjusted to start at a value of 0.0 by subtracting the integer 1.0 from all data points. Doing this allows the baseline-loop data to remain at zero even when summed together and the random response signal noise is canceled out. When the sample is a fluid, the fluid pulse-loop temporal region, however, frequently exhibits a characteristic change

in response, either positive, negative or neutral, prior to the sample pulse and often requires a baseline adjustment to overcome noise associated with drift in the first few data points due to charge buildup in the CCD camera. If no drift is present, typically the baseline from the first data point for each bead sensor is subtracted from all the response data for the same bead. If drift is observed, the average baseline from the first ten data points for each bead sensor is substracted from the all the response data for the same bead. By applying this baseline adjustment, when multiple bead responses are added together they can be amplified while the baseline remains at zero. Since all beads respond at the same time to the sample (e.g. the sample pulse), they all see the pulse at the exact same time and there is no registering or adjusting needed for overlaying their responses. In addition, other types of baseline adjustment may be done, depending on the requirements and output of the system used.

[0188] Once the baseline has been adjusted, a number of possible statistical analyses may be run to generate known statistical parameters. Analyses based on redundancy are known and generally described in texts such as Freund and Walpole, Mathematical Statistics, Prentice Hall, Inc. New Jersey, 1980, hereby incorporated by reference in its entirety.

[0189] In a preferred embodiment, signal summing is done by simply adding the intensity values of all responses at each time point, generating a new temporal response comprised of the sum of all bead responses. These values can be baseline-adjusted or raw. As for all the analyses described herein, signal summing can be performed in real time or during post-data acquisition data reduction and analysis. In one embodiment, signal summing is performed with a commercial spreadsheet program (Excel, Microsoft, Redmond, Wash.) after optical response data is collected.

[0190] Methods for signal summing and analyses are included in U.S. Ser. No. 08/944,850, filed Oct. 6, 1997; 09/287,573, filed Apr. 6, 1999; and 60/238,866, filed Oct. 6, 2000; an PCT Nos. US98/21193, filed Oct. 6, 1998; and US00/09183, filed Apr. 6, 2000.

[0191] Once made, the methods and compositions of the invention find use in a number of applications. In a preferred embodiment, the compositions are used to probe a sample solution for the presence or absence of a target sequence, including the quantification of the amount of target sequence present. The compositions and methods find utility in the detection of genotyping assays and sequencing assays, and in all sorts of target analyte assays, including immunoassays.

[0192] For SNP analysis, the ratio of different labels at a particular location on the array indicates the homozygosity or heterozygosity of the target sample, assuming the same concentration of each readout probe is used. Thus, for example, assuming a first readout probe comprising a first base at the readout position with a first detectable label and a second readout probe comprising a second base at the readout position with a second detectable label, equal signals (roughly 1:1 (taking into account the different signal intensities of the different labels, different hybridization efficiencies, and other reasons)) of the first and second labels indicates a heterozygote. The absence of a signal from the first label (or a ratio of approximately 0:1) indicates a homozygote of the second detection base; the absence of a signal from the second label (or a ratio of approximately 1:0) indicates a homozygote for the first detection base. As is appreciated by those in the art, the actual ratios for any particular system are generally determined empirically.

[0193] Generally, a sample containing a target analyte (whether for detection of the target analyte or screening for binding partners of the target analyte) is added to the array, under conditions suitable for binding of the target analyte to at least one of the capture probes, i.e. generally physiological conditions. The presence or absence of the target analyte is then detected. As will be appreciated by those in the art, this may be done in a variety of ways, generally through the use of a change in an optical signal. This change can occur via many different mechanisms. A few examples include the binding of a dye-tagged analyte to the bead, the production of a dye species on or near the beads, the destruction of an existing dye species, a change in the optical signature upon analyte interaction with dye on bead, or any other optical interrogatable event.

[0194] In a preferred embodiment, the change in optical signal occurs as a result of the binding of a target analyte that is labeled, either directly or indirectly, with a detectable label, preferably an optical label such as a fluorochrome. Thus, for example, when a proteinaceous target analyte is used, it may be either directly labeled with a fluor, or indirectly, for example through the use of a labeled antibody. Similarly, nucleic acids are easily labeled with fluorochromes, for example during PCR amplification as is known in the art. Alternatively, upon binding of the target sequences, a hybridization indicator may be used as the label. Hybridization indicators preferentially associate with double stranded nucleic acid, usually reversibly. Hybridization indicators include intercalators and minor and/or major groove binding moieties. In a preferred embodiment, intercalators may be used; since intercalation generally only occurs in the presence of double stranded nucleic acid, only in the presence of target hybridization will the label light up. Thus, upon binding of the target analyte to a capture probe, there is a new optical signal generated at that site, which then may be detected.

[0195] Alternatively, in some cases, as discussed above, the target analyte such as an enzyme generates a species that is either directly or indirectly optical detectable.

[0196] Furthermore, in some embodiments, a change in the optical signature may be the basis of the optical signal. For example, the interaction of some chemical target analytes with some fluorescent dyes on the beads may alter the optical signature, thus generating a different optical signal.

[0197] As will be appreciated by those in the art, in some embodiments, the presence or absence of the target analyte may be done using changes in other optical or non-optical signals, including, but not limited to, surface enhanced Raman spectroscopy, surface plasmon resonance, radioactivity, etc.

[0198] The assays may be run under a variety of experimental conditions, as will be appreciated by those in the art. A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be

used. The mixture of components may be added in any order that provides for the requisite binding. Various blocking and washing steps may be utilized as is known in the art.

[0199] The following examples serve to more fully describe the manner of using the above-described invention, as well as to set forth the best modes contemplated for carrying out various aspects of the invention. It is understood that these examples in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All references cited herein are incorporated by reference in their entirety.

#### **EXAMPLES**

#### Example 1

[0200] Immobilization of Crude Oligonucleotides to a Solid Support

[0201] 1. Introduce chemical functional group (such as —NH2, —COOH, —NCO, —NHS, —SH, —CHO, etc.) onto solid support.

[0202] 2. Activate the functional group before oligonucleotide attachment.

[0203] 3. 5'-terminal modified oligonucleotide attachment.

[0204] Crude Oligonucleotides were attached to supports and compared to results from attachment of purified oligonucleotides. As demonstrated in FIG. 3, in the presence of 2 M salt, crude oligonucleotides were immobilized as efficiently as purified oligonucleotides.

[0205] IN addition, the improved attachment of oligonucleotides to a solid support in the presence of increased salt was sequence and length independent. Thus, the method finds use in attachment of all oligonucleotides to a solid support (see FIG. 4).

[0206] In addition, when 0.5 M to 3 M NaCl was used for attachment of oligonucleotides, non-purified oligonucleotides were attached with comparable efficiency when compared to purified oligonucleotides (see FIG. 5).

TABLE 1

Seq. ID No.	Decoder (5'-3')
17	GGCTGGTTCGGCCCGAAAGCTTAG
18	GTTCCCAGTGAAGCTGCGATCTGG
19	TACTTGGCATGGAATCCCTTACGC
20	ACTAGCATATTTCAGGGCACCGGC
21	GAACGGTCAATGAACCCGCTGTGA
22	GCGGCCTTGGTTCAATATGAATCG
23	GATCGTTAGAGGGACCTTGCCCGA
24	TGGACCTAGTCCGGCAGTGACGAA
25	ATAAACTACCCAGGACGGGCGGAA
26	CATCGGTTCGCGCCAATCCAGATA
27	GTCGGGCATAGAGCCGACCACCCT
28	CTTGGGTCATGATTCACCGTGCTA

TABLE 1-continued

Decoder (5'-3')

TGCCTAACGTGCTAATCAGCAGCG

Seq. ID No.

29

29	TGCCTAACGTGCTAATCAGCAGCG
30	CGCATGTTGGAGCATATGCCCTGA
31	AGCCACTGCATCAGTGCTGTTCAA
32	GGTTGTTTTGAGGCGTCCCACACT
33	TCGACCAAGAGCAAGGGCGGACCA
34	GACATCGCTATTGCGCATGGATCA
35	GAAATACGAAGTCTGCGGGAGTCG
36	TGTCATGAATGATTGATCGCGCGA
37	ATATCGGGATTCGTTCCCGGTGAA
38	GCGAGCGTACCGAAGGGCCTAGAA
39	TTACCGGCAGCGGACTTCCGAATT
40	GTAATCGAGAGCTGCGCGCCGTCT
41	TCCCTGAGGTCGGAAGCTTCCGAC
42	CCTGTTAGCGTAGGCGAGTCGATC
43	TAGCGGACCGGCAGAATGAGTTCC
44	GGTACATGCACTACGCGCACTCGG
45	AATTCATCTCGGACTCCCGCGGTA
46	GCCAAATCTGGATTGGCAGGAATG
47	TGCATTTTCGGTTGAGGCACATCC
48	CCGCTCAATTCACCATGCTTCGCT
49	CTCGGAAAGGTGCAACTTTGGTGT
50	AATTCGACCAGCAGAACGTCCCAT
51	GCCAGAGTCTCAACCTCACGGGAT
52	CCAACAACTGGAACGGGAACCCGC
53	GAGAACTGATCGCTGAGGGGCATG
54	GGCACACTAGACTTGTGGCACCGA
55	CTTGGGCAAACGCTTCAGCCACAA
56	TCACATCCAAATATGGTCCGCGAA
57	GTCTGCCGGTGTGACCGCTTCATT
58	CATCGCAGAGCATAAACACCCTCA
59	GTTGGTATCTATGGCAGAGGCGGA
60	ACGAGGTGCCGCTGAGGTTCCATT
61	GGAATGAGTGGACCCAGGCACATT
62	TGTCAATATGCGTCCGTGTCGTCT
63	TGATGAGCCTCAGGGTACGAGGCA
64	CACCGCGGTGTTCCTACAGAATGA
65	TTGTTGCCAATGGTGTCCGCTCGG

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-Continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
66	TTAACCTGCGTCTGCCCCTTTCCT	103	CACGCGCTTAGTCGCGATCGCATA	
67	AGGCGCGTTCCTGCCTTAGTGACG	104	CGGAGGGAGGGAGCTAGCCTTCGA	
68	TAGGGCGATGGCACGAAGCTTCAA	105	GCATCCGGCCTGTTGATGACGCCT	
69	TGCATAGAGCCAAAGTCGGCGATG	106	AGGCCAATCGATCTTATTGCCGAG	
70	TTGAGAGGCAGGTGGCCACACGGA	107	CCTTCCAATGATTGCATACGccCA	
71	TCCGCATTGTGAGAAAAAACGAGC	108	AACACTTGATCAGGCGGGTCGTCT	
72	GGCGGTTTCCGTAGCTATAGGTGC	109	TGGAATCAAGGCCGTAAAGGACAG	
73	GGTGAAAATTTCGTAGCCACGGGC	110	GCTCCCGTAACCTGTCCACCAGTG	
74	CCGACGGAGGATGAAGACAATCAC	111	AGTGGTGAATGGCCGCTACCCTGA	
75	CCAGTTTGGCCCAATTCGCCAAAA	112	TGTTGAAGCGAGCTAAAACGGCCA	
76	GGATCTATTAGGCCGTGCGCACAG	113	CAGCGCTCCAGAATTGACAGCAAT	
77	CGGATGTCACCGTTTGGACTTTCA	114	AAGGTGGTGCCATTCATTTGGCTA	
78	ATCGCAAATCCTGCTCGTCCCTAA	115	CGTTAAACCGCAATCCGTTCGGCT	
79	CAGGGCATGCAATAATCGAGGTTC	116	TGTCTTCCACCTCGAAGGTTTCCA	
80	CATGCGTTGATATATGGGCCCAAG	117	CACGAGATACCGGCGTAAGGGTGG	
81	CAGCTGCAGCTTGTGACCAACCAC	118	CTACGGCAAACGTGTGGAATGGGT	
82	TTGTATGTCTGCCGACCGGCGACC	119	GTAGGGCGATGACGGGCGAACTAC	
83	GATGGCGCCCGTTGATAGGTATGG	120	AATCGACCTCCGCACACATTCGCA	
84	ATGAGAATCGCCGGCAATCTGCTA	121	GAGTCAGCATGGCGGCGGAGATTC	
85	ATTTGCACTGACCGCAGGCTCGTG	122	AGATAAAGACGCTGGCAACACGGG	
86	CAGGGAGAACGGTTAAGTTCCCGT	123	GGTACCTCAACGCGAACCACTTGT	
87	AGGCCGGCGATCGAGGAGTTTGGT	124	AAGCGATGGCTACCCAAGAGCGAT	
88	ACACGGTGGTCTCTGATAGCGACC	125	AGAGCTTATGCAGAACCAGGCGCC	
89	GTGCAACGCCGAGGACTTCCATCA	126	ATCGGTCTCACGCAGGGTTGGATA	
90	TCGGTGCCTGATAGCCATTCCGAT	127	TAGGTTGCCCGCCAGAAGAAACAT	
91	TGAAATACCACACAGCCAATTGGC	128	CGGTGCTGTTGCAAAAGCCTGTAG	
92	GCATCGTGTACATGACTGCCGCGA	129	TGATGAAAGTTTGCGGCAGGACAC	
93	CAGTGTTCTAACGGCGCGCGTGAA	130	GTTGAGTGCAGGATGCAGCGATAG	
94	CGCTTGCAACGTTGCACCTACTCT	131	AACATTGCGCGGTCCACCAGGGTT	
95	CGAAAAACTAGTGGGCTCGCCGCG	132	GGGCAGTTAGAGAGGGCCAGAAGT	
96	CTTTCAGGGGAACTGCCGGAGTCG	133	TCGAGCTGGTCCCCGTGAACGTGT	
97	TTGTGGCCTTCTTGTAAAGGCACG	134	GTCTTGGGGGCCGCTTAGTGAAAA	
98	TCCACGAACGGCGACCCGTTGTCT	135	ACTGTTGGCTTGCTCTCATGTCCA	
99	CGACCTTGCACGAAACCTAACGAG	136	AGGACCATTCGGAAGGCGAAGATA	
100	GTGCAGCTTCACGAGCCAGCCTGA	137	CTTGGGAGGCATCCGCTATAAGGA	
101	CGCTTTCGTGCGAATAGACGATGA	138	AATAAACGGAACGCACCGCTACAG	
102	TGCGCTTACAGGCTCCTAGTGGTC	139	TTGTACGTGCGGTCCCcATAAGCA	

TABLE 1-continued

TABLE 1-continued

TAB	TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')		
140	CGCACCAAACTGAGTTTCCCAGAC	177	CCTTCGTGCATCGGTGATGATGTT		
141	ACCTGATCGTTCCCCTATTGGGAA	178	TGAACACGAGCAACACTCCAACGC		
142	GGAACAGAGGCGAGGGGACTGAGC	179	CAGCAGATCCTTCGTAGCGGTCGT		
143	CCCTGCCTTGGCGTGTCGGCTTAT	180	GGAACCTGGTGAGTTGTGCCTCAT		
144	ACTCTGACACGCCAACTCCGGAAG	181	TCATAAGCGACAATCGCGGGCTTA		
145	CTGACGGTTTTCATTCGGCGTGCC	182	CCCAACGTCACTGAAGCTCACAGT		
146	TGCGGTGGTTCATTGGAGCTGGCC	183	TGTCAGAGCCCGCGACTCAGACGG		
147	GCATGGCCAACTAGTGACTCGCAA	184	TACACGAAGCCTCTCCGTGGTCCA		
148	AGGCCGTAAAGCGAATCTCACCTG	185	CTCAGAAGTCCTCGGCGAACTGGG		
149	CGAATATTATGCCGAGAATCCGCG	186	ATCCTTTTATCTACTCCGCGGCGA		
150	ACAGACGAGCTCCCAACCACATGA	187	AGGCGTGCAGCAACAGGATAAACC		
151	GGACGGTTTGTGCTGGATTGTCTG	188	ACTCTCGAGGGAGTCTCTGGCACA		
152	AAAGGCTATTGAGTTGGTTGGGCG	189	TTGCCAGGTCCATCGAGACCTGTT		
153	GATGGCCTATTCGGAGATCGGGCC	190	TCCACTATAACTGCGGGTCCGTGT		
154	GATCCAGTAGGCAGCTTCATCCCA	191	GCCCAGTCGGCTCTAACAAGTTCG		
155	AATAACTCGCGCGGGTATGCTTCT	192	CGGAACGGATAATCGGCGTCAGGT		
156	GGAGGAGGTTTGTCTCGGAAAGCA	193	TAAAATAAGCGCCTGGCGGGAGGA		
157	CTTTGGTATGGCACATGCTGCCCG	194	GCGCACTCGTGAAACCTTTCTCGC		
158	AGAAAGGCTCGAGCAACGGGAACT	195	AGTTTGCCAGGTACTGGCAAGTGC		
159	AATCTACCGCACTGGTCCGCAAGT	196	ACAACGAGGGATGTCCAGCGGCAT		
160	CGTGGCGGCCACAGTTTTTGGAGG	197	TTCGCAGCACCCGCTAGGTACAGT		
161	TTGCAGTTCAATCCATACGCACGT	198	TAACCCGATTTTTGCGACTCTGCC		
162	GGCCCAAAGCCCCAGACCATTTTA	199	CGTCGCATTGCAAGCGTAGGCTTG		
163	CGCCTGTCTTTGTCTCCGGACAAT	200	GAGCTGACGTCACCATCAGAGGAA		
164	TGAGGCAACAGGGGCCAAAAACTA	201	GGAGGCTGGGGGTCGCGCTTAAGT		
165	AGCGGAAGTAGTCCTCGGCTCGTC	202	TTGTGGGPACCGCACTAGCTGGCT		
166	GGCCCCAAGGCTTAGAGATAGTGG	203	CCCTCGCACTGTGTTCACCCTCTT		
167	GCACGTGAAGTTTAACCGCGATTC	204	TCATTGACTCGAATCCGCACAACG		
168	AGCGGCAGAAACGTTCCTTGACGG	205	ACAGGGGTTGGCCTTCGTACGTAC		
169	TCGTCGAGCAGACGAGATTGCACG	206	AGGCCGTGCAACATCACACAGGAT		
170	TCTTTGCCGCGTAACTGACTGCTT	207	GGGCCGTGGTCACGTAATATTGGC		
171	TTTATGTGCCAAGGGGTTAACCGA	208	GCGCGGACATGAAACGACAAGGCC		
172	TGTTACTGTGGTTCACGGCAGTCC	209	CTTATTGGGTGCCGGTGTCGGATT		
173	CGCGCCTCGCTAGACCTTTTATTG	210	GGGGCGGTTACCAAAAAATCCGAT		
174	ACAAATGCGTGAGAGCTCCCAACT	211	GCTAAAGCGTGCTCCGTAACTGCC		
175	CGCGCAGATTATAGACCCGAATGT	212	ATCTCATGCATCTCGGTTCGTCGT		
176	CAAATAACGCCGCTGAATCGGCGT	213	ACGAAAAAGTGTGCGGATCCCCT		

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
214	CCAAGTACACCGCACGCATGTTTA	251	GCGAGGACCGAACTAGACAAACGG	
215	ATCGTGCGTGGAGTGTCGCATCTA	252	ACGCACGCGTGACCGAAGTTGCTG	
216	TCCAGATACCGCCCCGPACTTTGA	253	TAAAAGGTCGCTTTGAAAGGGGGA	
217	TCTGCTGGCAGCACGTGAAGTGGC	254	TGCGATCGCTAACTGCTGGGACAA	
218	TTGAAATTGCTCTGCCGTCAGTCA	255	GGAGGTATAAGCGGAGCGGCCTCA	
219	AGTCAGGCGAGATGTTCAGGCAGC	256	ATGCTGACATGTCGTGCACCTCGT	
220	ACAAGCCGACGTTAAGCCCGCCCA	257	TGTGGTTAAAGCGTCCGTTCAACG	
221	CCCTAATGAGGCCAGTAACCTGCA	258	CGTTCACACCGGCGTAAGCTGCGT	
222	GTGAGACACATCCCCTCCAATG	259	CCTATCCCGGCGAGAACTTCTGTG	
223	CGACGGATGCAGAGTTCAGTGGTC	260	GTCTGCACTCACGCAGCGGAGGGA	
224	CCCGCATGCCTGGCGGTATTACAA	261	GCACGAGTTGGTGCTCGGCAGATT	
225	TTAGCAAAGCGGCGCCGTTAGCAA	262	AACGTCGCACGACACGTTCGTC	
226	CCCGACACGGGTCAGCGTAATAAT	263	ATGCGCGCTTATCCTAGCATGGTC	
227	GCGACGGCCCTGAGGTATGTCGTC	264	TCACGTTTTCGTCTCGACATGAGG	
228	CAAAAGTGTGTTCCCTTGCGCTTG	265	TGTGCCTCATCCTTAGGATACGGC	
229	TCTCGAAGCACAGCCCGGTTATTG	266	AGGTGGTGTGGGTCAACCGCTTTA	
230	ATGCTAACCGTTGGCCATGGAACT	267	CTGGATCGAAGGGACTGCAAGCTC	
231	CTTGCGGAGTGTTAGCCCAGCGGT	268	TAGATCAACTCGCGTACGCATGGA	
232	TGCTCCCTAGGCGCTCGGAGGAGT	269	GATCCTGCGGAGAAGAGAGTGCAG	
233	CCAATGCCTTTGAGTAAGCGATGG	270	TACGTGTGGAGATGCCCCGAACCG	
234	AGCAGATAACGTCCCAATGACGCC	271	GCGCTATGTCAATCGTGGGCGTAG	
235	TTGACCATTACGTGTTGCGCCCAT	272	AGCGAGGTTTCTAGCGTCGACACC	
236	TCGCGTATTTGCGGAATTCGTCTG	273	CGATGAAGACAGGTTTGCTGTTGC	
237	CTGCGTGTCAACAATGTCCCGCAG	274	ACCCAGGTTTTGCCGTTGTGGAAT	
238	TCTGGTGCCACGCAAGGTCCACAG	275	CCCTGTTAACGGCTGCGTAGTCTC	
239	CTCCGGGAGGTCACTTAATTGCGG	276	AGGCCGATTTCACCCGCCAATTGC	
240	TTTTCGTGATTGCCCGGAGGAGGC	277	GAGCCCTCACTCCTTGCCCTTTGA	
241	TCGGGATGTAGCTGGGGCTACCGG	278	GGGTGGACATCCGCCTCGCAGTCA	
242	CGAGCCAACGCAAACACGTCCTTG	279	GATGGCTGAGAACCGTGCTACGAT	
243	GCAAAGCCTTTGTGGGGCGGTAGT	280	TCGACGTTAGGAGTGCTGCCAGAA	
244	ATTCGACCGGAAATGAGGTCTTCG	281	CGAATGGGTCTGGACCTTGCATAG	
245	TTCGCTTGCTGAGTTGCTCTGTTC	282	GTGCACCAGACATTCGAACTCGGA	
246	CGCGTGAAGACCCCATTCCCGAGT	283	AGAGGCCCCGTATATCCCATCCAT	
247	AACCGTATTCGCGGTCACTTGTGG	284	AACGCCTGTTCAGAGCATCAGCGG	
248	GGGGCCAACCGTTTCGAGGCGTAT	285	AAGGCTCAACACGCCTATGTGCGC	
249	TTCGGCTGGCAGTCCAAACGGCTT	286	AGTCCGTGTTGCCAGATTGGCTCG	
250	GGGTGTGGTTAGAATGCACGGTTC	287	ATGTCCCATGTAAAGACGCGTGTG	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
288	ATGGAGTCTGCTCACGCCCAAAGG	325	TGATCCATATTGTCGGACGTTGCG	
289	CGGCCTCCAACAAGGAGCACTAAC	326	ACCTGCCGGGAGTTCATAGGCTAG	
290	CAGAGCCGTGGCAACATTGCGAGC	327	AGCATTGGCGTTTTTCCGCAACGA	
291	TCATTTGAATGAGGTGCGCACCGG	328	GGTAATATTCAGCGCGACCGCTCA	
292	GACGTACCGGAAGCGCCGTATAAA	329	ATAGCGTACGACGAGGTGACGCGC	
293	ATGCGAGCAATGGGATCCGGATTC	330	GGGTGAGGGAAAGAGCACCTGCCT	
294	AGAGTGAGGCCTCCCTGACCAGTG	331	TAGGTCACGATGCGTTTGACGCTA	
295	CGCACCGTAAGTAGATTTGCCCGC	332	ACTGCCCGTACCTCTGGTTCTGGC	
296	AGGGTATCGGAGCCAGGGCTTACC	333	CAAAAATCGGGTGAACATTGGCTG	
297	TGAACCTTTGAGCACGTCGTGCGC	334	CCTTTGGCCTGAAGTTGTCGTAGC	
298	TCCGCCTTTTTGGTTACCTCGAAG	335	GTGCCCCACGAGCGTATCGTTGTA	
299	GAACGCCAACGGCACTAACACATC	336	AGGCGCTACGTGGGCCTGGAGCAA	
300	CCGACAGCAGCCAAGACGTCCCAG	337	GGGTGCTACCATTGCATTAGTCCG	
301	TTGTACACCTGGGCCACGCACAGG	338	ACCACGCGCGTACGTGTAACCGAG	
302	CATAAAAAACCTGGGGCTCTGCG	339	CCATGATGCATTGGGTGCATTTAG	
303	TGCCAACTGTGCAGACCGGACTTA	340	GGTCCGGCCCTACGAAACGTTCGA	
304	GGCGAAAGAGCGAAACCGGCTCGT	341	CCGTGTGGCTGGAGATTCGTGTGA	
305	GGGATGCGTATTTTAGCGAACACG	342	GTTAGGGCGACGCATATTGGCACA	
306	TGGGATTCAGCGACCAGTACGCGA	343	GGGTCAGTCAGGTGCGTTAGGATC	
307	CCCGATATTCGCCCGGCCTATTCG	344	GCCGTGAAGTCGAATGCAGATCGA	
308	CGAGAAGATGCCTCACGCAACCAA	345	GCCACCACCCAGTGCATTCAGGTA	
309	AACCTTCACCCGTGGATGACGCTA	346	GAGCTTAGTTTGCGGTCATCGGGC	
310	GGCTAGACGATGGATACCCGTGCC	347	TGTTTGCCGCCATTAGGGAGTAAC	
311	GCCTCTTCTCGACGATGCGATTTT	348	GCTCCGCTGGATGTGCCGGTTTAG	
312	GCTTCCGGATGAACGGGATGGTTG	349	CGGTAGCATGCGAGATCCCTGTTA	
313	CCCTCCATGTTCTTCGAACGGTTT	350	CTACGCTCTACCAGTTGCCTGCGA	
314	TTGATGGGCGGCAATGCTCTTGCT	351	GTGCCTCCTGCTGTATTTGCCAAG	
315	ATTGTGAGATGCGCCAAATTCCCC	352	TTGCGACTCGACTTGGACGAGTAG	
316	TCAGCACAGCCAGACGGTCAACTT	353	TCTGGGAGCTGTTTACTCCAGCCA	
317	ACTCCACTCCTCGGTGGCAAACTA	354	TGCACGCGGAACTCCCTTTACCAT	
318	TCTGGGCATGCCTGGACGGAGACG	355	TGGCAGCAAATGAATCGAAAGCAC	
319	TCTCAACTCCGGTACGACGAAACA	356	AACTGGTGACGCGGTACAGCGAAG	
320	TTGCGTGGTCAAAGGCGCAACGTG	357	AGACGATTACGCTGGACGCCGTCG	
321	AGACAGCGATCCGCGGCTCATGAT	358	ATGCCCTCCTTCATGGAAAGGGTT	
322	CGCGTCTCTAACTGAGAGCAGCCA	359	ATTCTCGGAGCGTATGCGCCAGAA	
323	AGGCGCACATGTACGGACATTCAG	360	ATAGCGGAGTTTGGGTACGCGAAC	
324	GATGAGTGGCACGTCGGTGTGTAA	361	ACCTACGCATACCGCTTGGCGAGG	

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TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
362	GATTACCTGAATGGCCAAGCGAGC	399	GTCGCCGGATTGCTCAGTATAAGC	
363	CCTGTTAGCATCACGGCGCTTAGG	400	ACCCGTCGATGCTTCCTCCTCAGA	
364	CGGAATGATGCGCTCGACAACGCT	401	ATCCGGGTGGGCGATACAAGAGAT	
365	TGAGAGAGGCGTTGGTTAAGGCAA	402	TTCCGCATGAGTCAGCTTTGAAAA	
366	AAGCAGGCGAAGGGATACTCCTCG	403	GCAAAGTCCCACTGGCAAGCCGAT	
367	TCACGACAGACGGGCCGAGATTAC	404	CGACCTCGGCTTCATCGTACACAT	
368	AAGCAATTTGGCCTCGTTTTGTGA	405	CTCATGAGCGCAGTTGTGCGTGAG	
369	GCTGGTTGCGGTAGGATCGCATAT	406	CAGATGAAGGATCCACGGCCGGAG	
370	TTGTGAATCCGTTCTGTCCCCGAC	407	TCAAAGGCTCTTGGATACAGCCGT	
371	CTCCGATGACAATTGTGGAGAGCA	408	TCCGCTAATTTCCAATCAGGGCTC	
372	TGGGCTCCTCTGAGGCGAGATGGC	409	ACGCACGGCGCTTTTGCCTTAATG	
373	GGATAGAGTGAATCGACCGGCAAC	410	TGACAACGTCACAAGGAGCAGGAC	
374	TGCACCGAACGTGCACGAGTAATT	411	CTTAGTTGGGGCGCGGTATCCAGA	
375	GCCAGTATTCTCGGGTGTTGGACG	412	GCTCTAATGCCGTGGAGTCGGAAC	
376	TCGCTACCTAAGACCGGGCCATAC	413	CCGATTACAAATTGACTGACCGCA	
377	TGGCATTGACGAGCAGCAGTCAGT	414	AGACGTACGTGAGCCTCCCGTGTC	
378	CGCGTCCCAGCGCCCTTGGAGTAT	415	AATGGAGCGATACGATCCAACGCA	
379	ATGAAGCCTACCGGGCGACTTCGT	416	GGAGGCGCTGTACTGATAGGCGTA	
380	CCAGACAGATGGCCTGGAACCATG	417	TGTTTTTGAATTGACCACACGGGA	
381	TGGCGTGGGACCATCTCXAAGCTA	418	CATGTCTGGATGCGCTCAATGAAG	
382	CCGCATGGGAACACGTGTCAAGGT	419	GCCCGCTAATCCGACACCCAGTTT	
383	GCCCACTCGTCAGCTGGACGTAAT	420	CCATTGACAGGAGAGCCATGAGCC	
384	ATTACGGTCGTGATCCAGAAAGCG	421	GAATCACCGAATCACCGACTCGTT	
385	TGCGAGGTGAGCACCTACGAGAGA	422	AACCAGCCGCAGTAGCTTACGTCG	
386	GGGCCGCATTCTTGATGTCCATTC	423	TTTTCTGAGGGACACGCGGGCGTT	
387	CCTCGGATGTGGGCTCTCGCCTAG	424	GGTGCTCCGTTTGATCGATCCTCC	
388	TAGGCATGTTGGCGTGAGCGCTAT	425	CCGCTTAGGCCATACTCTGAGCCA	
389	CGATACGAACGAGGATGTCCGCCT	426	TAAGACATACCGACGCCCTTGCCT	
390	TACGCCGGTTAGCACGGTGCGCTA	427	GTTCCCGACGCCAGTCATTGAGAC	
391	CATACGATGTCCGGGCCGTGTCGC	428	TAAAAGTTTCGCGGAGGTCGGGCT	
392	ATCCGCAGTTGTATGGCGCGTTAT	429	CGGTCCAGACGAGCTGAGTTCGGC	
393	GGGTAAGGGACAAAGATGGGATGG	430	CGGCGTAGCGGCTACGGACTTAAA	
394	ATTGGAGTGTTTTGGTGAATCCGC	431	GCTTGGATGCCCATGCGGCAAGGT	
395	GAACCGAGCCAACGTATGGACACG	432	AGCGGGATCCCAGAGTTTCGAAAA	
396	GCCGTCAAGCTTAAGGTTTTGGGC	433	GAGCTTGAGAGCGAGGTCATCCTC	
397	ACCTGCTTTTGGGTGGTGATATG	434	GCATCGGCCGTTTTGACCATATTC	
398	AATCGTGGGCGCAGCAAACGTATA	435	CATAGCGCTGCACGTTTCGACCGC	

TABLE 1-continued

TABLE 1-continued

TABLE 1-Continued		TABLE 1-Continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
436	ACCCGACAACCACCAATTCAAAAA	473	GGGACAAGGATTGAAGCTGGCGTC	
437	GCGAACACTCATAAGAGCGCCCTG	474	TGTCGTTGCTCCCGAGTACCATTG	
438	TTTTGGTGTGGCCGGTTGAAGCTC	475	GTGGTTATCTGCGAGGGCTTTTGA	
439	CCGCCGAGTGTAGAGAGACTCCGA	476	GTTGTCCGAGACGTTTGTGTCAGC	
440	GACATCGGGAGCCGGAAACATGAG	477	GCTGGTGAACACTCACGAACCGCT	
441	TCGTGTAGACTCGGCGACAGGCGT	478	GCAGACAGGGCAAATCGGTGCAAA	
442	ATGCGCATATACTGACTGCGCAGG	479	CCCATCACAACGAGTGGCGACTTT	
443	ACAAGCGAACCCGAGTTTTGATGA	480	GC1TCTACAGCTGGCGTGCTAGCG	
444	GCATGAGACTCCGCGAAGACATGT	481	GAATGTGTGCCGACCATTCTAGCC	
445	TCCTACATGTCGCGTCACGATCAC	482	CCAGCGGAAGTTAGAGCTCTGTGG	
446	GACCGATCGCGAAGTCGTACACAT	483	TTTTTACCGACCACTCCATGTCGG	
447	GTCGCCAGGACTGGGCCGATGTGA	484	GCGGCTATGTGATGACGGCCTAGC	
448	ACCGATAAGACTTGCATCCGAACG	485	AGTACACGGGCGTGTTAGCGCTCC	
449	TCCATAACCAGTCCGAAGTGCCGG	486	TCCTGTGTGGTGGCGCACTCCCAC	
450	ACGCCCCTGCATCTCGTATTTAA	487	CCAACTAACCAATCGCGCGGATGA	
451	AGACCGCATCAATTGGCGCGTACC	488	AGTGAGTGACCAAGGCAGGAGCAA	
452	AGAGGCTTGGCAAGTAGGGACCCT	489	CATCTTTCGCGGAGTTTATTGCGG	
453	GCAATGGACGCCAGACGATACCGG	490	CTTCGTCCGGTTAGTGCGACAGCA	
454	GCTGGACTTAGTCGTGTTCGGCGG	491	CTCACGAAAACGTGGGCCCGAAAT	
455	GGGGCTCATGAACGAAAGGCCTTT	492	CGCAGCAGCTGAACTCTAGCATTG	
456	AGGCATCGTGCCGGATTGCTCCCT	493	AGGAGACATACGCCCAAATGGTGC	
457	TGCGCATGTCGACGTTGAACAAAG	494	ATTGAGAACTCGTGCGGGAGTTTG	
458	ATTGCATTATGCGGTCCCTCAAAC	495	CTCTTTGTAGGCCCAGGAGGAGCA	
459	TTCGGGTCACATCCGATGCCATAC	496	GCCGCAGGGTCGATAATTGGTCTA	
460	ACCCATCGCCGGAAAGCGATGTTG	497	AAACGCCGCCCTGAGACTATTGGG	
461	AAGCGCTGACTCGGCTAAGAATCA	498	CTGAGTTGCCTGGAACGTTGGACT	
462	ACTTCCAAGTCCTTGACCGTCCGA	499	CGGATGGGTTGCAGAGTATGGGAT	
463	TCTCAATATTCCCGTAGTCGCCCA	500	CTGACCTTTGGGGGTTAGTGCGGT	
464	AACAGTTCCTCTTTTTCCTGGCGC	501	GGAAATGAGAACCTTACCCCAGCG	
465	CGTCCTCCATGTTGTCACGAACAG	502	AACGCATCGTCCGTCAACTCATCA	
466	TGCGCAGACCTACCTGTCTTTGCT	503	TGGAGAGAGACTTCGGCCATTGTT	
467	ATGGACGGCTTCGCAGTCCTCCTT	504	ACGGAAGTCACGGCGTCGCTCGAA	
468	TGAACGCTTTCTATGGGCCACGTA	505	TTGCGCTCATTGGATCTTGTCAGG	
469	TGAACCCTGCCGCGAGCGATAACC	506	AGCGCGTTAAAGCACGGCAACATT	
470	GTTCTTGCGCGATGAATCAGGACC	507	AGCCAGTAAACTGTGGGCGGCTGT	
471	AGGGTACGTGTCGCAGCTTCGCGT	508	CGACTGATGTGCAACCAGCAGCTG	
472	ACCCTTGCTCCGCCATGTCTCTCA	509	GGTTGCTCATACGACGAGCGAGTG	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
510	GCGCAAATCCACGGAACCCGTACC	547	ATCCAGAGATCCGTTTTGCAGCGT	
511	ACGCAGTTTATTCCCCTGGCTTCT	548	GTCACCAGGAGGGAAGTTTCACCC	
512	AGAACCTCCGCGCCTCCGTAGTAG	549	TATCTTACGCCCCACGGTCGAGCT	
513	AAAGGAGCTTTCGCCCAACGTACC	550	TTCCGTCAGGCGGATCAACGGAAT	
514	AGTGATTGTGCCACTCCACAGCTC	551	ATGCCGGACACGCATTACACAGGC	
515	GCGATCGTCGAGGGTTGAGCTGAA	552	TGGGCCGCTTGGCGCTTTCATAGA	
516	GGGAGACAGCCATTATGGTCCTCG	553	CCTAGCGCGAGCTTTACTGACCAG	
517	GAGACGCTGTCACTCCGGCAGAAC	554	TTGGCCAGGAATATGGTCTCGAGA	
518	CCACCGGTCGCTTAAGATGCACTT	555	GTCTGCGGCCGACTTGCTATGCAT	
519	CGGCATAACGTCCAGTCCTGGGAC	556	AACTTGCTCATTCTCAAGCCGACG	
520	AAGCGGAACGGGTTATACCGAGGT	557	ACGTCAGCGATTGTGGCGAAATAT	
521	TGCACACTAGGTCCGTCGCTTGAT	558	ACGGCCTGCGTCAGCACATGCATC	
522	AGGGAACCGCGTTCAAACTCAGTT	559	ATACCTCCGCAGAACCATTCCGTT	
523	GAATTACAACCACCCGCTCGTGTT	560	AGTTCGCGGTCCCACGATTCACTT	
524	TTCAGTGCTCACGAAGCATGGATT	561	TGCTCAATTTGTGCAGAAAACGCC	
525	TTAGTTTGGCGTTGGGACTTCACC	562	TTATCGCGAGAGACGACCGTGTCC	
526	AATGCGACCTCGACGAGCCTCATA	563	GACGCGACGTGAGTAGTGGAAGCG	
527	CCGAAACCGTTAACGTGGCGCACA	564	ATGGTAGGGCATTGGGCTTTCCT	
528	TAAAGTAACAAGGCGACCTCCCGC	565	CCAAATATAGCCGCGCGGAGACAT	
529	TAATGATTTTAGTCGCGGGGTGGG	566	GCAAACCCTGATTGAATCGTGCCC	
530	GGCTACTCTAAGTGCCCGCTCAGG	567	TAGCGTCTTGCGTGAAACCATGGG	
531	TGGCGGACGACTCAATATCTCACG	568	CCACCCGACAGCGCTGGACTCTT	
532	GGGCGTTAGGCGTAATAGACCGTC	569	ACGAGCACTGAAGGCTGCTTTACG	
533	GCCACCTTTAGACGGCGGCTCTAG	570	CATATCAGCGTCGTCTAGCTCGCG	
534	GAGATGTGTAAACGTGCAGGCACC	571	TGATCCCGGACCGGCTAGACTAAT	
535	CAACCTCGTTGTCGAGTTTCTCGG	572	GGCCCCGACACTACAGGGTAATCA	
536	TAGCTCGTGGCCCTCCAAGCGTGT	573	GGCTCCAGGGCGAGATTATGAATG	
537	GTGTCGGCGCTATTTGGCCTTACC	574	CAAAATCCGATGGGCGGAAAATTA	
538	CCAGGGAAGCAACTGGTTGCCATT	575	CACAGGCGCATAGGGAGCAAGCTA	
539	TTCCGAAACTAAGCCAGAACCGCT	576	TAGCTATTGCCCCGATGGGCTACT	
540	GCAAACCCGGTAACCCGAGAGTTC	577	TGGTACGCGGTCCATAGCAAGTCG	
541	GCAAATGGCGTCATGCACGAACGT	578	GACGCTGTGGCTCGGAAACTGTTC	
542	AGTACTTTCGCGCCCAGTTTAGGG	579	CCTGGGTTCGCCGCGTGGTAACTG	
543	AAGATCTGCGAGGCATCCCGGCTT	580	TTCCCGCGTAGCCCAACAGCTATA	
544	GCAAGTGTATCGCACAGTGCGATT	581	TTCGCGGATTGCTGOCGCATAACA	
545	CCGACAAGGCCTCAATTCATTCTG	582	AAAAATGGCACCGAAGTTGAGGCA	
546	GTCTCGTCTCAACTTTAAGGCGCG	583	CATTCCGCGCGAGTTGAAATCCAG	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
584	ACGCACGTTTTTTGGGACGGTTAA	621	AATGTGTCGGTCCTAAGCCGGGTG	
585	TGTCCATGACGTCGTTTCTCTGGT	622	TAAGACGAGCCTGCACAGCTTGCG	
586	TCTCAGTCGGACTCGTATGCCAGA	623	GGCGTGGGAGGATAAGACGATGTC	
587	CTCCAAACGCACACATCAAGCATC	624	TGCTCCATGTTAGGAACGCACCAC	
588	TTCAACCAAGCGGGGTGTTCGTGA	625	CGGTGTTGGTCGGACTGACGACTG	
589	GGTGTCGGAGGGTGGTGACCTCGA	626	CCGCGCGTATCTATCAGATCTGGG	
590	AGCGCTTTTGGTCATGATTTGCAA	627	AAAGCATGCTCCACCTGGAGCGAG	
591	CCGAGGACTTACGTCTGCCCAGGA	628	ACTTGCATCGCTGGGTAGATCCGG	
592	GCCCAATCCAGTTCTTATGCGCCC	629	TGCTTACGCAGTGGATTGGTCAGA	
593	AAGCTTTGCGAAAGGTGTGTTGGC	630	ATGCAGATGAACAAATCGCCGAAT	
594	CGGGTTAACCCACGCAAGTTATGA	631	GCAATTCTGGGCCATGTATTCGTC	
595	TGATTAGCGCTCAATACACGCGTG	632	AGGGTTCCTTACGCGTCGACATGG	
596	AAGGGCAGACCTTTGGTTCGACTG	633	GTGGAGCTAATCGCGAGCCTCAGA	
597	GCGCCACAAGATTCACATGTCATT	634	TCGTAGTCTCACCGGCAATGATCC	
598	GCCATGTTCAAGGGCCTTTCGAAG	635	TTATAGCAGTGCGCCAATGCTTCG	
599	CGCGGTGTTTTGTCTAGGTGCCGG	636	CGAACAGTGCTGTCCGTCGCTCAA	
600	CAACATTGTGGTGGCACTCCATCC	637	TCCGCGTGGACTGTTAGACGCTAT	
601	CGATACGCGCCGGTTTGTTAAATC	638	CATTAGCCCGCTGTCGGTAACTGT	
602	GGCTATAAACGTGCGGACTGCTCC	639	GGAAAGAAACTCAGACGCGCAATG	
603	TGGGTAAATCACTATTGCGCGGTT	640	CGACTCGCTGGACAGGAGAATCGT	
604	GTCTTCATCGGCCCGCGCAAGCTA	641	CATGATCCTCTGTTTCACCCCCGG	
605	GCGACACCCTGTACTCTGATGC	642	GGCGTAGCGCTCTAAAAGCTTCGG	
606	GTAGCAGGGTCCGCAAGACCAAGC	643	AGTGATGCCATCAGGCCCGTATAC	
607	TCGCCAACGCAGGGTAACTGCCAT	644	TATGGAAAGGGCAACAGCGCTATC	
608	ACTCCGAAGCTTCGAGCGGCACGA	645	CTGTGGTTGATGGAGGATCCACAC	
609	TCCCGCCCACTAGACTGACTCGTA	646	ACTCGCTGGAATTTGCGCTGACAC	
610	ACCTTCTGGGGTCGCTCACCAATA	647	CAGGCCCGAACCACGCGGTTACAG	
611	ATCATCCCACGGCAGAGTGAAGAG	648	GGCGCAATGGGCGCATAAATACTA	
612	CGCTGGACTGGCCTATCCGAGTCG	649	GGTCAATTCGCGCTACATGCCCTA	
613	CGGTCTCAGCAACACTGTCGCAAA	650	TGAGGGCTGTTTGGTATTTGACCC	
614	CGAACGTTCTCCGATGTAATGGCC	651	GATGGTGGACTGGAGCCCTTCCGC	
615	ATACCGTGCGACAAGCCCCTCTGA	652	CCGCGCATAGCGCAATAGGGGAGA	
616	AGCTCATTCCCGAGACGGAACACC	653	TCTTCTGGCTGTCCGGCACCCGAA	
617	TTTCATGCGGCCGTTGCAAATCAT	654	GCGTTCGCAATTCACGGGCCCTTA	
618	ACTCGAACGGACGTTCAATTCCCA	655	TCGTTTCGGCCTTGGAGAGTATCG	
619	CTGCATGGTGTGGGTGAGACTCCC	656	AGGTGCAAGTGCAAGGCGAGAGGC	
620	CCGCGAGTGTGGATGGCGTGTTGA	657	CGCCAGTTTCGATGGCTGACGTTT	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
658	GCTTTACCGCCGATCCCAGATATC	695	GATGCTCGCCGTGTTTAGTTCACG	
659	GTGCTTGACGAAGAGGCGAAATGT	696	TCGGATGACGAGTTTCCATGACGG	
660	CAGTCCGTGCGCTTCATGTCCTCA	697	ATGCGGTCTACTTTCTCGATCGGG	
661	TACGCGTAAGAGCCTACCCTCGCG	698	TTGCGAGGCTAAGCACACGGTAAA	
662	GGCGAGTCTTGTGGGGACATGTGT	699	AACTTAATTACCGCCTCTGGCGCC	
663	CCAAAGCGAAGCGAGCGTGTCTAT	700	GTGACCGCGAACTTGTTCCGACAG	
664	GCCGTAGGTTGCTCTTCACCGAAC	701	TGCGGATTACCGATTCGCTCTTAA	
665	AAATCCGCGATGTGCCGTGAGGCT	702	TGATAGGGGGCCACGTTGATCAGA	
666	GGCTTCGCACCCGTACCAATTTAG	703	TCGCTCCGTAGCGATTCATCGTAG	
667	TGTAGAGTCCCACGTAGCCGGCAT	704	TGTCAGCTGGTAGCCTCCGTTTGA	
668	CACTAGTCTGGGGCAAGGTGCATT	705	AGCGTCGCATGACGCTTACGGCAC	
669	TGTACTCGGCAGGCGCAATAGATT	706	TCACTCAGCGCTGTGACTGCCTGA	
670	AACGGGTATCGGAAGCGTAAAAGC	707	GTTTGCGCTATAGTGGGGGACCGT	
671	CGGACTGCCCGTTTGCAAGTTGAG	708	GTCGCATTCTGCACTGGCTTCGCC	
672	ATCGTTCAGCACTGGAGCCCGTAA	709	TGATTAGGTGCGGTCCCGTAGTCC	
673	ATGCATCGAACTAGTCGTGACGGC	710	AAGGGACCTTGGGTGACGGCGAGA	
674	TTCCAGGCATTAAGGAGAGGGAGC	711	TCAAATGGCCACCGCGTGTCATTC	
675	GTGCGACATCTACTCCACGATCCC	712	CTCCGACGACCAATAAATAGCCGC	
676	CTCATCGTCCTAACACGAGAGCCC	713	GGCTATTCCCGTAGAGAGCGTCCA	
677	AATGGCACTTCGGCGGTGATGCAA	714	TGGATAACCTCTCGGTCCATCCAC	
678	CCGTGGGAGGGAATCCAACCGAGG	715	GACCGCTGTACGGGAGTGTGCCTT	
679	AAATTCTCGTTGGTGACGGCTCAT	716	GCCACAGAGTTTTAGCAGGGACCC	
680	TTGCTCTTATCCTTGTCCTGGGCG	717	CCCACGCTTTCCGACCACTGACCT	
681	TTAAGGATCAGGCGGAGCTTGCAG	718	CATTGACACAATGCGGGGACTGAT	
682	CGCGACTAAGGTGCTGCAACTCGA	719	AGCCACTCGACAGGGTTCCAAAGC	
683	GCTCGATTTCACGGCCCGTTGTTC	720	CAGGATGAGCAAAGCGACTCTCCA	
684	AGCAGAGTGCGTTGCAGAGGCTAA	721	CAAGGTATGGTCTGGGGCCTAAGC	
685	TGGAGGTGAGGACGTGCACTA	722	GGTGTTCGGCCTAAACTCTTTCGG	
686	AACCGTTTAGGGTACATTCGCGGT	723	TTTAGTCGGACCCTGTGGCAATTC	
687	TATGATCGCTCGGCTCACAGTTTG	724	CACACGTTTCCGACCAGCCTGAAC	
688	GACTTTTTGCGGAAACGTCATGGT	725	CTGGACGAACTGGCTTCCTCGTAC	
689	TGTCGGTTATTCCACCTGCAAGGA	726	TTCACAATCCGCCGAAAACTGACC	
690	CTATGGTTTGCACTGCGCCGTCGA	727	AACAGGATATCCGCGATCACGACA	
691	AGCAGGGAAATTCAATCGTTCGCA	728	TACGTCGGATCCATTGCGCCGAGT	
692	CCTAACCGAGCGCTTAGCATTTCC	729	CATGGATCTCTCGGTTTGATCGCC	
693	CCCGACCCTAACTCGCATTGAATA	730	AGCCAGGCGCGTATATACGCTCGG	
694	TTGCTTAATGGTGACGCCACGGAT	731	ATTTGGCACGTGTCGTGCCATGTT	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
732	CCGCGTTGCACCACTTTGAGGTGC	769	GCATTGGCTTCGGATTCTCCTACA	
733	TTGGACGTGACAAGCATGGCGCTC	770	AGGCGGCCCAACTGTGAGGTCTTG	
734	CTGAATCGCGCAAGTAAATGGGGG	771	ACACCATGTGCTCCGCGCTGCAGT	
735	GATAAGGTCCACCAGATTGCGCGC	772	ACGATGAACATGAATCGGGAGTCG	
736	CTAACAATTGCCAACCGGGACGGC	773	CTGCATCCCTGTAGCAGCGCTCCG	
737	GGTAACCTGGGTGCTTGCAGGTTA	774	GTGCCGTATTTCGACCTGTGCGTT	
738	ATCGGAGCCACCATTCGCATTGGG	775	GCAGTGCGCACTTCAGTTCAAAAG	
739	GTGAACTGGCTTGCCCCAGGATTA	776	GCGATTTTAAGCGATGCCTTGACG	
740	AGGCGATAGCATGGTCCCATATGA	777	TAGGTGACCTAGGCTTGCTTGCGG	
741	AACGGTATCGTGGCTAATGCACGA	778	CTGGATACCTTGCCTGTGCGGCGC	
742	AGTAGTGGTCCTCCAGATCGGCAA	779	CCCCTTACGGCTCGTCGTCTATGC	
743	CCGTTGAATTGGACGGGAGGTTAG	780	GCGCTTGCCCGATGCGATGCATTA	
744	GCATAAGTGCGGCATCGCGAAGGG	781	TTTCTGTAAGCGGCCTGGGGTTCA	
745	CGACAAGATGCAGCTGCTACATGC	782	GGCTGAGGTGAGCGGTAAGGATGA	
746	TCGCAGTGATTCCCGACCGATAAG	783	TCTTGGCCTCCCCGATCTAATTTG	
747	CAAGGCGAGTCCACTCGAGGGGAC	784	GGAGGTAACGCCGTGTACGTAGGA	
748	GCAACTTGCACGGCATAAGTGGCC	785	GTAATCCATTTGTGGCTGCGTCAA	
749	TCCGAGCTTGACGTTCGCGACGTC	786	CAAACCCATTCCAGCAGACGCCTG	
750	AGCGCTGGGCTGTGCCATCTC	787	TAGGAGGAATTTGGCATGCGGGCG	
751	TTCATGTCGCTGAGTAACCCTCGC	788	ATAGGTAGGATGTGCCCGGCGTTG	
752	CGAACCGCTAATGCCCATTGTCAG	789	GCAAGTGCTTAGCTCGTCAGCCTC	
753	CACGGAAGGTGGGACAAATCGCCG	790	CTGGCTGTCGCATCTCGTTAAC	
754	CACAGATGGAGACAAACGCGCCTT	791	CTAACGTCGTCTCGCGCAATCACT	
755	TTTTCGCAACTCGCTCCATAACCC	792	TTTTCATAAACGTTGTCCCCGAGC	
756	ACGTTACGTTTCCGGCGCCTCTAA	793	AGCAGGAGGACGAACCTCCGCTCC	
757	TATCGGATTGCGTGGGTTTCAATC	794	TTCAAGCACCATCGTGCAATCCAA	
758	CTTCCACAATTGTCTGCGACGCAC	795	AGCGTCGCCAGTGATCGCTAGTGG	
759	TGCACAAAGGTATGGCTGTCCGGC	796	TACATTCCCTGCCTCCGTGGGCTT	
760	ACCGTGGCCGGGCCATAAGCTACG	797	CGCTTCGCGTATTCAGTAGCGGTT	
761	TCCGATGCCAGTCCCATCTTAAGA	798	TCGGACGCGTCGACACTCATTATA	
762	CTGAAACCGTGCGAATCGAGGTGA	799	TCTGAGCAGGCCAGCGCTCCAGCT	
763	CGGTGTTCCGCGTGTCGAAAAAAT	800	TTGAATTGCCAAGCCCTGAAAGCC	
764	TCTAGCAGGCCTTTTGAATCGCCA	801	AGTTTTCGCCTTGATGCGTCGGTG	
765	GAGTCACCTCTGAGACGGACGCCA	802	GTTTCATAGGCCACGCGTGCTAAA	
766	TCTTCTGTCATCCTGCAGCAGCAT	803	GGAGCGAAGACTTCGTCTGCCCAA	
767	GCGGATGAAACCTGAAAGGGGCCT	804	ATTGGCCGAGGGTGAATGCAGCCT	
768	GGGGCCCCAAACTGGTATCAAGCC	805	TGATCCATCCGAATGCTTTTCCAT	

TABLE 1-continued

TABLE 1-continued

TABLE 1-Continued		TABLE 1-Continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
806	GCACACAGTTGTCTTGGCCCATGA	843	GGCGTGAATAGAGTGACCAGGCGG	
807	CTGGCGGCAGTGGAAAAAACAAC	844	ACGTGCCAGCTGCGGGCACTTTAT	
808	ATCTCCATGCGTAAGACTGCTCCG	845	AGTGGAATAGTCGCGTCGTGCCGC	
809	TCTCCTCTCGTCGCAGTTCGTGGA	846	ACTCGCCTATTACCGCTGGATTGG	
810	TAGCGTATTCACTCTTGCCGAGCA	847	GAGACCGGATTGAGATGATCCCGT	
811	CAATCAAAAGCCACGGCGCGATGG	848	AAAATGGCAGGCGGCAAGCAATTG	
812	AGCGTCACGGAATTCAGCAGATCT	849	CTGGCAGTTTACCACCGAACCAGT	
813	GACTCCCTGTTAATGCGCCCAAGG	850	TTACATTGCCGATTTCGCATGTGA	
814	TAGGCACTGCCGGTTCAGATTCAA	851	TAAAACTGAAGGGTCGCCTCAGCA	
815	AACAGGGTGATAACGGTGGCCAAT	852	GGCTTCGCATGCCTTTGCAACATT	
816	CGTGCGTACCATGTGTAAGTGCGT	853	AAGACCGAAGGTCTCTCTGAGGGC	
817	GACCAATTCTACTTCGGCAGCCCA	854	GCCTATGGCTCCAGCTCAGCAGTA	
818	ATCGGACCGATTTGCTTTTGGCTG	855	CGTATCATAGCGTTCGGTGGACAA	
819	TCCGCCGAAGCACACGCTTATTCG	856	CATGCGCTCGCACTCTGCCTGTCT	
820	AACGGTACGCATTGTGAGCAGTGT	857	TGGGCAATTCGGAAACGTCGGTCT	
821	TGGCGACTACTGTTCCCCTGAATC	858	TTGCGGAGATGCGACGGTACATTG	
822	CAGAGGGGACAGCCGTATGCCTTA	859	ACTTTCGCACGTCGATCTGGACTG	
823	CGGTGGTTTTATCGGAATCTGCGA	860	CTAACTGCCGCGGCAAACTGATTA	
824	TTGGCCTCCGACCTCACGACATAT	861	GGCCGCGGATTTTATTCCTTGGAT	
825	CGTTTCGCTAGCATCTGGCGCCGA	862	GAATTTGGAACGGTGTTCCGATGA	
826	ACTAAGCGGTGGAGCCGGTGGATG	863	GTCCATCCATCTACGGCATCAGGA	
827	ATATTGGCTGCGTTTACGGGCCGC	864	TAAACGACCTGGCACATGTGCGTA	
828	CCGCTATGGTGGCAATCCCGATAC	865	CACCATCCAAGAGCCAATCCTAGG	
829	GTTGCATGTGGCTCAGGCGGCATA	866	ACTCATATACGATCAGTCCGCCGC	
830	ATTCTGGGGAGTGACCCAGGGCTT	867	GTGCCAACCGACGATCAACCGAAC	
831	CTCTCCAAGGAGACGAGCCAATGT	868	TGGGGTTCGTACAGGTCGGTTCAT	
832	GAAAGGACGGGATTTGGGGGCTAA	869	AACAGTAGAGGCGAGGCCTGCGGG	
833	TATGTAGTACCTTGGCTCGCGCCA	870	TGCATCGAATCCGAGATGGATCTT	
834	TCCCTTTCGATGAGCGGCTGTACT	871	GCGTCACGTTATGTCCGCTCTGTC	
835	TAGATCGGGCAGAGCCCGTATCTT	872	GGGACATGCGTAGCGCAATATCAC	
836	GGAATGCTTTAGGCTGCCGAGCTG	873	CACACGTCACACCATCCAAAGTGG	
837	ATGGTAGCAACATTCAACGCCAGG	874	ATGCTCAGGTGCTAAATACGGCCA	
838	CTATGAAACGTGTGGCCCAGCAAC	875	AAAAATGTTTAGCGCGCTGACTGG	
839	ATGTTGCTAGTGCCTTTCGGGCCT	876	ATAGTCCGTTTCCGTTCCCAACGA	
840	CCAATGTGCGCAGACTCAGTCATT	877	TCGATCTTCTGGGTTGCAGACCAG	
841	GATAGTGCTCGCAAACGGGCCTTC	878	GTCGGCGCAGCCGATCCTCATGTC	
842	GCACCCTGTTGCCTCATTGAGCGT	879	GTTGCGGGGTGTCGAAAAGGATCT	

TABLE 1-continued

TABLE 1-continued

TABLE 1-Continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
880	ATCTCTTCCTCGGGTGGATGCCAG	917	TAATTCATGGGGCTAGCCGAACCA	
881	TGATGTGCGTTTCAGCTTTTCGCG	918	ACACTCTAAGCCGATTCCGTTCGA	
882	GTTAAGGGGTGAGAACATCCGGCC	919	GTGGGCGTGAGTGACACGCACAAA	
883	AAGTCGTCTCCCTGCGTCTCGTCC	920	ACGACTCCTCGGGCAAAGTACGTA	
884	CCGACCTAATAAGGCGCAACAATG	921	TGTGGTCATGGCGCTACTGTTTTC	
885	CATCATTGGCACCGTACCAATGCC	922	CTTTCGCTAGCCAGAGCGGGTTCC	
886	TGGAGAAAGGGAAGTGCAGCAACG	923	ACAGGGCGTGTTAGCGTGTGACAA	
887	TGGTACTCCTTGTCATGCCTGCCA	924	GGTACTTCCGGCGTATCGGGCCAC	
888	GGCACAGGTTCTCTTGCAGCGCGG	925	GTGGGTTTTGTTCACCCTTCTGGG	
889	GAATCTGGGCATTGCTACGAGACC	926	ACGCAATTCCGCATTACTTACCCG	
890	CGAAATGGGAGCGTCCACTACCAC	927	CGCCTCGACTGCGGTCAAGCACAA	
891	ACATATGAGCTCGCGTGCTTGCAT	928	GTGAAATGGATCCAGAGAGGGCCA	
892	TCGAGCACGGTCACTGATAAAGCC	929	TATAAACGCTGCAGGGCTCCGTTA	
893	GAGGGTCCCTGCTCAGAGTTGGTT	930	GTTATTCAGGCGGCTTGTAACGGG	
894	AAATGCGATCGCCCCTTATGGAAT	931	GGGTTCTAGCGTGCGCGTTCAGTT	
895	CTACCCGAATGGATTGCGGATGGC	932	TTGGGCTCGAGCGGTACACCACTA	
896	AGGGACTGGCAGGTCTCTGCGCGT	933	CCGTCTTCAGGACAACGGTATGCG	
897	TAACGATCCATTCCACGAATGCAG	934	GGACCCTTTGACAGATTGCGGCAC	
898	GGCCGCACGTACGATTACGCCTTG	935	TAAATTTTATCGCCAGGCGGCGCT	
899	TGGGGAATGCATCAGTTGTTGGCT	936	GCCGAACGCAAGATCGCTTGAACT	
900	TATCTGGGAGTAGCAGGCAGGGCC	937	TAGGCCATTGGTGCCCTAAGACGG	
901	CCGAAGGTTTCACGCTCAGGTCGC	938	CAAACCACAGCTTACAGGCTGCGT	
902	GAACCCAGCTGGGACATCCTTCAG	939	TAAACGGAGACTGGCACGGTAGCA	
903	TGCATGCGAGCAAATAACCCGGAC	940	TAGCGCGCATCACACTTGGAATCG	
904	AATTGTCCGCCAAACGCTTTTCAG	941	TGCTGACACAAACGAGCCGTTTCG	
905	GTCGGCTTCGAGCGATCGAGTGTG	942	CGCTTAACGGCATTGACTGTCCAC	
906	TCGCGTGCTCTACGTAGCCCATGA	943	TTCCACGGCCGTGTATTACGGATA	
907	GGCTTCCGCGATAACGTAATTCGC	944	TTTATGCCGTTGCCGAGGAAGACT	
908	TGTAGCCGACTAGGGCCGAAGCCC	945	AGTGCCGAGATAGGGGACTGGGCG	
909	AAGCGAACGCCCTGGCTGAATATT	946	CTAGTCTCCACGCCCTCGGGACGA	
910	TGTCACGCGACGTGCTGCAGATTT	947	CCGCCATTCGGAAGATGGATGATG	
911	CCGTGTCCGTGTTGTCGACAGGCG	948	TGACGGTGAAAGTCGATTGCGAAG	
912	CCCCACACGTTGCGCCTATATGTG	949	ATATGCGTCACCACCCGGTTCCGA	
913	GGCGGGCACAACTCAACACAGATG	950	CCATCAGTGAAGGGGTTGCTGCCA	
914	CGACTGCGGGATCACCGGTGATTA	951	CATATGTGCTTGGCTTGCGATGAC	
915	TCGGGACATGACCGGTACGGAGTC	952	TCTGCTTTGGAAGCCTGAACTGCT	
916	TACCTCGAGTGGCCGTTGATCGGG	953	CGATTTGGTCAAGAAGGCGGAAAT	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
954	ATCAGAGGCCTTCCCGCCTCGTTA	991	ACTTTCAGCACGCGAACAGCGCAA	
955	ATTGTTGTCGTTGCCACATCGCAG	992	CTAAACGCCCTTGATGCATGAGCA	
956	TGAAATGTGTCTGGACGCGAGTCT	993	GCTTGCCTTTTACGATCGTCGCTA	
957	GCGGGCGATGCTCCTTAAAGGGTA	994	CAGACATCGTACGCACTCGGCATC	
958	CCGCAATCTCCATGCGTCGACCGT	995	TAGCCGCGCGCTCCTATGCTCTT	
959	TGCCGCGTAATCACCTGGAACTTG	996	GATGCCCTTTTGGTCCCCATGCCA	
960	TTCCAGTAGCCAGCGGTAGTGTGA	997	TGAGCTGCCTTGCCACGATGCCTC	
961	CTGAATTCCGCCTATTGTTCGGCA	998	CCGCCGTATACGTGCCATAGTTTG	
962	GCTTGAACCTCGAGGCGATGTTCT	999	TAGTGCTCTCCGCGCTCATCCAAC	
963	CAAGCGTGGAAGTACGACCCGCCA	1000	CCCTAGATAAGTTGGGGTGGGACG	
964	GTGTGCACTGGATCCGAGCCCTAG	1001	TGAAGGGCCACCTGATATGGTTTC	
965	TCCCTGGGCTAGCATTGCGAGGTT	1002	GCCGCCTCCGACTGGTTAACCCGA	
966	AGAACCAAAGACGCTTGTTTGCCG	1003	CGCACGGCTACTAACAGCGGATCA	
967	CGTCACATGCAAACGTTCCCTCCC	1004	CCGGACCAATTCCAACGAGCATCG	
968	TGACCGCATGTGTATTGAGTCGCT	1005	CATTGAGGTCCACCGTTCACATCC	
969	GCGGGCCCAATGAGTATCCGTCAT	1006	AGGACGCAGCATGTCCCAGCCGAG	
970	TAGTGACTGTGAACGCCCCTGGTT	1007	TAATCGCGGGCCATACTACCAACG	
971	GGCACCGTCTGCCGCGCGTATATC	1008	CGCAAATTTCTCCGGTCGGCAAGC	
972	TCGATGCAGTCTTTTTCCCGTCAA	1009	GTGGCTCGACTAATGCCTTGCGTG	
973	ACCCCGTGGGGTTTCGCCATTTTT	1010	TGTGGGCGTGTTCCGGCTCACTGT	
974	CTACACGCGCAGTTGTGACTTGTG	1011	GTTCTTCCTTTTCTGCGGTGGGAA	
975	CGCAGCGACCTCATCTCTGGAGCC	1012	ACCTCGAGTCAGATTGTGCGCCTT	
976	CGACCCAGCACTCCTAAAATCGGT	1013	CAAGTGGACAGACGGTTTGTTCCG	
977	ACGCGCCGCTCATCACTACAATCT	1014	TCCAGTTGAGTCGCGCCGACGAGG	
978	CGCAACTTCCTGTGGCAAAGCCAG	1015	CGCAACAGGTCAGCCCTTATTTGC	
979	TCGTTGGGCACATAAGGCAACTGA	1016	GCCGTGACTCCTGCAATGTCGGTA	
980	CCGCTTGTAATTGCCATTCTCCGT	1017	ATCAGCGCAAGCTGGTCTGAAACA	
981	GTAACCAGGGAGTCCTGGGCTGTG	1018	CCCTGGCCAGAACGAGAGGCCATG	
982	AGCGCAAGATCTGGGGGCAGTCAC	1019	ACGATCAAGGACTCGTCAGGGTTG	
983	GCGTACATCTGCTCATCAGCATGG	1020	TTCATGGCACCAAGACCACCGTTA	
984	CCTCTGTGGCAGGAAAGAAACCGT	1021	ACAGCAAGGAGATGGATTGCGACG	
985	CCTATGCAATGGACCTGCATCGGA	1022	CGTAAATATCTGCGGCGGTGTGAA	
986	CTCGGTGGATGGCGAATAAGGATA	1023	GGAAACACGTGTTCGTCTGTTGGC	
987	CCTCACTCGTGATGGCGTGACGCA	1024	CGATGTTAGGATTCGGATAGGCCA	
988	TACGCTCACAGAACGCCATACGCC	1025	ATCGGACAAGGACAAGTGGATGGT	
989	CCGGAGAAGTTACGCGGATCGGAC	1026	GCCCGGAGGACAAAGTTCGAGTTA	
990	GCGCCCTCACTGCATTTTTGGTAT	1027	AAATCCGACAAATGGGCACATGGA	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
1028	CAGTTAGGGGATGCGGATGAGTGA	1065	AGTTGTCTCATCCTGTCCGGGACC	
1029	CGGCAGGTGGAGATTCCGACATTG	1066	CTTCTTTGTGCACACTTGCCAGGG	
1030	TAGGGCAGCCAGGTTCACTCATCT	1067	CACCTCATCGGAGCATAGCAACCC	
1031	GCACCGTATTAGCAGTAGGCACGC	1068	ATGCGATCCATGACAAGGGTTGCT	
1032	ACGCATTACAGGTGTGCGAAGGGA	1069	CCCGTGGAGATGATGTGCGGCTTA	
1033	CGTGACTGCACGTGTTCCACAGGG	1070	CCCAATAGACGCCACAGCCAGTGA	
1034	GCTGAACTACCGCCTAAAATCGCG	1071	AACGACCACGACCCTCGCCGAGTA	
1035	AGCACGCCAGGGAGGATCGAGTTA	1072	GGTGCTTTGTCTGAGGCGAGTGAA	
1036	ATGAGGCAAGGAATGGGTCATGC	1073	CTGTCGGCGCTGCTCTCCGAATTT	
1037	GGGTCTCTCGTAATCAAAGGCCGA	1074	CTCGCCGGAGTGTTGTAAGCATTG	
1038	TATCTTGCGCAACGCCTCCATTTA	1075	AGCAATCATGAGAGGTGGCCGGTG	
1039	GGTTACACCTACGGAATCCAGCGG	1076	ATTTGCCACCGGCGACAAAAAGAT	
1040	ACACCGAGTTGGTCCGGTCAATAG	1077	CCGCCCGTGTTGGCATGTCTTTTG	
1041	TCCCAGATTAAACGCTAGCCACCG	1078	ATCGGAAGTGCTGACTGACACACG	
1042	TTGGTGAAACTGGCCCGTCGGAAG	1079	CCTCAGACCCTATCTGGGTTGACG	
1043	CCAGGGGAGTTGACAATGAGGCTG	1080	CTGTGTGGTCTGGTCCGGCTGTTC	
1044	TCTGCGTTATTGGACCGTTTGTCG	1081	GTCCCCATTATCGGTGAGTGCAAC	
1045	TATGGGATGCTAAACCGGCGTACA	1082	ACAGGCACGTAAGTGCTCAATCGG	
1046	CACAGACGTCTGTCGGGCTTGTGT	1083	AGCAAGATAGCGGGAGTGCCCCTA	
1047	AGAATGCCGTTCGCCTACTCCCGT	1084	GGTTTACGCCATGACATCCCGTCA	
1048	CGACGGATAATGCAGGCCTCATGA	1085	GTGCAGGCCTTTGTGTGTGAATCG	
1049	ACCCTCTAAAGCAATAGGTCGGCG	1086	CTTCGAGGGTAGGGCTTCGAAACG	
1050	CACTCACGGCAGAAGCCTGCTTGT	1087	AGTCGACACTTGGGTTTACCACGG	
1051	ATCAGCCCACATATTCTCGGCCGT	1088	ACATAAATCTCGCCCGCTGCACTC	
1052	CAAATCTGGGGTCGTCCTAAACGC	1089	GTTTGGTTTTCCACGGAGGTTTGA	
1053	TGTCGCCCATGGCAGGTTAAATAC	1090	GCAGGAACCAGATTAGTGTCCCGG	
1054	GGGGGCCCATCAATTCATTATCGA	1091	TTTGCTAGAGCGCGGAGCTAAAGC	
1055	GTCGAGCAGCTTTAGTATCGCGGG	1092	CTATGTGGCATCGCTGACATGCTC	
1056	CCGCTAAGCACCGAAGGCTCACAA	1093	CCTAAGTCGGTTTGCAGCTGCTCT	
1057	TAGAATTAGCGAACGGTGATCCCG	1094	GCGTTCGTCCACAGGAACGGAAGG	
1058	CACATGACATTTGGCAAAGGTCCA	1095	TAACCCGCGCCCGAGAAATTGTCT	
1059	TCAACGCACTGGCGATGACTAGAT	1096	TATGGTGCTCAGAGCTGTTGCCAA	
1060	CGGGAAATGTCTTTAGCCGTCGAA	1097	TCATCGACCCACTAACGTCAGGGC	
1061	ATCAGAGCAAATCTGCAGCGGGGA	1098	TGCTCAAGCTACGCGTCACTTCCC	
1062	GGCCTGTTTCTGTCCAACTGGGCT	1099	AGCGGGAAGGTCTGAGGAGGGAAA	
1063	ATTTCACCTCGCTGATCGCTTCCG	1100	CCGATGTAGCACCACCGCAGTGGC	
1064	AGTGACGCCGAGTCGCGAGGGTTA	1101	AAGTTCTGGGAATCACACGGCGCG	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
1102	CACCAGCCTTACGTGCGGCGTTAA	1139	CACGCGTAGGCTGGTGTCATTC	
1103	CGTTTCGCCTCCTCTTCCGAATGC	1140	TCGATCCCGCGATCTGGCCTATTG	
1104	GAGGAGGCCAATAGAGCAGCGCGC	1141	GGAACACTCAACCACCGTGGATCT	
1105	AGTAATCTTGCGGCACACAAGCGG	1142	TCACACCAACTGGCCACAGATG	
1106	TGAGGACAAACCGCGCGTAGGATA	1143	TGTGCTTAGGACACCAGGCAACCC	
1107	TCGTAGAGACGCAGTGCCCATCTC	1144	GACATTTAACCCGACCGATTGTGC	
1108	CGAAGCTACACCCCGAGTGCGGTG	1145	GGCACCGAGCCAGTAGGCCTCTGA	
1109	ATGATGTGATCTTCCCATGGCTGG	1146	CTCAAGCGTGCATGTTGGTAACCA	
1110	TGTACACGTATCGCGTTCGCCTAG	1147	AGGAAGGCCACCATCCAATATTCG	
1111	GGTGTGCTTTTACGCATGTACGCA	1148	TTGGAGCCCTGACTGAACCAAATC	
1112	AGGCGGGATACGTGGATGCTAGCC	1149	TACGAACGCCAAGGTTATGCCAAT	
1113	AAATTAGGCACAGCCCTCCCACAG	1150	CGCACCAGAGTTATGCAGGCTCAA	
1114	ATAAGTTTGGTGAGCCATTCGCGA	1151	CCAGCTTGGACGAGGAAGGATGTG	
1115	CCTATTTCGGCGGACCTCGATGCC	1152	GTCACGCCTTTCAAATGACCCACA	
1116	TTACCGGAATATGCACTTGGCCGC	1153	TGCTAGACCCAGCCCGAGTCTCGG	
1117	CCTCTCGGACGGTCCCTTTGATCG	1154	TATTGTGGCACTTGGGTCCAGTGC	
1118	CAAGCGAATGCTGTATTACGGCCT	1155	CACGTGTGAGACCGGAAGTGCATC	
1119	GCATTTCCCATGCCAGAACGTTGA	1156	AACCTCCAGCAAAACGTCGAGGTT	
1120	GTTTTGGCTAACCGTCCTGCCTTG	1157	GGCAGCCTGATGCTACAGCACCGT	
1121	AGGTTTTGTCCGGGCGAATGATGT	1158	CGGTCCGTCCATCCTTCAGAGTTA	
1122	ATGTCCACGAGTGCGTCCGATATC	1159	CTATTCGCGGACCCTACGCAGTTT	
1123	AGACGCGTACGAGGGTTCTGCGCC	1160	ACCTGTGCAGTCAGCACGAGTGCG	
1124	AATACCGTTCCCATCTGTGCGAGG	1161	GAGAACCACAGGTGGTCCACCCTA	
1125	ACACAAGGTGCCTCATCGAATGGT	1162	CCTCGCTAGAGAAATCCACGGGAT	
1126	GCCGGCAAAATCCTACAAAATCCA	1163	TAACATCGGTGCAAACCGTGGCGC	
1127	CTTATCCCATGTGCCGGTCTGACT	1164	ACCCAGAAGACATGGCATTCGCCT	
1128	GCGGCCATAATGCATAGCACGGAA	1165	AAAAGCGCTGCTCTAACACCGCCG	
1129	TACGGTGCATCGCAGTATGGGTAA	1166	CAAGTCTGTCCATTTCCCAACGGT	
1130	CACCAGATGTCGAGGATCATCGCC	1167	CCGACACATGGTGGGCTTTTTAAG	
1131	GCTCCTACGCCCAAAGAGGTATGG	1168	ACAGACCAGCTTTTTGCGCAGATT	
1132	AGAATATGGGCAGCAGCACTC	1169	CGGCGATCCATTTCACTTCAAAGT	
1133	CTGCAGTCGCACGCAGTAGACCCG	1170	GACGTTATCATGACACAGGTCGCG	
1134	ATGTCCCTGACCGGAATCTTTCCA	1171	GGCAGAGTTGGATCGGATCCTCAA	
1135	TTCGCCACGAGGCATTAGTCCGAC	1172	TTGCTGGCAAACAGCTCCTGAAGA	
1136	ACGTCGTTCCCGAGAATACGGTCT	1173	CCTCAATGCCACCGAATTCGGTAT	
1137	ATCCGCTGGCGCTTTGACGAAGAA	1174	GGAGTTAGCGTGATTAGTCGCCCA	
1138	TGPACCAAATTCTTACCGCGTGGA	1175	GAACTCGACGTGTCACGGAAGGGT	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
1176	CACAAGCGACATTTCTGGTGCACG	1213	GGGGCAGAGATCACGCGTTCCTCT	
1177	CCAGAATGCGTGAATTCGCGTCCT	1214	TTTCGCCCTACGAAGCGAAGTTTC	
1178	CAAGGGAGCCCTGCGAATTAGAGT	1215	TACGGGGTGATGTTAAGCTACGCG	
1179	ATTCTTGCTTCGGACGACTAGCCG	1216	CCTGTGAGTCTGAGATCGCCGTGT	
1180	TGCCACTTTGATTTCCAGATTGCC	1217	ACTGAAGCTGGAACAGGCCATTCG	
1181	GATGGTCGGCAGATAAGTGGTGGG	1218	AGCACTGGTTCACATGGGAGTCCA	
1182	GTTCACACGGGTTGACCAACATGT	1219	TAAGGAAGATCACACTCCCTGCGC	
1183	GATTCAATTGCCCCATTCCTGCAT	1220	CACCACACGCTAAAATTGAAGCCG	
1184	TACCGGAAACTGAGCCTCGTGCTA	1221	GCTGTCGCCAGGATCATGTATCGT	
1185	GGATCTTTACTCAGGGGCAGAGCC	1222	TTCGTTCGTGCACTGGATTCTTGA	
1186	CGCGAGTGCTTTGTTCTGTGTGGA	1223	TCAGCTCTCCTTGTGCTTGCAGTG	
1187	GTCGTCGCGATGGCGTACATCCTT	1224	ACGACGAGGTGAACTTCGTGGGAA	
1188	ACGGGAATCTCCCGAAGTGCGAGC	1225	AGCATTGCCGCGGGCCTTGGTTTA	
1189	GGTCGAAATGAGCCAGCAGCAGAT	1226	CAGAGGGCAGATGTGACTCCTCAA	
1190	CCATTGGAATACTGCGTGCGGCTT	1227	CGATATTTCAGCCTCTCAAACGCG	
1191	GGAAGACTTCGCGAGGGCACAATG	1228	TGCCAGAAATGTTGCCGATTCGAA	
1192	AGGGTGACTTCGAAGGTCCGAACT	1229	TAGGCCACCCGGTGTTCACAATTC	
1193	TCGTCCCTCTGGTGGTCGAATCAC	1230	GAGAGTCAGACCGAGGGACACGAG	
1194	TGTGCAAATTATGCTGGGCGTGAG	1231	GAGGCGATCCTGGAACCACGCAAC	
1195	GTCGCCAACTGTCATGTGTGCCCA	1232	CCAGAGAGGCGGGCTACTGACTCA	
1196	CCTCGAACCCTCAAGACGAAACGA	1233	CACACAGTCCCATCGTACGGCAGT	
1197	CTTCATCACGTGACCTTTGTTGCC	1234	TTACGTTGCGGAAGCGTGCCTCTA	
1198	CCTTCATTCCCAGCAGGATGGCTT	1235	ATGTACACGCTGCAATCGTGTCCC	
1199	CGGGGACCTCAATGGAGCGTCTTA	1236	ACTCGTCGTCGGAAGCGCCCAGGT	
1200	CGCCTCTAGCGCTTGTTACGTCGA	1237	ATGCGAGAGCAGAATTGAGCCGGT	
1201	CTGCCAGACTCAAAACAGGGACGG	1238	AAGTTGGTTCGTATTCACGCGTGC	
1202	CTCCTTACACCGTGTGAGGGAACC	1239	TGGGCTTATCGCCGAAGATTGCTA	
1203	TTTCATGCCATATCGCCTCGCGCA	1240	CAACGGCGAAGACCCAGAATTTTA	
1204	TCTGGCTTTTCCTCGATCAATCGT	1241	AGCGTACGGCGAAAGTCTAGGGAC	
1205	GTCTGACTGTCTGCCCTGTATGCG	1242	ATGCATCCAGCGTCCCCTTGATTA	
1206	GGTTAATGGAACGGCGTTAACGCG	1243	ACCGTCATCAGTCGCAGGCTTCTG	
1207	CTTCGCACTGCGGAATCTCAAGCT	1244	TCTTGACGGCTGGGCATGATTGGA	
1208	TGCCAGAGGCGTAGGAGTCCTGGA	1245	TTAACATTCGGACCCAGGACCTGG	
1209	GACGGGCGAGCCAGTATTAACTCA	1246	TGGTGTCGAACTCCCTTGCGTGTT	
1210	GACCTCCAAAGTCAGTCTTGGCGG	1247	TACTCCAGTCGCCTGCGCGCAAAC	
1211	CGTTAGAGCATGACCGAACACGTC	1248	CGCAATGCCGTAAGCATGCCAAGC	
1212	GTGGGCTCAAAAATTGGGTACGCC	1249	AGTCCGCGCGAAATACGAACAGTA	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
1250	ATGTTGCACGCGCACTGTATCACA	1287	TGGGGACGAATCCGAATGTAGTGA	
1251	GGGATCAGCATCATTGGAAAGGAG	1288	GTCATGTAATTGCATCCCACGGGT	
1252	ATCGCCTAACTACCCGCGGCGTGC	1289	CTTTGCGCGGTGGTCAATAAAAAG	
1253	TGGCCAGGGAACACAAGCTCGGTA	1290	CACTCGAGATTCAATGGGCATGGT	
1254	AAACATGGGTCGCGTCTGAGATCA	1291	CTCGGGGATGCCCTCTTGGCATTA	
1255	GCGAGAGCTGCGATTCCCTTTTAG	1292	CGAAACGTGGTGCAGAAACCTGAA	
1256	CCGGCCAAACAAGAGACGAGCGGA	1293	GGAGTTCACGAGTCGAGCAGTCGC	
1257	AATGGGGCACAGTCTCGCTTGACA	1294	AGCCGTTTTCAAAGATCTCGACGA	
1258	TGTCTCGGGCCTTCAGGACACACT	1295	TGGCTGGACATTGTCTGCAATGCA	
1259	TCCACCTTCATTAAGTGGTTCGGC	1296	ATCGGCTGCCTCAGTCCCTAATTT	
1260	GCTTCGGAATCATCCACCTGTCAT	1297	CCAGCATGGAGTTAAGTGAGCGCG	
1261	GAGCCGATGGGCTATCGTCGTCGG	1298	TTCATATTTACGAATGCCGGGTGC	
1262	CACGAATTACGCACGCACAGAGGA	1299	CGAAATCGCACAGGAATTCGCGTC	
1263	GCTGTGACGCTCCCCTCAACTAGG	1300	GGCAATTTCGGGACACTCGTTTCA	
1264	CGCTCTGAAAACGCGGGCTACGTT	1301	TTTGTGATTGGGGGTATAACCCGA	
1265	GAGTGCTGGACACCGTAGCCAGGA	1302	CCCAGCTAATCCAGCTTGGGCTGT	
1266	CCAACCCCAGTGTAGGCGCAAATG	1303	AAAATCGTTTGGCTGTAACGTCGC	
1267	GAAGTAGGGGATGTTGGCCGGCGG	1304	AGGAGATTCATCGACTTCCGGGAA	
1268	CAACGTGGGCACCTGTTTTAGCAG	1305	GCACGGGGTCTCAATGCTTAGGGT	
1269	CTAGCTGCGATCCGAACCTCTACG	1306	GCGCAACAAGTAGCCTACCGAGGC	
1270	CATTGAACCATCAGCCAAGCTGCG	1307	TAGCAGGCTGATGCCGTCTACACA	
1271	AGACTGGCAATTTTTCGAGGCCAA	1308	GCAAGCGGCGATCGTACAACTTGT	
1272	CTGGCCGTCCATGAGTTGGTCCAG	1309	GCACCTCTGGTAAGCCTGAAAGGG	
1273	CATGCTGAAACACGGGATTGCCAT	1310	CGAGGGCGGTGAGTGCATACCGTG	
1274	CGATATGTAAGACAGCCGTCGCAA	1311	GGATTAACCGGAACTGCCCTTCTG	
1275	AGCGTAACCTACTGGGAAGGCACC	1312	GATATTGGGTCCGGCGCGCATTAC	
1276	GTGCTCGTGGCACGTACAGGCCTT	1313	GGCCTTTAATCTCCGGTCGCAATG	
1277	GTTCGAACCCCGCGATGTTAAATG	1314	AACCTTAGTGCGGCTAGGTGGGGT	
1278	GTTGTTAGGAGGCTCGAGGCTGCT	1315	CACGCTGACGCCAGTGTGGTGAGG	
1279	ACTGGTGCTACGCGGGATATTTGA	1316	GGTTCCCTTGACCCACCGAATTGA	
1280	CTGGGAGCTATCCTCAGCCGAATC	1317	TTCTGACAACATCGACCCTGGCTC	
1281	GAACTCGCCGCTGCCGAAGGGTAG	1318	GCGAGCGAAGATAATCCCCAAACT	
1282	TTCGATCGAGGAGCAAGGAGAGTC	1319	GTACTCTGTGCAACGGTCCCGAGT	
1283	GGGGAAAATTGAGGCCTTAGCCAT	1320	ACACGCCAGGAACAGTGTCTGTGA	
1284	CTAAGGTCAAAGCGCTGTCGCCAG	1321	AAGGGAATTTAGCGCGCGTGACTT	
1285	GTGAGGCTTACCCCGTGCTCTTGG	1322	TGACGTACGCGTTTTAAGTGGGGA	
1286	CCGTAGCGGTGCTCGACCAGGTTC	1323	CTTAGAGGGACGAGGCCATGAATG	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
1324	GGACGACTCCGCAAAAAAGGTCGT	1361	CCTTCCTGGTACTTTGTGGGCGAC	
1325	TCAATCCCAACATCCAAAGCCTCA	1362	CTACATGCTCACCCCACCAGAGTG	
1326	GCACTGGTCTACCAAGCTTGTCCC	1363	ATTTTCAGAATAGCCCCGCCTCGA	
1327	ACTTGTCGGAAACGAGACCGAGCA	1364	CAATTGCTACGTTGACGCCCTCTG	
1328	TCAGGAAAGGCCTAAAGGCGAAAG	1365	CTGTCGCCTAATCCTCGGTGGCCG	
1329	GGAATGTAGTCAAGGAGGACGGGG	1366	TTTGTGTTGGCTCCGTACATTGGA	
1330	GCACGTGGTAAATGAATTGGCGAG	1367	ACGTGACGGGAAGGTGGTTGAATC	
1331	GATCATCAGGGGTTATGCGTCGCG	1368	AGTTCTTGCGTTGCACGAAACAGA	
1332	CTCACTCATTCTGATTGCCCGCGG	1369	GCTCGCCGCGCGTCTTTATGTCTG	
1333	GGGGTGATCTCTCGAACGTCACCC	1370	ATGAACATCGCGAGGCAAGCCTTT	
1334	AAGGTTGCTGCTAGCGTACCTCGA	1371	CAACCGCGCCCACCAACATTAAGG	
1335	TATAGATCGCCCAACAGGCAGGAG	1372	TGATCGAGGACGGCTTGGTAGCCT	
1336	GTTTGGACCTGTTGGGAGTGGGCA	1373	GGAGGCATGCCTTCCGAGAGCAAC	
1337	ATTGGGGAAAACCCGGTCTCAAGG	1374	CACCGATCCTCAACGCAATTGCTA	
1338	TCGACGATAAAGTGCTCACGGGAC	1375	GGCCATGAATTGGGAAATCCATGT	
1339	CGATAGAATTCAATGCAGGGCGGA	1376	CTGTTCCAGGCGTAACCAGCGGGC	
1340	CGGTTCGCTACGGCGGCTGGTTTC	1377	TATGTCTGGCTCGCCATCAGAAGA	
1341	CCAGGTTTCGGTTAGTCGCGCTAG	1378	GGAGTGACCAGCACAAGCATCGAG	
1342	ACGACCTTACACTCGGATCCGACG	1379	TCGGACTGGAAGTAACTCGCATGA	
1343	TCGCGTTAAATGGACCAAGGGGCC	1380	GTAGGGTCAAGCACGATTGAAGCC	
1344	CCAGAAAGAAAATGGCGCCCGGAT	1381	CACCGGCGGTTCGACTAACGTGAC	
1345	GATACATCGCCGCCTGCTAGGCAC	1382	GAATGACGCGCAGTGCATTTGAAC	
1346	GAGATCACACTCGGAAACCGGATG	1383	GTGCTCGTCTAACCGCGGATAGAG	
1347	ACTTCGCGGAAAAAGGCTGGCATT	1384	GCGGACCTGGGTTAATTGACGCGC	
1348	CCGAGCTGCACGAGCACAAAGT	1385	TTTTTGATGTTGCGCACCGGGCTA	
1349	TTCCACAAGGCGGCATAGTGAGGC	1386	TTGCGTCAGCGCATCTGCTCGATT	
1350	AGCAAACTGGAATCCGGAAAAACC	1387	ATGAGCACGCCAGTTCGTTCCTTT	
1351	CGCTATGTCGCAGCATGCATTTAC	1388	TCAACGGTAAAGAATCGCCCCGCA	
1352	AGTCACGCCCAACGTCGGTTCTTT	1389	CGCGATTGACTGAACCACACCTCT	
1353	AGTGGGCGCACTTGGCCTTAAATA	1390	GCGTGXAAGATGACGGCCGGTATA	
1354	ACTTGCAACTTCGGCCGTTTGACT	1391	CATGATTCCACCTCGATCGGCTAG	
1355	CAAACATCAGGTTCATGCCGTACG	1392	CTACGACAAAGCAACCGTGCAAAA	
1356	AGCGTGACCACCCTACAATGGCAA	1393	ATGCCGTGTTCATCTTGATGGTCC	
1357	GCAGGCATCCGGCAGAGATGTCTC	1394	TTCGTGGAGGGACTTTGGAGATCC	
1358	GAGCGGCTAAGAGGCCAGACCAAA	1395	GAAGCGCCGTAACGTACACCGTCG	
1359	CACAGAACAGGGTGTTTCCCGCTA	1396	AGCGTGCGCTTGGCTATAAGGCTA	
1360	ACTTTGCAGAAGGCCCAACACAAG	1397	ACAGTCAGGAGTAACGCCGCTCAA	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-Continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
1399	ACTGTGTCGCAATCAACCCGCAAA	1436	TCGTCACTGTTAGAGAGGCCTCCG	
1400	TGCAGCCAATGCGGAACTTAGAGG	1437	AGTGTCGTGAGCCCTAGCGGCGCT	
1401	CCCGCTATCCCGGTCTTGCAGTTC	1438	AGGACGCAGGGATTCAAGTGCAAC	
1402	GAGGGCGCAACATATGCAGTGCTG	1439	ACCGATGCGCGGTCGGTCTCATAC	
1403	CGTACGGACATCGATGACGCAACG	1440	GGCAGAGGGTTAGGGGGTTTTTTT	
1404	AGTCTCCCGAGAAACGCATAAGGC	1441	GGCAAAGGGTGTTTATGGGAGACC	
1405	AGGAAGTGGATGAACGCGGCTGCA	1442	ACAAGGCTTCGGCTGGCAGAATAC	
1406	GGGTTGCTCACCCTCGTCATCAGG	1443	CATATCCGTTCCTATCGCCAGACG	
1407	TAGGAATGCGAGTTCCGGCGGTAA	1444	AAGCCTTTGTGGCCAAGGCCGCGT	
1408	CTCCTCACTTCCAAGCTGCGGATA	1445	CCGAACCATGGCTTTATCCAGTGT	
1409	TCAATAGCACCTAGCATGCTCCCG	1446	GTTCAGCAGTAGCTCCCTCCTCGA	
1410	TGATTCCTGCGCTTTCACAGGTCG	1447	GCGCAGTGACACCATGATGC1TVC	
1411	GTATGTGCGGGATGGAAATCACGC	1448	ACGATCCATTTTGCCAGCATGCAA	
1412	TACGGCAACTGTCGATACGAGGGC	1449	TCCCTTCATTTCGGGTTTTTAGCC	
1413	GGTTCCCTATCCAGCACTCCTCGC	1450	TCTTCTTGCCCACATTOCCTTTTG	
1414	ATAAGCGCGCCACAGGTATGTACC	1451	TGCCTTTTGATTGGTGGTCACGGT	
1415	GAAAGTCGCCAACAGACTCGAGCA	1452	GACCCTCACGGTCATCAGAGGGAG	
1416	CGCTAATGCCTCATAGGCGTGTGC	1453	CCGTTCAACACAGTGATACACGCG	
1417	ATCCCCGCCGCACGAAGTACCAAG	1454	CACCAGGGGATAGGTGCGGTACGC	
1418	GACGCTGCTGATGGCTTTATCGAT	1455	GGTCGGAACTGATCTGTGCGATCC	
1419	CTCTCCCCGTCGCTTCAGAGATTA	1456	TGCTCCTTCCTAGGGTCATCCGTG	
1420	TCATGTGGGCCGTCGTATCAGTTT	1457	GTGGACTTTGACGCCGGCTACCGC	
1421	GGCCTGAAGGTGAATGGTTACGTG	1458	CTGATCTGTCGGCGGTTACTTGCC	
1422	AGCCTCCAAAGCCGGTAGAGTTCC	1459	AGAGGAGCGGAAAAAACCGGACGA	
1423	TTGTCGTAGGCGCTCACCTTAGGA	1460	GCGACGAAGATCCAGCAAGCTC	
1424	GCCTGAGTCCGGGTCGGGAAAGAA	1461	GGGACTTCCAGCTGAGGGACGAAA	
1425	GGCACTATACCGGTTCTGGACGCG	1462	GGCGCACTCCAATACCCACTGTTT	
1426	CCGTGTATACGGAAAGGTACGCCA	1463	GCGCTTGGAGACTGTCAGGACGTG	
1427	CCCAAGGCAAGTGTGCATCAGTCC	1464	CAAACCGCTGGTTTCTCCACCTGT	
1428	GGAGTGCATCATGGCCAAATCTGG	1465	GCGATTGCTTGGGATCGGTGACTA	
1429	CCATGTTACGTCTGCGCACCACAG	1466	CTCAGCGACATTTTTCTGGTGGCG	
1430	GGCGTTGAGCTTAAAAGCAGCGAC	1467	CAGCGGCGTCGTTTACTCAGGACT	
1431	TTGGCACTCTGCAAGATACGTGGG	1468	GACAGCCGTGAACGCTCAGCCGTT	
1432	GATCTGCACTGCAAGGTCTTGGGG	1469	GGGCCGTAGAGGCATCGGGTAAAG	
1433	CGATCAACTTGCGGCCATTCCTGC	1470	CGCCGCTCACCTGCTTAAAGCATT	
1434	CGGCTGGGGTCACAGAAACGAGTA	1471	TGCCAAATCGCAACTCTTGAGACA	
1435	GCGGCTAGTTGTACCTAGCGGCTG	1472	CCCCGATCGGGTGTAATTCTCCCT	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
1473	CAAGGTCCAGGTGACGCAACCACT	1510	CTCTCGCCCACATAACTGCACAAA	
1474	CGAGCCTTCAGTGGTATGCATGCG	1511	AAACCTGCCTAAGCAAGCACTGGA	
1475	CAGCAGCGTGCCCATCTCGACTTA	1512	TTCCATATTGTACCCCGCGCATGC	
1476	CGGACCAAGATGGCAGTAATCCAG	1513	TGCTTGCGATATCACGATACTGCG	
1477	CTACCACGCTCTGCGCGGGCTGTA	1514	TTAGTGTTCGAGCCTTGAGCCGGC	
1478	ACGTGGTTAGGCATGAGCTGCGTC	1515	CTTGTTGCGCGAGTCCGTCTGGGA	
1479	CGACATATCCGACATGACCGGATG	1516	GTCAGCTGCCTGCTGGTGCTCTTC	
1480	GCGCCCAGGCTGTGTTAGAAAATA	1517	CATCCCTCGAGGTGTAGGCAACAC	
1481	AGCTGGGACTCCGGACCTTGAGTG	1518	CAGATGCACTCCGACGGGATTCAG	
1482	CGGTCGTAACCGCTGCTACAACTT	1519	CTGAGCCTCGCGAAGCTGTGGCAT	
1483	TCGTTCCTCTGGAACAATTCAGCA	1520	GCTATGCCACGCCGCAGATAGAGC	
1484	CGGCATCTCCGGACAAAGGTTAAC	1521	AACACCAACCATACCGTCCGTTCA	
1485	TATCTTGTCGAGCGCCACTCGGAG	1522	GCCCAGAGCTAAAGCATGTCTGGG	
1486	TGCAAGGGAGAAAGCCCCATGAGC	1523	AATGCTGCAATGCTAGCGTCGCTA	
1487	ACTGCATAGCCCAGATCCGCTTGC	1524	TCCGGACCCACTATCCAATCCCCA	
1488	TGTGATTCAGTCGAAGCCAAGGCCG	1525	TAAGACCATGTGGCACCAAGGTGC	
1489	CATCCATCTACAATTCGGGCCAGT	1526	ACAGCCACACACACGCGCCCACTA	
1490	ATGAGCCGTTCAGAAAGCCAAAGA	1527	TAGAACCGAGCACGGCGCCTTGTA	
1491	ACACTGGAATTGCTAGACCCCGCG	1528	TTCGAGTAAGCTGGCAGGACCACT	
1492	CTGAGCTGCGTGGGACAACTCCGC	1529	CTTTCGCAGGTTCGCAGACAATCC	
1493	CAGCTACTAGGGCGCGATGTACCC	1530	TACGTCCTGTGCTGTTGACACCGG	
1494	ATAATGATGGGACGAGAAGGCCCC	1531	GTTCGGGTCAATGTTTCGGGGAGA	
1495	CGACCGAGTGTTACGACATGGTGC	1532	CCCTGTTGTGAAGGGGTTTTGTGA	
1496	TGCAGTACCCGCCGCTCCACTAGT	1533	GGCAGATTGGTGAACCCCAGATAA	
1497	ATGCTAGCGCGCCTGTCAACGTAC	1534	CCCTCGGTGTGTTCAAGCCAAATC	
1498	AGACTCACTGCCGGCTGATCAAAT	1535	CCCGCGAACATTTGAACAGCTTAA	
1499	GCCTGGTGCGAAGATAGGGATTCC	1536	CCGTGTCAGTTGCTCCCTGGCACG	
1500	GGAAAGTTGGCGGATCCGAGCACT	1537	TCCGTCTCAGCCGCCTCCCTATCC	
1501	GGCAGTGAGCAATGTGTGACGAGG	1538	ATAGCTGGGTCACCACAGGCGGTC	
1502	TGAGGTCCTCCCGGCGGACTACGA	1539	ATAGGCAAGCGGTGTAGCACAGCG	
1503	CTCGCCTTAGATCGTGGTTCCGCA	1540	TTAGAAGCCGGTCTGGATTTGCGT	
1504	GTCGAGGAATATCATCGCAGCCAG	1541	TGCCGACCTTTACCAGGATCCTCG	
1505	GCGAATGCAACGAGACAAGAAGGA	1542	GCCCACACTATAACCAAGCTGGCA	
1506	TTCGCCACCAAGTCGGCATTTGTT	1543	TTGCGCCACTAGTACGGATCTCAA	
1507	CGGTGGCTGACACTTGCCGGATTC	1544	CTTGCAGTTTATGCTGACCCGTCC	
1508	CAAGGAGCAATCAGATGGTCGGAG	1545	TGCCTCCAAATTACTTACCGCCGT	
1509	GTGACCCGGTCCGTTCTAGCTGTG	1546	CCCGTATGCGGAAGCTATGGGCTA	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
1547	TCGTTCAACCCCACACTTCAGTTG	1584	CCTCCATTTTAGCGCGTTGCCAAT	
1548	CAATGTGGGGGACATTTCAAGGTT	1585	TTCTTAGGATCCGCGCACTCTTGG	
1549	TAGCGTCGCACAAATGGCTGACCG	1586	GTCGAAGGTGTCTACCGTGCGCAG	
1550	GGTGGCTTCGTGACAATATCGGCC	1587	GTCACTCGGCGGCCCAATCACTCG	
1551	CAGCGGCGTCCGAAATTGGCTCTC	1588	TCTCGGTCACCCGTCTTGACCCTT	
1552	GGCTTGCTCTCGTTTTTGATTGCA	1589	GCCCTCGACGAACTCATCCTGAAC	
1553	ATGCGAGGAGGACACGACCGTTCC	1590	TCCGGCGTACTCTGACACGGCGAT	
1554	CCTGTTCACTACGACCCACGGGAA	1591	AGCCAAATGCTTTCGTGGTTCGGA	
1555	GTGCCACGGAGTGCGACTGTTGCT	1592	ACTCCACGCCGCATGTTGCTGTGA	
1556	ACACATCCAAGTCTGACGATGGCC	1593	GCTTCGAGTCGGTGGCATCTGTAT	
1557	CAGCCCGAAAGGAAAGCCTCCGTG	1594	GGTCTTGGGCCATCGACTTGCTGC	
1558	AACTGAATGTAGGTGGGCCCCTGT	1595	GGTATCGGACTGCACTAAGGGCAA	
1559	ATTTTCGACGATAAGCTGGCCGGT	1596	AGCCCATGCGTTCCGGATGATTTG	
1560	TGAGGGAGAACCCGAAATCTGCTT	1597	GCCAGGGTTAAAAGTGATGGGCTC	
1561	GGCGACTACATCCCCAATTGCTTG	1598	GACGACGTGCTGGCTACGAAGGGG	
1562	GCAGACGCGGCCTTCCATACTTTT	1599	TCCTATTGACCGTGCATCGTGATC	
1563	ACAACCACATGACGTGTAGCTGCA	1600	ACCCGCCTCGACTCCACAACTAAA	
1564	CTGCTGGGCGCGCAAAGCTTGTTG	1601	GATGTGGATCACGACCTGCCAGTA	
1565	AAGCCTTCTTTGGCTTGCTCCGCT	1602	GTGCCATTGCCACCCATAATGCGT	
1566	TACCTGCTGCCTGGAGCAAGGCAT	1603	TTAGCCTGTGCACCCAGTCAGGAG	
1567	GACGCCGCAGCCATGAGTGAGTGT	1604	TCCGATGGGAGAGGCTGATCTCAC	
1568	AGTTGGCCGCTTATTTTGCTCACC	1605	CACTACTGAAGTGGCCTGGCGCTG	
1569	AGGCGCACGGAGAACATTTGCCAA	1606	TGCGGCCATAGCGATGTGATAGAT	
1570	CCAGGCGCCTTCGACAGATCCTCA	1607	GATTGCGCTTAACGGAGATGCACG	
1571	GTGTCCCCTCCAGCTAGCCAGTTT	1608	TCACGTTTGACAACGCCAAGCATT	
1572	GACAACAAGCCAAGGTGACACGTC	1609	GCATTGTTTGCTAAAGGCGGCATT	
1573	CTACACCGCTCGTGACTCGGCAAA	1610	AGTCGCTCTACGCGTGCAACGCTG	
1574	TGGTGCCATCAAAGCACGTTGTAC	1611	TAGCTCCATGGAGGTCCGAAAGGG	
1575	ACAATGCGTGTTGCGAAACGCATA	1612	GACCGGTTGGACCTCACTGGCTTC	
1576	TTGTCCAGCCATTGTATTTTGCGC	1613	AAGCCGGACAGTCAATGTGCGTAT	
1577	ACGAGAGATAGCGGACTCCTCCGA	1614	TGCCTCGCTGAGTTCTTCACCGTG	
1578	AGCTTTGTCGTCAGGCGAGCTCTT	1615	TCGTAGACCTTGCTTTTGGGCTCA	
1579	GACAGTCGGCGTGCAGTTTGTTGT	1616	ACCGCTATGCGCCCTACAAAGCAT	
1580	AGCTAGCGACGGCCAACTCACGTA	1617	TAGCGTCACCGTAGCTTGGGGCAG	
1581	CTCCTGTTCGGGGCCGTTACTGGT	1618	CTCTCAGCAACTGATGGCACCGGA	
1582	ACTGACCGACGCAGTGCCACATAG	1619	AAAGGAAATGTGGTGCTGGTCGGC	
1583	AGGTAGGGTCTGGTTTGACTCGCA	1620	CCGGCTTAGATGGAGAACAAGTGC	

TABLE 1-continued

TABLE 1-continued

TABLE 1-Continued		TABLE 1-Continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
1621	AAGTAAATCGCCTCGCCCAAACCG	1658	CATGCATCCGATTAAGGGGATCAC	
1622	TGGGCTGTTCAGCCTACCGGACGT	1659	ATTGCGGGAGTCCCTAGCTTTCTG	
1623	GTTTCGGTTCAGCCATGGGCCTAC	1660	GTGTGGAAGATGCAATTGGAACGG	
1624	GGCCAACATTTCTAGGGGAGTGCC	1661	ATACAACGGTAGGTGACAGGGGCG	
1625	TTCTTCGTTGGGATTGTCCTCACC	1662	GCCGTGGGAGTAAGGGTACAAAGG	
1626	TGCACATTGGGGTACGGATCTGAC	1663	GCACGTAGGTCGGCTACTACTCGG	
1627	GGCAGTTAGACGGCAAACTGCAGG	1664	ACTGTGATCTCTTGGGCAAAGGGC	
1628	CGCGTCAGGCTATGAATGGCTCTT	1665	CATGCCTGAACAATCTCGCATCCC	
1629	GCTGAATGCAAACCTCGGAGCCAT	1666	GAGCCTGGCTCCACAGCTGTGCTC	
1630	CGCTCTGGCGGATTCATTGTTTTC	1667	CTTTCGATACCATCGTTGGCGATC	
1631	TTTTCAATCAACCCTCCGGACGTA	1668	CCCGGAGGTGAGGCATTGAATATG	
1632	GTGGTGGAGTCTGAAGCACGACAG	1669	CTCATTCAGCTAAAAGCGGCTGGA	
1633	AAACAGGTCCGGATGATGTCTGGA	1670	GAAATGCCCTGGGGACTTTTTGCC	
1634	GTACCGCGTGTACGCCACCGTTAG	1671	TTTGCCTTCACAACAGACGCAGCA	
1635	TCCAACCTACATTTGCGGAAGGAA	1672	AAATCCCAAGACGTCGGGGCGTAT	
1636	GACGTACCGTCGTCCCGTGAGTTG	1673	CAACGGGCGTAGCTAAACCGTAA	
1637	GGCAATCCTACAACCGACGCTGAT	1674	GGCCAACGACAATGCGAAACCTTC	
1638	GGCGGCTGCAGGGTCTACATCGAG	1675	GACATCACGCAAAATCTCAGCGCA	
1639	ATACTACGCTGCAGCTGCGCGGC	1676	ACGTTCCGTCCACAACCGTATGTT	
1640	GGATCGCAATCCCTCCGATGACGA	1677	GCTCATAGGTCTTCCGTAGCCCGT	
1641	TGGCCTTGCACGGGAGCCGAATCT	1678	GAAACGAGTCTCTCGCGCCCTAGA	
1642	AGGTGCCGACGAAACGACGAATAT	1679	CGGGACAGAAGCAAGTTACATCGG	
1643	GCTGTTTCACCGTCGTCGTTGTTG	1680	TGACCGCTCGATACCAGGAGGGTG	
1644	CGGTCCCAATGTTACAACCCAGAC	1681	CTGGCAATAAAGACCTTCCGACCA	
1645	GCAATTCCAGCCACTTTTGACCAA	1682	TGCGCGACGTCATGTTGGTGATTA	
1646	ACGGGCGAAAGCTCGGTACGGATA	1683	GTTGGTTGTGGGAACACCCCGCT	
1647	CGACCCGACTTTTGCTTTCGAGTG	1684	TGTGGGTTCGGAAACACAGGAAGT	
1648	AATTCAGTGTTTGCGTCATGGTCG	1685	GGAAAAAACGGCAATTAGCCGAGT	
1649	CCTGTATGAGGTTCTGGGTCGGCT	1686	TGGTGCGGAGTGCCCTCTATTGGG	
1650	TGGCATACTTGGTGCAAACCCCCT	1687	AACCAACAGGCTGCAGCCCAGACT	
1651	TCGCCAGTACAGAAACATGCGGGC	1688	AAACAGATCCATCTGCACGCCAGG	
1652	CCCGCTGTTGCTCTCATCGTGGAG	1689	GGAATACCGCGGCGATTATGGCTT	
1653	GCCACAATCTGACCCTGGGAATCA	1690	TACTGTTCGCGGCAAACCGTCACT	
1654	GCTCAGTCTCGGAAGTTTCGGCTA	1691	GATCTCTCGTGGAGCACGTTTTCC	
1655	CTTCACGGGCCAACGACGGTCGAG	1692	GGCATAGCAAACCTTGACCTCCAA	
1656	CGACAGTTCCGTCCGTCTTGAGGA	1693	ATCTGGGATTCGCGAGCCAATATC	
1657	ACGGAGACGCAGTCGAAACGTCCC	1694	CGATCAGGATATCATTTACGCCCG	

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TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
1695	ACGGTACCGAAACGGTCTCAGCGT	1732	GCGCGAGTGTCATGATGTTCACGT	
1696	CTCCCATACCTGCGTTCTTACCGA	1733	GACATTCGTGACTTGGTCGTCCGC	
1697	GCACGAGAACCTAATTGTCGCACA	1734	TCATTAGTGCAGGCACCGATCAAG	
1698	GCCACACGATCAAGACAGCGCATG	1735	GAGTTGTGCGGAGTCATCGGAGTC	
1699	CCCGTTAACTCACGAGCGGTCAAT	1736	GCCTTTACAGATTTGGCGGGCTAT	
1700	AGAGAAGGTCATTGCCTGTCGGTG	1737	ATGGCGTTTGCGAAGTCGATACAG	
1701	CGGGCCCTCTTAAAGTAGAGCAGG	1738	TGCATCGGCCTCAATCAGAGAACT	
1702	ACATCGCGTCCGAGGGAGTTAGCG	1739	ACAATCATGGCAATCTGGCAAATG	
1703	AATGCCTAATCGAGCCAGCGGATC	1740	GACGTGGAAGAGTGCAGATCAGCA	
1704	CTCGATCTTTTAAACCGGCGCTT	1741	AGGGCAGGGACGGACAGTAAGTC	
1705	CGTTCCTGGAAGGCAGGGTCTCAC	1742	GCATAGGGCGAATCTAGTACGGGC	
1706	CCTGTGCTTACTATCGGCGATCCA	1743	TCCGGCGCATCCTCATTAGCAACT	
1707	GTTAGTCGCCCTATTGGCCTGGTT	1744	TGGCCGCTTCCACTAATATTGGAC	
1708	CCGGTGAGATGACTGTAAATGCCA	1745	CCGGCGGACGGCTCTTGTCAATGA	
1709	CGTGGTTTAAAACATCGCGCTTCG	1746	CGAGCAACCCAAAAGGAAGCAGTA	
1710	TAAGACGCAGAAGATGGGGTCCAC	1747	GCGTATGATTCGGCAATCCGCCAG	
1711	CACCACAGCTTCTTTGTTCGACCC	1748	AGTACCGCTACAACGCTGGTTCGC	
1712	TCGGGTCCGTACCACCACTTTTGC	1749	GGGCAGGCCAGGTCCACCTGAGAA	
1713	CCAAGCCCCGAGTACCGAAGATTT	1750	CCACTTCTGTGACCGAACCGTGCT	
1714	TCCGTGATATGGTCGTGGCGCGGT	1751	CCTGGTACCAGGCAGCAGTTGATT	
1715	TGTCTGTGTCATGGCACCTCGCAT	1752	TTAGGGTACCGTCGAGAGACGCCA	
1716	AGGACTGCACTGTGCACGTCTGAT	1753	GGTTGCTTGTGCGCGTGAGGTAGT	
1717	CCATCCTCATGTACAGCGCCGCTG	1754	TGCTTCGACCGATGAAACTCGAAG	
1718	GTACCCGCGCCTTCCTCGACACAG	1755	TGCCACCCATACTATGCCCAGTGG	
1719	ACGGGTCCTGGTCGACTAAGGCTT	1756	TGTGCGGCAACGCGTGAAGACGTT	
1720	CGTATCGAAGGCGTGTACAACCGG	1757	TGAGAGAAGCTGGCCTCGGATCAG	
1721	TGCCCGCCCTTTATGCAACGCTCA	1758	TATTGCGAATTOGAGTACGTGCCC	
1722	AAACTTACGAGACGGCGGCTGCCA	1759	CGAGAGGGTTCCCCAGTGATCGA	
1723	AAGTCTGACAAACGGAACGGGTGT	1760	TGCCTGGGGTGTCGTTCTAATTCT	
1724	TAAGCGCAGACCAAAGTATGCGGC	1761	GTGCGTCATTGTGGGTCATCCCAA	
1725	GCAGTTTTTCAGATCCTCCGCAAA	1762	AGGGCTCCCAGCATACCAACGTTG	
1726	TCGGAAGCATTTACGCGATCTCAG	1763	AACTAGCCGCACCTTTGTGCAGAG	
1727	CACAGAAACGGTTGAACGAACGCC	1764	TTAGCCCAGCCCTTCAATGGGAAC	
1728	GCATGCTCAGATGGTCGTGCTCAC	1765	CGGCCTCGGTTGTACGGGTAGTCT	
1729	AAGGATTCTCGCTTCCGGCATGAT	1766	TCTTTGAGGCGCGGACCCGCATAT	
1730	GGTGGGGTAGCGCTGGTATGAAAA	1767	GATGGTTCGCCCTTGTGTCGCAGC	
1731	ATTATTACGGGACCGAACCAACGG	1768	GAGATTCAATACAGGCCGCGGGTC	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
1769	AGGGCGAAGGAAGGTTCCGTTTTT	1806	CAAAACTGACGGGTATGGGAGCGC	
1770	CTCGACCCCTGCCACTACTGGTTC	1807	AGGTGTCGCTGGAACCCGACTTGT	
1771	TGTTCCGCGGTCTACGCATTACTG	1808	CTTCCAAAAGCGCAATTGGCTTTG	
1772	GAGACGACGTCCTACACCCGCTAA	1809	TCGGGCTTCTCGCAATTCTGTCAG	
1773	AGATTGCGACAGCGACACGTGATT	1810	GCCAAAAGAATGCGCTGGGTAGGT	
1774	GATACCGTTGGGCATTTCTCGGTA	1811	TGGTGCCCGCACCGAGAGACTGTA	
1775	GATTGGGAGGCATTCAGCGACGGA	1812	CGAGGCCGTAGTGGGGACTGCTCT	
1776	AGGAGGAAACGAGGGCGTAGGTTC	1813	CGATGTGCGCATAGAGGGGACTTT	
1777	GCCAAACAACGTCTGACGCCTAGC	1814	TGTGCAATCGGCCTTCTCAGAGCC	
1778	TTTAATGCGGAAAGGATGCACGCG	1815	GATCACCTGGACCGCTACCGTTTT	
1779	TTATCGGCCGTTAAAATGGGATGG	1816	ATGGGGAGTTAAGGACCCTGCACC	
1780	CCTTGGATTCGTTCATCGCTAGCA	1817	CATTGTGGACAGCCAATGGTGGCT	
1781	AAGTGAACGTGCAGTGGTCTTCGA	1818	CCATCACCATGCCACGGTAAGATC	
1782	TCCTTACCCCTCGTTCAAACGCCT	1819	GCACCCGTGTCGTTGGTTAGCAAG	
1783	ATTCCTGAACCATGCATGGCCTGT	1820	GGAGTGGGTTCCGCGAATTCACTG	
1784	AGCGAGACGCTCGATCACGAACTA	1821	GGGGATTTCCTTTCGCAGGCTCGA	
1785	GCTGGTCTGGCTCGCTGTTTAGAA	1822	CATTGATCATGTGCACTTGCACCA	
1786	CGTGCGCGGCATAAAGATAGGTCT	1823	AGCAGCGCTGCGCTTGTTTCGGAT	
1787	TCTGGCACTCACATCGGACAGTCT	1824	CGAGTAACGCGGTTGCTTTGCGAA	
1788	ACCATTGGAGGACCACAGAGCTCC	1825	TGGCCTGGAACATAGGTGGAACTC	
1789	TCCAGGGTCGGAGTACATGGCGGG	1826	CGCACACCAAGCGTTTATTGAGAA	
1790	ATATGCCGTCGGATCGTACACGCA	1827	TCACCTTCACAGTGGGCATACAGC	
1791	TGCTGGCGTCAACACTTCCCGATT	1828	CAAATATCCCTGAGCCCTCGAGCT	
1792	CAGGGCGGTGCGGTGAACTAGCCA	1829	GGGAGCTGGTGAGCAGATGTAACG	
1793	CATGGACTGCCGTACATCAGCTGG	1830	AGGATTGCTTTTGCGTTATGCGGA	
1794	CCGGCCATACGCTGGCAAGATTAC	1831	ATCGTTTGGGCGCTACGCAATTGT	
1795	AGCGGACACCTGTACTCTCCTCCA	1832	CCGATTTGTCCCAAATGCAACGTT	
1796	GGAGCCACACCAGTCGAAGATGGT	1833	AAGGGTCAAGCTCATGGAGCGGAA	
1797	CGCCACCGGAAATTGAAAAGACTG	1834	TCTGACGTCGTTCAAGGGCTCGCT	
1798	TGAAACGGATGTTGCTTCTTGACG	1835	CGCACCACTCCGAGGTATTTGTCT	
1799	TTGAAGCGGTGAAGAGCCTGTCCT	1836	AAGGGGTGAAAAAGGAGAAGCCGA	
1800	CGAACCAAGCTGCATTGTCAGTGG	1837	AAACCACGCAAATGGCGATACCAT	
1801	GAGTCTGCGCTTGCAATCTTTGCG	1838	CAGAAGGGATGACGCCTTAAGTCG	
1802	GCTGGGTATAGTTGCCTGGCAATG	1839	CATGACGAGAGCGGACCTGAAGTG	
1803	GCAGGCGTTCCATATTCGCAACCC	1840	CTGGACATGTTTGTTTCGCCACTG	
1804	GCGCCAACTAATACCTCCACCGCG	1841	AAGACCGACTCTCGTCGTTTGCAC	
1805	TGGCGTTCAGTGCAACGCTGGTTA	1842	GCGCGATTACATACCGTTTCCGTA	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
1843	CACTGACCGGACCCAACCTAACAT	1880	ATCGTGCCCGAAGACACTTAAACG	
1844	AGTGCAAGTCTAGACACGCCCGAG	1881	ACCTGAACCAGGGCGATTGCTTTA	
1845	GGTTGGTGCGAGATCCTGGACTGT	1882	ACCCTATACGCTGGGCTAAGCGGG	
1846	GGTCGTCCCGAAACGTAAACGAGG	1883	TGTTTCGCGACTAGAAGCCTTTGC	
1847	GACTAGTACGATCACGGGGCGGGT	1884	GAAGTTGGCGGCTCACCCGTATTA	
1848	CCGACCTGACCCTGTGTACAGGTT	1885	TGGCTACACCGCTTAGGAGGAACC	
1849	TGCTCACTGCCCACACTGTTATGG	1886	CCACAGTTGCGTGACTTACATCGC	
1850	CGAGGAAACACATTTCTTCGGGCC	1887	ACTGCCACTGCGTCTGAAGAGTGG	
1851	TGGCACCGGGTGGATTCTTGTCTA	1888	GCGCCAGCAAATTTCGTGTGGTGT	
1852	GAGGCACGGTGATAGTGGTTGTGC	1889	TGCCTCCGTCGAGCCGAATAGCCA	
1853	ATGCAGATGGATCTTTTTCGACGC	1890	GTACAAACGGGCGCTATTTCGTCC	
1854	TGCGATAGCCAAAGAGTCGAGGAC	1891	GCTTCCCTGGCTCTGAACGGAAAC	
1855	ATGGCGTGTCAGCGAACTGCCTGG	1892	CGGCTACCCAGGCAGATAAGCTGA	
1856	CAATGCAGCTCGGAAGTCAGGTCG	1893	GGTTGGACCCGACAGGGAATTTCC	
1857	AGGATCAGTGCACATGTCCCCTCA	1894	GGGGAATACCCGGCGTTTGTAATA	
1858	CACATCTTGGCTGTCACCCGAGAA	1895	TGGTTCGGTGAGGTTATGTTCGGT	
1859	CGCATTATCACCTCAATGCCAGTG	1896	TCGGTAGGGTTCAGTCGCTGAGGA	
1860	ACATCCGCAGACTCCCTATAGCCC	1897	TTCGGAGTGTGCCGGTGCTAGTAC	
1861	GTGAACCCGAACGAGGGGAGTCTC	1898	TCGTACTGGAATGATGGCCGGGCC	
1862	GCGTAGGGAATTTGCCTCACGACT	1899	TCCGTCGACCGTCCAGCGAAGTTT	
1863	TTTACGCGTCGCTCGGTTGTAGTG	1900	AGGGAATATAACAACACCGCGCAC	
1864	GAGAGGCGTCTAGGCGGTTCTAGC	1901	ATGTCCCGGAAACCAGCTACCTCA	
1865	GCATGCTGATAACGAATGCTTCCC	1902	ACCAGCGACTTAGATAGCCGTCCG	
1866	CTGAAGCTCGTGTGCGATGAGGGA	1903	GGAAAACCTCCTTTGCGTCAACCA	
1867	ACAACGGCATGAGGAGGCTTTTTC	1904	ACGTGCGTGCATACCCAAGAGGAC	
1868	TTTGGAGACGCCAGTACGCGTGGT	1905	ACGCCACTTTCCCTAGAACCAACG	
1869	GCTATCATTTGGTGTAAGCCCGCC	1906	CGAAGTACGCAATAGTGCCACCCT	
1870	TCAACATCCAGGGCGGTGCTTGGT	1907	GATCCCGGCGGATCACCTATCAAT	
1871	TTCGATGTAATCCCCAAAGATGCC	1908	AGAAAGCGACCGTTTCAGGCTAGC	
1872	GGACCTTCGGCAGGTTATCGCCGT	1909	CGCTCCCTTTCATAGTCCTCTCCG	
1873	AGTAAGAAGAGGCAGGCCCCACCT	1910	GTGGGTGGTCATAACGACAGCAGA	
1874	AACGGCTCCCCGTCGTACTGCTTA	1911	CTGGAGGCTGCATCGTTCGTAACA	
1875	CCTATACCGTCGTGGTTCCACGTT	1912	CACCATGAGTTTCGGAGCGAGGAT	
1876	CCGCGCAGGCGCTAATACTCAAGG	1913	CAAGCTGCGTTCGATGAGAGATTG	
1877	AAATGGGCCAGTGAAATCCTTGGT	1914	CCTGGGAGCAATGACCGCTCTGGT	
1878	ACGGTTTCGAATACTGCTGGGCAG	1915	TCCGGCGCTCTACCAAGATGAGAC	
1879	CCGCTTGAGGTTCAGGTCAGAGCT	1916	CGACCGCGTCGCGTATACTATCCG	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
1917	AACATTCGCTAGTGGGGTCCAACA	1954	GCTAGGAAAGTCGGCATTCATGGG	
1918	TGTATGATCATCCGACCGAGCAGC	1955	AAAGCCCCAAAATTCCGCCTAACC	
1919	AGTGCGCCGAGAGGGTGAATAGAC	1956	GCGCAACGCTAAGGGACTATCAAG	
1920	AGGCTTGTTCTGGACCAGCACCAT	1957	CGTCCGCTGGGATGAGTCTCCTGC	
1921	GGGGCCACATAAAGAATTCCGAAC	1958	ACAGGCCTCGTGATTGGTGTGGGT	
1922	TGGTGAAGATAAATCCGCATGGCA	1959	CATTCTCCTTCCGGGACCACGCCT	
1923	ATTTCCACCACGCTCTTGCCAAAT	1960	TCGGAGTTGACCAAGCTCAGTGCG	
1924	CGCGTAAAGCTGTCACCGATGACC	1961	ACGCGCCACTGCAATTGCAAACAC	
1925	TCCCCAACCGGTAACAACAGCGAC	1962	AGTTCATGGAGCCGGCGTATTGTT	
1926	CCTCTGCTCGCCTTACACCCATGG	1963	ACGTTTAATGCGGGGCCCGCCTAC	
1927	CAAGCTGCTCCTGTGCTGAAGGGC	1964	TGAGGCTTTAGCCTACGCGCAGGT	
1928	AAACGAACGATGGTCGGTAGACCG	1965	CAGCGTTATGAGCGCGGAGTTTAT	
1929	TCAGTTCGATGGCTATTGCGCCTC	1966	GTCCACGTGACCACGGATAGTTGG	
1930	GGCTCTCAACGGACGCAAATCATA	1967	GATTATGCTCCTACGCCTGCTCCG	
1931	AGTAGAGTGTTGCGGCTGCCGATC	1968	TCGTCAAGGGCATGATGTGTGGGA	
1932	AGACACTAGACCGCCGTGACCTGA	1969	GATGGACCGCCAAAGACACCTTGA	
1933	ACCGAGCACCGAATTTCCTTGTCC	1970	TACACGAGGATGGGGTCAAGCTTT	
1934	CCGTGGCCAAGATACGAACGAATT	1971	ACACGCACAAAACGTTTGAAAGGC	
1935	CCTCCTACAGCATCCACATGAGGG	1972	GTTATCGTGGGCCGATGGTACTGA	
1936	CACTCGGCAAATACGTATGCGCAT	1973	ACATGACCGTATCCGCCTGCTTCG	
1937	ACCGAGTTGAAGCACGAATTTGGG	1974	GAAGGCGAACCACTGAAACTACGC	
1938	GACCACCTCGGAAGATCGTTCTGC	1975	TGACTTTTGCAACGGGTGGAACCA	
1939	TCAACTGGGCAAACGAAGAGCACA	1976	TGAATTCGTAGGTTTTGGGTGCGG	
1940	GCTTAGCCTCACACGTGCATACCA	1977	AGCATTTATGAAGCGGCCATTGCG	
1941	CTGCGGTCTCCAAGTACCATTTCG	1978	TGCTCCTCGCGTTGGTACCGTGAG	
1942	GTTCCGTATTACGGCGGCCATAAG	1979	CGCAGCAAGAAACAGCAACTGTTG	
1943	ATCGACGCAACCGGATAGTCTCTG	1980	AGACGCTTGGAGTGAAAACTCGGA	
1944	CGCAGATAAACCGGCATCTTTCAG	1981	CATTCGTAGAATGCCCCAAATGGA	
1945	ACCTGCCAATACGGGTCTACGGTT	1982	CCAGAAGGTTCGGGACCCGTCGTG	
1946	ACACCTGTTGCCATGCTGATCCGT	1983	GAGAAGCCGGTTCTCAGAGCACAT	
1947	AAACTGTCTACTGCGCAATTCCGC	1984	TTGCGTTGCAAGATATCTGGCCCG	
1948	GCAACTAGCCCGTGCTAGGATCGT	1985	GGGTTGCATGTTCAGGCAAGACGA	
1949	TCGTAGTGGTGGATTGTTGTGCGT	1986	CTCACGAAGGTGACATATCACGCC	
1950	GGCTTACTCCTCAATTGCGACACG	1987	GCCCGAGATACGGGTTCAAAAAGA	
1951	CACGACTCCCTGCCAGATTTGATT	1988	CATCTTCGCGCTTCTTCACTCCGC	
1952	CTTAGACGTCGGCAATGTCACGTC	1989	TTACACGGTAAGCGTACGGCCGCC	
1953	CTCAGAGCACAATCTGCCCTGCCT	1990	ACCTTCGGACAATGTGGCGTTCGC	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
1991	TGAATGGTTCTGCTAGGCCCACAC	2028	ATTCGTGGGCGCATCTCGGAATGT	
1992	CACGCCTGTCTGACATATGGATGC	2029	TCCCGTCCTGTAATCCAGGGAACA	
1993	CGCCTCAACCCAATCTGAGAACGT	2030	CTTCGCTGCACCTACATTGCGCCA	
1994	TTACGCTTACTGCGAGCTGGGTCC	2031	GCGTGTAGATGACTGTGCTTTGGG	
1995	GGCTTGTGGGGCAATACGCATCTT	2032	CTATGGTATCGAGACATCGGCGGA	
1996	CACTCTCCTTTGGATGCGGAACAA	2033	CCTCGTACTCCGTCGTATGCACAA	
1997	CTTCGAAGCACTTCAGACTTGGGC	2034	TGGTGCGTCCGTAGTGCCTGCACT	
1998	GACCAGCCATCACGTAACGGCCCT	2035	CGCGATCCTAGTTGAAAGCTTTGC	
1999	AGGAACCGGATGTGGTTATGGAGC	2036	ACGATCCAGGTGTTGGGCACTAAG	
2000	ATCCATGGGCAACTGAGCCTATGC	2037	CCAATCTAGGATACACCACGCCCG	
2001	GGAACAGCACTTGTTACCGCCCAC	2038	GATACGTGGGGTATAGGCGGGCCC	
2002	TGGCTCGCTTCAAGCCTGTTTGCT	2039	CATGGAACAAACCGTCGTAGGGGA	
2003	CAAACGTGAGGTCATGACCACCAT	2040	ACACTCGCGCAGTATTCGAGTCGT	
2004	ACCGATGTCTTGAAGTCCGGAGGT	2041	CTCAGTCTCGAAGGTGATCCGACC	
2005	CGAAAATGCATGATGATCTCCCCT	2042	TCCCAATCCCCGTGGTATCGTCGT	
2006	TTTGGTATTCTCGCTGCACCGTTG	2043	AATCAACGTAGTTCCGGTGGTCCG	
2007	GCGTACTCAACCACATTCCCGACC	2044	CTTAACAACCCAGGGGTTTGGGCT	
2008	AGCAAACAACAGCGGTCCGAGCAT	2045	CCATCCTGAGAGTGACGGAGGTGC	
2009	GGACTAGGAGCGGGGATAGCTGAG	2046	CTACCGCTGCATGGCGTTAGATTG	
2010	CCTTAACGAAAACCTGTCGACCGC	2047	TTATTGGTGGCGGACGGAGTGAGT	
2011	CTCGATCGCATAAGCAAGAAACCG	2048	TTAAGGGTGAACTCAACCGCGTGA	
2012	CCCGTTGTTTGGGCGACAAAAAGT	2049	TTTGATTGAAACGCTGCGCACTAC	
2013	CGGCGGCTCTCGCATGATCTCGTT	2050	TCATGTGTAGGTCGCGGCCGTCAC	
2014	CGGATGGAGAGGAGTCTACGTCCC	2051	CTCCGAACCTTCTGGGCCTCTTTT	
2015	ACCAAATCAGACTAGCGACTGCGG	2052	CTGTTGCCCATTGGCCCGACACTC	
2016	CAGAACAATATCGTGCGTCAACCG	2053	CACGATCGCTGAGCAACACATCAC	
2017	CCTTTGCGCGCTCCGAGTAAGGTA	2054	CGGATCATAAGCGTCCGCCTTCGT	
2018	GGAAACGGCACCTATCTGTCGTGA	2055	AGGTTAACGCAACATGTGATCCGC	
2019	CGACCGACAAAACCAAATGCCGCC	2056	GGGAAAAACAGCTAAGCCTTGCGA	
2020	CCAAGGGTGTGGGAGCTGAAGAGA	2057	ACTTATTGCCGGGATCCGTACACA	
2021	TTAAGTGCGCATAGTCCTCGTGGG	2058	TGCGGTCTGGAAAGGAAGGGAGGG	
2022	GCCTGGTGGGGTAAGTCATGATGC	2059	GCTGCCACCTGGACATCGCATACA	
2023	GAGCAGCAGATTGATGCGCTTATG	2060	GCAGGCATGACAGTGGCGTAGTAC	
2024	TGCGCCAACTTCCGGAATATTTGC	2061	GCGGCCCTGATGGTTTGGCTGAGC	
2025	AACCCCATCATGAAATGCTCTCCG	2062	TCCCCATTTAGTCCCCTCCATCAC	
2026	GTCCAACGGTACTGGCGTGATGTT	2063	GCAACACAAATGCGAGCGTAGGAG	
2027	ACTCGGCTGATCGTGAGATGGTGA	2064	GGCGTTTGTATTCGAGCCACGTAG	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
2065	GGTAACGTCGCACGTGGAATTCCG	2102	CACTCAGCGTAGCCTGAAGCCTGG	
2066	ACTTCACAACGGTCCGTTGGACAC	2103	GAATTATCGACCGCAGCGGTGTCG	
2067	CCGAATTATAAAGCGCAAGGCACA	2104	GTGACATCACATGGTGGCCGAGCG	
2068	GGACCCGATAAGACTCTGACGCCG	2105	AGCACCTTGCCGAGTCACCAGTGA	
2069	ACCCGTTTCTCGTAGGAACCTGCT	2106	TAGGTTGCAGGAATGGTGGGCACC	
2070	CACGTTCGACTGTATCTGGTTGCC	2107	GTCCCATACGTGTGGTACGCGGAT	
2071	CCTCGGATGGGCCCATGACCTTGA	2108	TCGGATACTCTCGCGTGCCACGGG	
2072	GGACGCCTGCTGTAGGGGTTTGAT	2109	CAACGTTCGCCCCTAAGCCCAAAT	
2073	CTCGAGCGTGGGCTAAAAGAGCAT	2110	GTTAGGTCACCGCGGCATATCCTA	
2074	TTTACTTCTTAGGGCGCGTTTGGG	2111	GTTCACCGGCCTCTACTTGGGTTT	
2075	ACCACCAACATAGCGCGCACTAGT	2112	AATCCGCGTCTAGGTCATGTGGTC	
2076	TGGTTACACGGCAGCCCGCGTAAG	2113	GCTACGCCTCTGGAGGTGGTACCC	
2077	TTATGGTACGTTGCTGCGTGCGGG	2114	CAGGGAATGCTACAAAGGGTCCAA	
2078	ACCGCGGATCTAACGAATCCCATT	2115	AAGGGTTAGCTGCCCGGTTAACAG	
2079	CATGATCCCGCCCTTAGGTTAAGC	2116	CCTCGCAAGCGCGATATTTATGCC	
2080	TACCGCTTCAAAGGGTTGCCGAAT	2117	GCCTCCCGGTCATGGTCAAGGGAA	
2081	GCACCGCGTCAATATTACCGAGGA	2118	GCTGTTGAGCGGCGACCTGTGCAC	
2082	GTGTCGCGGCTTTACAGAAGGAGA	2119	CGCTGACTTAGCTCTGATGTGCCG	
2083	GCAAGCCATACCGCAATAAACTCG	2120	TTCATGGCATTCATCACGAAGGAA	
2084	ATGAGGTCGTGCTGCGTTCACGAG	2121	TAGTGTTATGCCCGCGTGTGAATG	
2085	CGAGACTAGTGCCGATGCAGGGTA	2122	CATGTAAGGGCACGGTCGTGGGCA	
2086	GCCTCATCATAGACGCTGGATGCA	2123	CAGGAAGCTCGCTCCGTGATGCAC	
2087	GACAGGCGTCGGTAAGCTCTCAAG	2124	CCTGCTGATAGCAACCTCACTGCA	
2088	GCTACGAATCTTCCCTGTCGCCAC	2125	ACTACGAGGGCAGGGTCTAGGCG	
2089	TTTGGCAGAACGTACCAGTGGGGT	2126	CATAATGTGGGTGCTGACGCCGAT	
2090	GGACAATAAGCACCGGAGAATGCG	2127	TAGCGAATCCACACAGAGCCGCTC	
2091	TCATGAACCTTCTGATGCCGCGAA	2128	TCGCGAAATCCCTAAATCCTGTGC	
2092	CGCCGCATTACCTTAAAAACGTGC	2129	TGGCACGAATCAAGCCACCAACTC	
2093	ACGAGTCCAACCGCCTCATTGATT	2130	GCGGACCGTCTTTGCTATCTGACG	
2094	GCGAAGAGTTGCTACTCTTCCGCC	2131	AGGCCCCGCCTTGTAATTGGTCAT	
2095	CGTCGGCAACAATCTTTTTCGTGA	2132	CTGGTCCCATACGCCGCTGACTAG	
2096	AATCCTGTGCACCCGTGAGACGCG	2133	TGCTAACTGCGGCCCTACAGAGTC	
2097	AACCTATATGCATCAACGCGAGCC	2134	TGGTTTATGTTCGGTAGCGTCCG	
2098	GAACTTGGCAAAACAGCCCGGAAA	2135	AGCTCAAACTTCTCCCACGGGATG	
2099	CTCTATGGCCGTTTGCCGTCTGCA	2136	CGCGAAGATAGTGAAATCCGCATC	
2100	AGTGCACCGGGTTGTGGACACAAT	2137	GAGTGAAACCTCTCGCGGGTTGCA	
2101	CCTGGCTTTTCACACGCCAAGAAA	2138	TCGAATGCTCTGCAGTGACGTCAA	

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TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
2139	AGGTGGCAATGATCGACGACCCTG	2176	TTTCGGCAGAATCTCCGATTCAAC	
2140	ACCTTAACACAGCCGACCAGGTGA	2177	TGGCGAGCAGACCTACAAGACAGA	
2141	GTCCGGAGCCGTGCAAAGCAATAA	2178	GGCGACAGACCGGTACATCGGCCA	
2142	TCTGCCTGACTGCTACATGCTCCC	2179	TCTAGACCTGCGTTTCGTGGGACC	
2143	CTTTTGGGGATTAGAGGCCGACAA	2180	GCCGAGCGTGGTACCATACGTTCA	
2144	GGCATAAAGGCTTCCGTTCCTGTC	2181	TAATCACACCCGCTTTCTGTGGCT	
2145	GCGGACCGTAAAGCGGGCAGATAG	2182	GGCCGGAGCCATTGGACACTTCTT	
2146	TTTCAAGAGTGCATCGAATCCACG	2183	CCTGTAGACCTGCATGGATCGCTG	
2147	CCGGCATCCCTTCTCGCTGTTGCC	2184	GTGTGTGTCTGCGTTGGGGCAC	
2148	ACACAGAGACGCGAACGGAGTGCA	2185	ATCGCCGTTCCCGCAAAATAAGCA	
2149	AGCGGCATTCTCCCACTCGTTACT	2186	TGGATCAACGGGGTAGTGAAAACG	
2150	GGAGCGTACTGCGCCTCGCAAGTC	2187	AAGCGACGATGCTTTCTTGAGCTG	
2151	AAACCCGAATGACACGGCAGATAA	2188	CACGGGCACGTGTTCTACGCTTGC	
2152	GGTCGGGTCCATATCCAAGTAGGG	2189	ACGGGCTGGGACAAGAGCTAGAAA	
2153	AACCAGCGGATCGATAAAACGACA	2190	GGTAACTGGCTCCGCTCTCACATC	
2154	GGTGTCCACCCGTTAACGCCGGTA	2191	ACTCTGGCTGTTGGCGAACGTGAC	
2155	AGCGCGACGTGGCTTGCCGTTAAA	2192	GACCGAGGACCAGTCCTTGCTCTC	
2156	TCCCACGGCTATAGGTCCAACGAC	2193	AGTAGCTCTTGCGGCCTAACGGCA	
2157	ATCAACGAACGATGCCGTTAGGTG	2194	TTCTTGTCCTGGGGGAGAGCAGTG	
2158	GAGGCTAAGCCGTATGGCCGAGGC	2195	TTAGCAGGGAGGTTGTCGGCTCAT	
2159	ACGGTCCGAAATGGTTAGAGGCAC	2196	TCGGGAGAGGGCCTTACCAAAAGC	
2160	ACGCAAACCATTCCTCGAGTAGGC	2197	AGAACGTGGATTGTACGCTCCGCC	
2161	TTACACGCTCGCTATTGGGCCATA	2198	CTTCACAGCCTGGAGCCACCAATG	
2162	CTCGGCACGGGTTTAGAACGCCGG	2199	GAGATCGATGAAACGCACCAGCGG	
2163	ATTCGGTAAGGTATCGGGCTAGCG	2200	GGGTCCAGAGTTGGTGTGGGATAA	
2164	AGCACACCGTTATACATGACGGCG	2201	CCGTCCACCCCAGATAGGAATCAC	
2165	AGTCCCTGCCGTTCGCTCATGGAA	2202	TGCCTCGCTTCTGTGAATCTACGA	
2166	GGGCTTATGACCAGTCAGGTTGGA	2203	GATCACAGCGTCCGCGCATAACGG	
2167	GGTCACCACACGAGTGCCTGGTCT	2204	ATGACGCCTTACATGACGCACCTT	
2168	TTGATCGTGTCTCCCGAAACCCTC	2205	GCGTGGAATAACGCCCTTAGTTCA	
2169	ATTGTCGCGATCGGCATTTCTTAA	2206	GGTCTACCATTTCTCGCCCGACCG	
2170	GGGTCCAACGACTTCTCGCTGCTG	2207	ACACCTCTCTGGCGTAGACGCTCA	
2171	CAAATTCCTTGGGGGCCATAGTGG	2208	GTAGAGGTGCTCAGGACTCGTCGC	
2172	CCAGAGTATCCGCCGTTAGACGGT	2209	GTAAGCAGGAGGCGAAGGCGCGAA	
2173	TCCTGCAGATCATCTCGTGTCTGG	2210	TCTAAGGGCCGTTTCAATCGACCT	
2174	TGCGGGAGATTTGAACAAGCTGTA	2211	AACCTGATTTCAGGGTCAGCCCGA	
2175	TTAGACGCCGAGCTAGGCAACGTC	2212	GTCACGCGATTGGCCCACCTATTA	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
2213	ACGATGCCGCGCATGTAACCTAGT	2255	CATTTCGGGCCCTAGCTACTGCGC	
2214	TGAGAGATGTCTCGTCAACGCCTG	2256	CCGATCCCGCACATCCGTATCCTG	
2215	GCATATCTCGCGGTGACAGACGAA	2257	TATCACCGGGAGCGTCTTATCGTG	
2216	TATCCTGGACCCAGCCTTGGAGGA	2258	TAGGGCTCGTGCACCGATTAGAGG	
2217	GACCCAACGTCGAAATTGTGCGAT	2259	GCGTGGCACTCGCTTGTCTAGGTA	
2218	TGAAAATCGGGGCATCTAGTTTGG	2260	CTCAACGAACTCAAGGGCCGCTAC	
2219	CCGCGAAAAGGATTTGTGTACGCA	2261	AGCCTGGTATCGACCAATCCTGCA	
2220	CATTCCATTTATCCGCAGTTCGCT	2262	TACGCGTTCTAGTTGGCCGGATCC	
2221	CCTGTCTGTCGAGCCAGCGTCTAT	2263	TTTATGGGTTTGTGCCTGATGGGT	
2222	TCAGCGCGGCTAAACAAGTTATGC	2264	GGGACCCCTAGCAACGTCACCTTA	
2223	ACGCCTACGAACGACCCAAGAGAG	2265	CTGCCTCCCCAGGAGTCATTGGAT	
2224	TGCGCATCTACCATTGTGTGGATC	2266	AACCCCGCAAGACCAGTACCAATC	
2225	AAGTCCGCGCTCGCTCCTGTAATA	2267	GGTCACATACGCGCTAAAAAGCGC	
2226	GCTGGGTCATTGCTCGAGTAACCA	2268	AAATGGCTCCGACCAGTTAGGGAC	
2227	TGGAGCGTTCTGGCAATGACCGAC	2269	AACGCGGCACGCTTAAAGGTGCAT	
2228	CAAGTCAATTCTTGGCCAATTCGG	2270	GATCGCACGCCGATTAACCTTACA	
2229	CGTTCATGCAAGGATCCCAGGTTA	2271	CCTCCTGATTGGGAGTGCGGAATT	
2230	ATGCCAATAGAAGCTGGGGATGCT	2272	CGGAGGGTAATAGGCTCCTCTGCG	
2231	CCTAACTCTCCCTTGAGGCCGTTC	2273	ACAAGAACTGGACATTACCGCGGG	
2232	ATCTCGGCGAAGGTTCCAAACATT	2274	TGTCGTCTTAAAGGCCTTTGTGCG	
2233	GCGACAGATTACGCTGCGGTTTTC	2275	GGTGACCATGTGGCGTTTTAGCTT	
2234	AAGCCCAGACGGCCAACACGTTAC	2276	CACGGTTGCGCACGGTACCAGAAC	
2235	TCAAGTTCAAATCACATCCCGTGG	2277	CCTTTATTGTTTGGTCCCCTGCCC	
2236	GATTGTCGTTCTGTGAGGCG	2278	GTGCGCCTGCATTCTACCGTCAAT	
2237	ACCGAACTATGTTCCGGCATGGCA	2279	GTTTACGTTGATGGCTTGCCGCCG	
2238	CGTCATCGGGTGTGCAATGCCGTT	2280	CCGTCGGTGGTAGGACGTGAATGT	
2239	CGGACGGAGTCACGTTTGTGCACT	2281	TGATCGCCCCAGAATCCCTGTGCT	
2240	TAAACAAGTCGTGTGCCTTTGCCG	2282	AAGCAGCCAAAAATCGGTTGCTTT	
2241	TAATTACTGGCCTGTGGAGCAGGC	2283	CGACGGGACTTAGTAGCAGGGCCT	
2242	GGAGCGGCCCGAATGGTGCTCTTA	2284	CCGATTCGCGAAACGACCAAGTAG	
2243	ACTAAGCAAGGCTTGGATGTGCGT	2285	CCACCCCAACTCCAATCTTTCTCA	
2249	AAACTAGCTAGCCGCACCCGCAAG	2286	GTGCAGTAGACGACTACCGGCGTC	
2250	GTTGTTCCACCAGTGATCACGCAG	2287	TTCGCCCATCGTATCAAGCAATTC	
2251	GCCGCTGACAAGATGATCATCGTT	2288	GAATCGCGACTACCCGTCGGGTCA	
2252	CTTTCATAAAGCCAACCGATGCCC	2289	CCAGCACTCGCCATCGGTTATAAT	
2253	CTGACTGCATCTCGAAAGCGGGTG	2290	CGAACCGTAGAACTCCGGTCGGTG	
2254	ATTTCTTCGGAGAATCGGCCACGT	2291	GCACCATGACAGAGCCCCAGGATG	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
2292	TGGGCTACCGCAGAATAAGGGTGA	2329	TTGAATTGGGTGTCGGAGCGTTCT	
2293	TGGCCTGTCGTGTCGAAGGAAACA	2330	CGGCGGCAGACAATGCTTTGAAC	
2294	GCCTCACCGATAGCGAGCGTTTGC	2331	GGGTCTGTCAAAGAGGGTGTCTGG	
2295	GTGCGCCGGCTAAAACGAGACA	2332	CTTTGTGCAAGACGAAGCACCCTT	
2296	CCGCAGACGAGTTTCTTGTGACAG	2333	ATCGAATTCCGAGGAGGTCTCCAT	
2297	GTTCGCAATCGCGTGCTAGGAAGC	2334	TCCGACCCTCAGAGTCGACTCATT	
2298	TGTTGTACACATGCATCCGGTGAA	2335	ATCAACGGCCACCTCCTCGCCGAG	
2299	CACTGAACACGATATAAGGGCGCG	2336	AGCCACGGAATAATTCCGTCCACC	
2300	CGCGATGGTTCTTAGCAAGACGAT	2337	GATCGCTTGCGTATCGCAAAGACT	
2301	TACACCAAGGAAGAAATGGGGACG	2338	TCCACGCCTTACCATCAACTGCAA	
2302	CGTGCCTTGCGTTTTAGGTGCAGC	2339	GCCAAGCGATAGGCCAGAACTCAG	
2303	GTCGTTTGTCTGGGCATTAACGGC	2340	AGCGTGTGGGTCATTTTAGCACGA	
2304	CAGGCTCTCGTTCGGTACAAACGT	2341	GTTATGCGCGGCTTACGAGTTCGA	
2305	CGGACACTGTTTCACCAGAACCCA	2342	TCTGTCCACGTAACTTGCCTGCAG	
2306	TACCCATGATGCGGAAGAAGCGTA	2343	TCGGCAGCCAATGATCATACCTCT	
2307	CTGTCCTTAAGCGGATGAGAACCG	2344	TAAGCCCGATCCGGTCCTGTGTTT	
2308	CGGGAGATGAGAACGGTTTTGTGC	2345	ACATGGCAGACTAACAGGCCTCGC	
2309	TAGATCGCGACTGTACTCAGGCCG	2346	CATGGCTGCACTCTAAGTCGAACG	
2310	TAAAACAGTTCGCGCGACTGTCGT	2347	TCTTCAACCCACGCGGAACGATTG	
2311	CGAGGAGCTCCACATAAGCCCAAT	2348	CTCGTGTCTCCAGAGGATTGTCCC	
2312	TGGCTAGGGATGGGGAATCATCTT	2349	TGAAGGCATCAACCCAGAGGATTT	
2313	AGGATTGGGTGCCTGGATGCATTG	2350	ACAGCTCGAAGGCAGCCACATTGG	
2314	TGTATCTACCGGCCTGAAGCAGGT	2351	ACAACGAGTACCGCGACAGAAGGG	
2315	TCCCTACGCGCATGACTCGCTTAC	2352	ATAACCGAAAAACCAGCCTGCGAT	
2316	TGGTCGATCACCTGTGACAGACGC	2353	ACAACTCAGCACTTTCGACGTCCA	
2317	TGGGGGTAGTCCATGCATCAATTG	2354	CGGGTTACTGGGTATCACCAATGC	
2318	CCCTGCCAGGATTACTATTCCGGA	2355	CATCGGTTATCGCTGCACGCGCGT	
2319	TCCCGCACGGGGAATTTAAGTAGA	2356	GAAGGAATCCCGGATAGTCCGTGG	
2320	GTGATGTGCAGGAACTTCTGTCGC	2357	GCATGGTCTCAGCCAAAGAACCTG	
2321	ATTTAGGCATGCATGCGCTTCTCA	2358	AGCCTGCGACGTTTCCCGACAGAC	
2322	TTCGGCGCTAGTGGACGCCGTCAA	2359	AAGAAAGGCGCACGGGATCGATAT	
2323	GAGCTTCATCTCATCAGTTCCGCG	2360	TGTCGCGAAGCCAACTTTCAGTAA	
2324	GACAACTCCACTGCTCCAATCGCA	2361	GCGGCATGCAAGGTAGGTCTGGAT	
2325	GGCCAAGGATGGACCTTACGATGG	2362	GGTGGCCATCTCCTCGAATTGCAT	
2326	GGTTCCGGAATTTGTCACCGCTTC	2363	GCGTGCATAAGTTGCACATTGTGC	
2327	GCGCTGGATAGTCTGCGAGAAGCC	2364	TTGAGGTAGCGTTTTCGCGCATAT	
2328	TGAGTCCAGTGCTGCCACCATGAA	2365	ATCCCACTTGTGAGAGGGCGCATT	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
2366	CGGTCAGCGAGCAGACATCAACCT	2403	GGCTACCCATAGGCTCAGCAGCAC	
2367	GCGTATCTTCGGGTCGAACACTTG	2404	GGCTTGTGAGGGTGTGTTCTCGAC	
2368	ATGCCATTGAACTCGCACTTTGCG	2405	TGTGTTACGGCGAATGCAACAGTC	
2369	CGATTCCCATCATAATGTGGGTCC	2406	CGATAACAGGTCGCGCCGTTACTA	
2370	CAATTTGGATAATCCAGCCACGCC	2407	TGATAAAGTGAGGCTCCAGCGCGA	
2371	CGGCTTACCCTATGATTCCGTGCA	2408	AATTGTGCACGGATCTGCACGGCG	
2372	GGTGGACCATGCGCTGTGGTATGA	2409	GCCGATACTGAGCATTTCACTGCC	
2373	TATTTGTCGAAGATCGCAAGCGCC	2410	GCAATGTACTGTCACCAGTGGCGA	
2374	GTCAGTGGGTTTTGAGAGCCCGCA	2411	GGCATATCGGTAACACTTGGTCGG	
2375	AGGGGTCGGGAAATCTGACAAAA	2412	GGGTCTCAAACCAGCGTGGCCGCT	
2376	TGCTTGCTATCCGAAAAAAGCAGG	2413	GTCTCCGGGACCATTGAGCTGGAG	
2377	TTATCGGATCAAATTCGGCTTCGG	2414	GGCCTTCGGCATTCAGACGGGTTG	
2378	TGCAGCAACGAGTTACCCGGACTT	2415	CGTGATAGGCCACAGCGCTCAATT	
2379	TATACATGTCCGGAGGGGCACCCA	2416	GGCAGGCCCGCGAGGATGATTAAC	
2380	TGCAAAACCGGAGGATGAACCCTT	2417	CGGGTATGGTTGATAACAGCGTGG	
2381	TCGGTCTAATGTCCACGCAGACAC	2418	ACGACGTCCTTGGGACCGTA1TGT	
2382	ATGTGTTTGCCACGCGCTCCTATT	2419	CTGATATCGAGCCTGAGCCTTTCG	
2383	TGGCGAGGCACGGCTCTAATTCGG	2420	TCCCATTGGCCTGTATGCTGGCCT	
2384	GCGACGACCCGAGCGACTTTTACA	2421	GTGTCGTCGATTGTTTCATCGACG	
2385	CTCAGAGAGTCTATCCGGCGCCCT	2422	CGAAAGCCAGTAGCCGATTGCGTG	
2386	GGAACATCTCCTGGGTCCCTCAGA	2423	GGTTCGGCTTATTCCACTGCGACA	
2387	GCAACGCAGGGAAGTACTTAGCGA	2424	AGCGAGGGCTAACTTTTTAACGCG	
2388	TGACTTGGGCGGACAAAGAAACGC	2425	CGGCGCTGATGACGGGACTCGATT	
2389	AGATCATCGGGACGCTTCATGCTA	2426	TCACAGTGCTCGGCGTAAGGACTA	
2390	CCCTTCTGACCGCTAAGGCCATAA	2427	CCCATTACGAGCACACCATGGC	
2391	CGTGAGCCGTGGGGTGTCTCTGTA	2428	GGCCGCTAATCTTTACGCATCACG	
2392	TACCTTGGTCGTCTCCGCTTTTGT	2429	ACGGCTTCCTAGTGTCCAGCCCTT	
2393	TCGCCGCAAAATGCTACGTGAAAA	2430	CTGTCAGGTCCTACCCAATGGCTC	
2394	GAGTGACCTAATGGCTGCCCGACT	2431	CACAGCCCATCCCACTGAACTGCT	
2395	AAAGGAACTTGGCCAACCCTATGG	2432	ACAAACGATACACGCAACGCTGTG	
2396	TGTTTTCGCACTCCACCTAATCGC	2433	TGGCGGCCAGCTAGCAGGCGAAGT	
2397	CAATGGGTTTCATAAGGGCAGGCA	2434	ATCTCGAAACGATGCGTGCCTAAA	
2398	GCCTAACACACAAGGGTCCCTCTG	2435	ATCTCGAGAACAGCGTGCGTGCGG	
2399	CGTCATGCGGTCCGAGGATCGATC	2436	GAAGAAATCCGCCGACATCTACGG	
2400	CCACACGGGCACGGAGTAATATCT	2437	GCGGAGCAACCTTGGCTGTTTCTA	
2401	CATCAGACATAGGTCGCGTGCCGA	2438	CGCGTTCCGAAGACTTGTTTG	
2402	AGATGAAACCAAGGGAGGACGCAG	2439	TGACCTGAAGCCCATCCATAAGCA	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
2440	TGGTATTCATTCCGGATAAGCGGG	2477	TACAGGCGTAATTCCTGCGAGGGA	
2441	GCGTTGCGGGTCATTGATGCAAAC	2478	CCGAAGTGCGAGAAGCACGTTGTT	
2442	ACCGCTTTCTGTGTAGAGCCCTGA	2479	AAGGACTGGTATGGCCGGAGCTTT	
2443	CAAATAGACAATCGCAGCTTCGGG	2480	GGACACCGCCAACCTCATAGTTGC	
2444	TGTCCTGACAAATCAAGGTGCAGG	2481	AATGGTGTTCGCCTGGACTACCAC	
2445	AAATTGCACTCGCGGAGATTTCCT	2482	TAGGAAAGCGTACACGGGAATCCG	
2446	TGACGCCCATTTCTATATGGTGCA	2483	TCTCACCCCAATGATGAGGACGTC	
2447	TGTTCCGACAGGGCACTGCTAGAC	2484	CGTGTCCGTGTGACACTGTCCATG	
2448	TCGCTGGCTTGGGAAGGCCTTCGT	2485	TCCAGG CTGTTGCGGATACGGTAG	
2449	GTGCACCTCCGTTGGCGTAGAATG	2486	GTAGGCAAAATGGTCGCGATCAAT	
2450	CTCATTTGGGACCGATCGGGTTGC	2487	ATCTCCGTGGACCCGATTGTGACA	
2451	GCCAGTGTCTGTCAATGGATGGGA	2488	GAATATGCCGTCAACGCTATGGGC	
2452	TTGCCCGGCAGGTTCTGTGTAATG	2489	TTCCGGAAGCGTTTGGTAACTTTG	
2453	ACCCGCGAACCGAGACGCACTTCT	2490	TTCGATAGGAATACCAGGGCCTGG	
2454	TCCGTGCGATTGGTCAAGGTTGAT	2491	GGCCATTTGAGGAGGATTATGCAA	
2455	AGGGCGTCTCGGTTGAACCTCGGT	2492	ACCTVCTGACCTGGACTTTTGGCG	
2456	TGACCGTTCAAAGAGCAAGCCAAC	2493	GACCAATCCGCAGTTGAGCAACAG	
2457	ACACTCACCTGCTGTCCCTGCTGA	2494	TCGGCCACTCACCATGAGTGTAGG	
2458	GCGTTTAACTCCTTGGGTGGTGGT	2495	AGCGCTCACATGTTCGAAAACGGG	
2459	CGCCTGCGCAGGTAACTCTCCGCA	2496	TAACGCAAAGGCGCGATCCTCGCT	
2460	AATCGAATTTCCCAGCGGCTGTTT	2497	TGGGTGGGCCAAATATTACTGCAA	
2461	AAGCAGGTGGGATCCTGGGGATCA	2498	GTCCTCGAAAGGGGCATCCAAACA	
2462	AATCCCAGACTCGCTCTTCGTGCT	2499	CCCATCTGGTGGGAGGCGTTATCA	
2463	ACGGTTATAAGGGCCGGCTGCGAC	2500	GTGCGCGGTCTGCAAACTCGCCAT	
2464	TACGAGAGCGGGCTTAGACGTCGC	2501	TGTGTTGCCAACCCTAGGTCATCA	
2465	GCGATTTTGACCCACGGTTATCGA	2502	CTGATGCTGTTCTCGTCGGTTGAC	
2466	AGCTGTATAATTTGGATGGCGCGA	2503	AAGCTGCAAAAGGTGAGCGTGGCA	
2467	TCCGCGAGTCTTAGCCGATTGAAC	2504	TCTGACGCGTGCTTGGGAGTCTAT	
2468	GGCATCAGCTCCGTAAGCCGATAG	2505	GAATTACTTGGAGGCGCCGTGCAA	
2469	TGTTATTGGCAGTTCGAGCGACAG	2506	GATTCTTCCCGACCTAGGTTGGCC	
2470	GCGAGCCTTTTTGCTTGGGAAGAG	2507	CGCAGCGTATCCCATGTTGCTTGA	
2471	AGAAGAAAAGGTCAGCGTCGACGA	2508	GAGATGGAATTGTTCGCCCAAAGA	
2472	CGGGTCGACCCTTGAAGCATAACC	2509	GATGCCTGGATCGGTCTAGCGTCA	
2473	CTCGGTTTTCACAAACTTACCGCG	2510	GCAGCGACTGCTAAGCTATCTCGG	
2474	GCAGTCCTATCCGGAGCCTGACAA	2511	AGGGCTAATTTACATCGCCTTGCC	
2475	AAGGTGCGCTATTTGTTGTCGGTC	2512	AAGTGCACATCCTCACGAAGCGAT	
2476	AGTGGAATCCATGCCGACACCTGA	2513	TCAGGCAGCCGTAATTAAATGCGC	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
2514	CCACTGGGGAAATCGCACTGTTGG	2551	GACTTGAAACCGCCTATGCCCACA	
2515	TTGTCCAAAGCCACCTACGACAGA	2552	CGATCGGTTGTGTGTCTTACC	
2516	TGGGCGGAATAGATTGGGTGTCTT	2553	AGTAGCACAATGCCTCATTTCCGC	
2517	TAGAATTCGCCTCTTCTAGCCGCC	2554	CTCGCTATCTACGCGTCTCCGAAA	
2518	CATTACTTCCTGCAGATGCGATGC	2555	AGCCCGTTACGGCATCTAGGATTC	
2519	GGAAATGCTAGCTGGGGTAATCGC	2556	TCGCGATGGCGAGAGTTCAGAATA	
2520	GCCGCCACTTGCGAATCTACATCT	2557	TTACAGGATTCCAAAACCCGCAAA	
2521	ACAATAGCGGACAGCTCGCCAGAT	2558	CGGTACCAACGCGCGGGCATATGA	
2522	AGTTAGGCTCTCGGTGCGGTCCAT	2559	TGCCAGTATTATCCGTGCCAGCCG	
2523	TGGGCCTGAGAAGCGGTTAATAGG	2560	ATTTCAGACCTCGGGACAACCTGG	
2524	ACGCTCTGAGCGACGCCTATCGTA	2561	GAAGTGCGCGTAACTTAGGGAGCC	
2525	CCTGGTGATCGTGTCCCAGACTCA	2562	TTGGCCAGGTCATCACTCTGCCAT	
2526	GCGTGTCCATTCGCTTGAGGTTTC	2563	ATCGGCCGGTATTAGCTGCCCTCC	
2527	ATCCTGAACGGCGATGACCACCAC	2564	CGCAGGTAAGGCCGAGCAATGTTT	
2528	TTACGTTTCTCACCGATCAACGCC	2565	TTGGGAACGTGCTAGGCGGCCCTC	
2529	GCCGTCTTGAGTGGCTAAAAGGCA	2566	CCGCAAAAGTAGAACAGCCTGGGT	
2530	ATCTACGATGCGGCTCGAAGTGTT	2567	CATCTCGGCACACTGGTGCTGTAT	
2531	AACCAAGACTCGTCCCCAAACGAA	2568	ACGCGTAAATCAACGACGTGGTCG	
2532	AACTGCGGTGGTGGAGGCAGGTGC	2569	CGTAGGTGGTAAATGTTGGCCCAG	
2533	CCTGAGTGGTCGGGCTGGAAAAAT	2570	GTTGGGATGCTGCTTCACTTTGGG	
2534	TGCGATCTTCTCCACCTACAGCGC	2571	TTCGAGCCAGAATAAAACGGTTGG	
2535	AGGCGCTTAGAACCGTGAAGGCAG	2572	AGAGATATTCGGCCTCGGTCGAGA	
2536	TGGAAAATTTTGGGAAACGCTGGA	2573	CGACAAAGTTTCTCGCGAGCAACT	
2537	CCAGCGCCGCACCTTCTCCAATAG	2574	ATTGCCGCGTCTCGTATCAAAAGA	
2538	TAGACGGCTGGCGAATCTTACGGT	2575	CGGAGAATGGATGCAGGTTCTTCG	
2539	TACCATACAAGAGAACGAGCCGCA	2576	TATAATCATTTGCGACTCGCCCCA	
2540	GTAGCCGAGAGCAATTTTCACCGC	2577	AATTTTCCCCGATTTGAAGAAGCG	
2541	GCAAACTCCCCTGCCCTTTAGCCT	2578	TCGCATACTTCGTCGGCGAGTATT	
2542	ATCCCGCTGATAACCGCCAGGATA	2579	CGTGAGCCGTTCTCATCCAAGCGG	
2543	AGTCTCAGTTCGGCGCAACGGTAG	2580	GCAGAATCGAATTGGGGTGGGTTT	
2544	AACCTACAGTCGCCGCAATGCATT	2581	CTCTCGGTTTCTCAACCGAGCTCG	
2545	ATACACGTTTCAGCCGGCAACAAT	2582	GACCAGTTAGTGCAATGGTTGGCG	
2546	ACGACGGGACGTGCCCTCGTTGAT	2583	TTCTCGCACAGCTAGTCAGCCGAT	
2547	AAGTCCAAACTCGAATGGGGCAGT	2584	CCAAGTCTTGCGTGAGCGATCCTG	
2548	GATTTATTGGCGCGGTAACGACCT	2585	GCGAAAGTGGCTCGTATTTCTCCA	
2549	TGTTTTCAGAGGCTACCCTGCCAT	2586	CCTCGGGACTGTCCGACTGAAAAA	
2550	ACGGTCTCAGGGAAATGCGATCTC	2587	AGGCGAGTGTACGGCTCATCCATG	

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TABLE 1-continued

TABLE 1-continued

	TABLE 1-continued		TABLE 1-continued		
_	Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
	2588	GCGGCTCTGCCTACGATATTCACA	2625	GCAGTGAGCTGGGTTCAATGCTTC	
	2589	TGCACCTGTCTGTAGATTTGCGGT	2626	CATCATCCACACAGGCAGGTGTGT	
	2590	CATAAAGCACGGACGGACTTGAT	2627	AGACAAAGGTCCCCATTGCGAAAT	
	2591	CCCTCAACGTAGGGCGTGACTTTC	2628	ATACTCGTCGACGAGAGCGGAAA	
	2592	GGGTCATCGTGCAGTTATGCCGTA	2629	GCAGAATGTGTTGTCTTCGCAGCC	
	2593	CCCGGATAATCCTTTGTCCAGCCG	2630	CACCATGCCTTCATCTTGGCCTAG	
	2594	TCCGATAAGCGAACTCACATGGGT	2631	ACTCTTCAACGCCAGGTTAAGCCA	
	2595	CCTGCTGGTTCGGTCGTAAGCGAA	2632	GCGACCTGCGGCGTGTGTATTCTC	
	2596	GAGGCACCAATCGGTCTGAAAATG	2633	TCGGTGTATGCACCCTTTCTCCAT	
	2597	TACGAAAATGGTTGCGCCGGGTCT	2634	ACCGTCGAATCTTGCGGCCAATGT	
	2598	CCCAAAGATCGTATCACCACCCAA	2635	TAATGCATGCTCCCGGCTCACGTT	
	2599	AATTGCCGGAAGCAGTCAGAATCG	2636	TCTGTACACACCACGTCGTGCACA	
	2600	CCGAATCAGCCGTATTTGCTGGAA	2637	CATGGGGTTGTCAGACGACACCTA	
	2601	CCCGCTTATCTGTACTCGATCGCA	2638	AATCTGATGCTCGCTGTAGGACGG	
	2602	TTTTGGGGATCCCTATTAGGCGCA	2639	TCGAAACCGCGGGAAAGGGTAAAA	
	2603	AGTGACAGCGCTCACCACGGTCCC	2640	CGCTAGGGCCTAGGGGCACAGACA	
	2604	CCATGAGTGTTTCGGGACATCGTA	2641	TGGGGGACGGGCGTCTAATCCTCC	
	2605	GCCACATTCTGCTACCTCCGTGTT	2642	AGGCATGCACCCATGCTGCCAGAG	
	2606	TCCTGTGCTTTGTGACGTGCTAGG	2643	TCCCAATGGCCTGTCAAGCATAAA	
	2607	GACCGCATATACACCTGATGGGCC	2644	GAACCTGAGCCTTTGCTAGCACGA	
	2608	GTAGGCCCGTCGTTAACCATCTCA	2645	CGAATTGATAGCGTTACGGGCGAA	
	2609	CGGCTCGCGAAATGGAGTTTAGCG	2646	TTGCACGCGCGCGAACGACTATTC	
	2610	GCTGATCGGCTTTTCACCGCTATA	2647	TGCGGTGAAGCAGTCCAAGGTCAG	
	2611	TATCAAATCGTTGGCACGCGACTA	2648	TGAGGACCATCCAATGGATCGGTT	
	2612	TTGGCGAGGATCCCTAGGCGTACT	2649	TCGGTGATTGGTAATTTGGATCCG	
	2613	AAGTCCTGAGGCCGTTCGGTTTCT	2650	GCGGGCAGGTAGTTTGACTGGATG	
	2614	ACTCCGGACATCTCGGCCAGAGAT	2651	CAAGCACAAGCCCATGAAATTTCA	
	2615	CCAAGGGGAACACAGGATCGTAGA	2652	CGGTACAGCGGATAGCCAAGGATA	
	2616	GTGGCCTAAATCCGCCTTCTCAAC	2653	CCATGCTCTTCGCTGCAGCATACT	
	2617	CACTCCGTCTCGTCCATTAATGCG	2654	CGCGGCAAAGATTAATTCCCGGCG	
	2618	TCAAGAACCCAGTGCCGGTCAGCA	2655	GAAGACCCGTCCGGGTTTCCATAC	
	2619	GAATCAATTTTCCAGGGACGGGAC	2656	CTGGCAAGGAGGATGTGGCTCGTG	
	2620	GAGAGCATACGCAATGTTCCCTCC	2657	CTGTGCAGGGGGTGGCTCTGTTGA	
	2621	ATCGGTGTGCTGGAGCGCCAGAGT	2658	TTCAATAATGATCACGAGGCCCCA	
	2622	GCCTCTCCTATGACGATGACCCAC	2659	TGGTGATGCGAAGCCTTACCTTTG	
	2623	TGGGCGCGCTTTTAAGACTACATC	2660	CTGCCACCATCTACGGCGCAGTCT	
	2624	CGTTGGGTACCGTTCTATCAACCG	2661	TTTGCCCAGCTCTCGCAGAAGTTA	

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TABLE 1-continued

TABLE 1-continued

	TABLE 1-continued		TABLE 1-Continued		
_	Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
	2662	AATTCAGACGCCACATCGACGGTC	2699	CGGTGTGCTTCAAATGCCAAAGGA	
	2663	CCGTGGTCTGCCTCGATTACCTAC	2700	TTGTTCAGACTTAGGCGCTGCCCA	
	2664	GGCGAGGAATTTCGGAACCTTATG	2701	CGGCGGTACTCTTTCCACTGTCCT	
	2665	ATCCGATGATCAGATACCGGCTGG	2702	AAGACGATTGCCCACGTGCCAGAG	
	2666	CCATAGACTAGCGCCAGAGTGCCC	2703	AGGTGAGCGCAGGCATATTGCAGT	
	2667	TGTGGACCTAGAAAATTGCCAGCC	2704	CTCGGGCCTGTACAGCAAAGCCGT	
	2668	GAATAATCATCGCGGTCCTCATGG	2705	TGCGCGCTAGTGCTGCCTATGATC	
	2669	GGGATTGGCTCTTGGTTGGAAGAA	2706	CCATCCTTTGCCTTGAGGGTAAGG	
	2670	ATTGTGCTTCCTCGAACTGGGAAA	2707	AACAACAGCGTAAGACGGACAGGG	
	2671	TGCCCCACCCCGTAAGTCAATAAT	2708	GAGGCGGTCGAGGCTCACAATATT	
	2672	TCAGGACCGACGGTGCACTTAGTG	2709	CGAGGTTAGACGCCTATGACCCAC	
	2673	CCAGCCGTCACAGTGCAATTTCCG	2710	AACTTGCTATACCGGGCGCAGCAA	
	2674	CTTAAAGAGGCGCGAAGCACAACA	2711	CGCGGTGAATCGCATACACAGCGC	
	2675	TACCGCTCGTCGCGATCACAATGA	2712	CACCGAATCAAGCCATATGGCTCT	
	2676	CCGAGTGCGCGAAGTGTCTATGTG	2713	TTCACAGCTATCCTAGGCGCTGCC	
	2677	GCACCAGTGCCCGATCAAAACGTA	2714	AGAAGCGCGAAGTGTACCCCGCAT	
	2678	TGCAGGCTTCTCAACGGCTGGGAG	2715	TGCATGGTATTTGCGTGCGATAGG	
	2679	CTCCGTACGTATCCCGCGTGATAC	2716	GGCCGGACCTATGTGAGATGGAAA	
	2680	GGAAGTGCAACTTAAAGCCCCGCC	2717	TCAACCTGAGTCCTGATCCCAAGC	
	2681	CGAACCGGCAGTCGATCGTTGCAT	2718	TGCTTACCGTTCAGGGAGGCGTGT	
	2682	CCGTTAGTGGTCGACAGTTCGGTT	2719	GGAGAGTTACGCGATGAGCCACCT	
	2683	TCAGGCTACGCCCTCAGCACTACA	2720	CGGTATGCGGTGTACAGCTTTCGT	
	2684	TATACGGGCCGAGGTCCGTATTCG	2721	GTAAGCCGGGTCTCGTGTCGCCGT	
	2685	CCAACGTGTGACGAAGGGCCATTG	2722	GCGTAGTGCGAACGCCCCGACCTA	
	2686	CTGCTCAGCGGTGCTTGAAAGACA	2723	TCCTCGCGGCTTACGTCAAATTCG	
	2687	GGAGATTGACTTCGCGTTTCACCA	2724	CGACGTTCAAAGCGGGAGAGGAGG	
	2688	ATGGTTCAGAAGGTTCGTCGGGTT	2725	CGAGGCACCCCGACATGTTGAGAT	
	2689	GAGTGGAGCATTCTCGGCCCTCAA	2726	CTATTTCGTGCCGCGTCGGACAAG	
	2690	TGGATTGGAACCAATCCCGCACAA	2727	GGCTGCTCAGTGACGTGTCAACTG	
	2691	TGCTCTTGTGGTCACTCGAGAGGA	2728	ATCACTCGTGCGTACCCGACCGTC	
	2692	TTGGGAGCACGGTTACCGCCTGTG	2729	CGAGATGTCCTATACCGTGGCGAA	
	2693	CAACGCGAGCTAACGGTAGTTTCG	2730	TCACACCGAGCCCCATAAATGAAA	
	2694	AACGCTGAGCGCTCACCTTCACCT	2731	AGCTACGTGTCTCGAGCAAAAGCG	
	2695	CCGTCGTAGATCTGGAGGCTTCAA	2732	TCAGGGCGAGTTTTTTCAGCGGCG	
	2696	GGATGGCATGGGCACACTGTAACC	2733	TTCGTTCTGTCTATTTTTGCCCCG	
	2697	TCGCTCGTAGATATCCTTCACGCC	2734	TGGTATGCCCAGGATCCAGCCTAC	
	2698	GGAGCAATACCGCGTCCAAAACAC	2735	TCTCAGTCGTTAGGCCAATGGCGG	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
2736	AAAGATCACCGTGGAGCGATCGGC	2773	TACCCTCCGGACCAGCTGTAATGA	
2737	TAGCAGGACTTGCACTCGTGATGC	2774	TATCCGCACGGTATAGCAGTTGCA	
2738	TGCCCACGGTACCGTTCAAGGCTG	2775	CATCAGTCGGGCTACCTTCAGCCT	
2739	TGAGGTGCGTCGCCCTAAGTAATG	2776	CGGATTAATGCCTTTCCTCGGAAT	
2740	AGCAAGGGTTACAACCCGCAACCC	2777	TTCGTCGTGCCAAGCTAATGCAAG	
2741	CACAACAGCCAGTATTCGCCACAA	2778	CCACTACGGATCAGCACAGGTGTC	
2742	GGCAACACCATACTCGACGAGCTC	2779	GGCCGAGACCACCAGTAACAGGTT	
2743	GGCTGGATTGACAATTTAGCCCCT	2780	CGCGCGGAAGCATTGAAGTTACTA	
2744	CGTGAGAAATGCTACACGCGTCAG	2781	TCGGCTTACCGCTTCGTCTGACTT	
2745	CGCATCTGCCCCATTTTGTTCCTT	2782	GACTGACGTCAAGGCAAGCAACAC	
2746	GTCGGCCTAGTCGGCAGAACGGTG	2783	AGAGGAAGGAGGGCTGTGACAGA	
2747	TCGACACGCGTAGCAGCGTGGACA	2784	TTCCAATGCGAGAGATGGCAGGCT	
2748	TCCCTCACCTTCCAAAAATGTGCT	2785	AAATGGGGTGCTTCGAATATGTCG	
2749	GGGCAAGAACATGAGAACAGACCG	2786	GCTGTCGGATTATTGCACGCCTGT	
2750	TCGTCCTGGTACGACTTGCGTAGA	2787	CCGACTTTGTTTATGTTGCTGGCG	
2751	TGGCGGTTGCATGTGATGATCAAG	2788	GCTGCGATATAACCCGTCCCAGAA	
2752	CCTCGCGTGAGTAAAAACCGTCCG	2789	TGAGCTGGGCGTCAACTCCGAAGA	
2753	ACTTCCGCCACAGAATGCGGCCAG	2790	CCCAAGCATCCTAAATCTCCCTCG	
2754	GTGTAGAGCTTGGGTAGCCCCGTT	2791	CGACAGCAATCCACATGCATTCTT	
2755	CGCAGCATCCGAGTTAACACACAT	2792	TGAATGGTCGGGAAACCAATGCAT	
2756	ATGAGCCTGGGATGATCCGCTGGT	2793	CTTTGCATCGAGATGCGGGGTAGC	
2757	CCTGGCATAAGTGCCGACATGCTT	2794	TCCATTTCCTCCGCAACTCTCAGG	
2758	GCGCATGAAAAACTACGACGGACG	2795	CCACTACGCCATCCTGACAACGAG	
2759	AAAGATGGGTCGATGGGAGCGTCT	2796	TAGTAAGGCCAATGTACGCCGTCC	
2760	ATCCTGGGCACGAGCGGATTTATC	2797	GTCATGCATATGGGGCCTGTTTTC	
2761	TCACCGCATTTGATAGTTACGCGA	2798	ACCGGTAGACGTTAGCGGGTTCAA	
2762	TGGTGGAGCGGACTCTGGTGTTAT	2799	TTGGTTCAAACGGCCACACGTCTC	
2763	CACAATGAAAAAACAATGGCCCCA	2800	GACACAAACTGCAAGGGAGGCATG	
2764	CCTTGCCGCGCTTGTGGTACCAAC	2801	CTCGAGCGCTGTCATCATATCGGC	
2765	CCGAGACCTTTGCCACACGAAAGA	2802	GCGGCTAAGGCACAAGTAGACGTG	
2766	ACCGCGGTGTACACCTGAGCAGGC	2803	ACAGCCTAAATGGCGCAAGACCGA	
2767	GTCGTACGCTTACCGCAGCGGAGA	2804	GCCAAATGCTTGGAATTTGCTTCG	
2768	TCGTAATTTGACCGACACACGCAG	2805	CCGATGATGTAAGCCGTCGGCCCT	
2769	CCTAGACGGATACCCTGAGCGGAA	2806	AGGAGCAAACAAACGCCAGTGACA	
2770	AAGCGACAGCAGAGGTTCAGTCGC	2807	ACGAATTGGGTAGCCGGACTGAGA	
2771	GCGTGGACGATATCACCTGGGCGT	2808	CTGTTCCAGTTCGGCAAGTGCGGC	
2772	GTCGGAGAGCCAGTGGTACGGCTT	2809	AGACAAGTCAGGAACGCGTTTCCG	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-Continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
2810	AGACGACGGCCAGATACGCTGCCA	2847	ACAGAAAGGTGGGGAGCCTAGCGT	
2811	AGGAAGCGCTTCTTCCGGTTCTTC	2848	AGGCTTGCGAACATGGGTAGTGAC	
2812	GATGGACGCAAACACAAGGCGATC	2849	GCGTGGGCCTTGCTCCTGTTTAAC	
2813	CGCATAGCAGTCTCCGCATCTTGG	2850	GAATACAGAGCGTCCGATGTGCCC	
2814	TGGTTCCGGTGTGCAACAGATAAA	2851	GCGACTCTGTAGGGAGCGCGATAT	
2815	CCGTATGCCACCTCCAGAACTCAA	2852	GGTGCACTCATATGCGTCGCATCG	
2816	GTAAAGGAACCCCTCGGGAATCCT	2853	CTGTCCCACGGGGAAACCTTACTT	
2817	GCCTGATGCTCGTTAAAATTGCGT	2854	TGGCTTACTGTCGCAATCTAGGCC	
2818	TCGCACTTGGACCATGAGATCTGA	2855	GCACTCAGTTTCCGGTATCCCATG	
2819	TTCTCAGGCTGGGCAAGAGTCTGT	2856	GTGAGGTTCACGTAAGGCACAGCG	
2820	CGGACCTGGGGATGCTGGGATTAC	2857	GTAACGCCTTTGTCCCCAGCGTAT	
2821	TCGAGCCGATAGGGTTGGCATTGC	2858	GCATTGATATGGTCGGTCTCGCCT	
2822	TACGTGTGTCCCACACGCGTCGTA	2859	GTGGGTTTAAGTGACAACGGACGC	
2823	TGTGAAATTCGCGTTTCGCATCTT	2860	CAAAACCCTGCCGAAGATGTTGGT	
2824	TTGCAATGCTCCAAAAAAACTGCC	2861	TCCGAGGAGACTGAACCTGCTACC	
2825	TCTCATCATGGCTGTGGCTTTGAC	2862	CGGGGAAGAACGGATTCGCTAAAT	
2826	ATTACACCGCTTGGTTTGGAGTGG	2863	TGGTTAGCTTATGTCGGAGCCACC	
2827	GCCGTGCAATGCACAGAGTTCAAG	2864	ACGCGTCGATGAACTAAGGCTCGC	
2828	GAGATCAGACCGTGTCGGATGCTG	2865	TTCTCCTGACGAGTACGCAGTGGG	
2829	CCACCTATCTTGATGCGACCTGGA	2866	TCCGCGGTTGCCGGTTTGTTAGGA	
2830	CCGATCGCCGTTTATGTCTACGGC	2867	TGGCGCATCTTTCAGGGGATGATG	
2831	GAAAATCACGGTAAGGCACGTTCG	2868	TCTTTGGTCCTTGGTGTTTACGCG	
2832	GATTCTCGCTTCCCAACGAGCATA	2869	GAGAACTCCCGCTACAAAGGAGCC	
2833	CCAGAGCAGCATTCCACAATGGTG	2870	TTAACGTGGGAACCGTTGGTGAAT	
2834	TGTGAAATGTGGCAGTCTCAGGGA	2871	GGGACACCATCCTTGGGTTTGTTA	
2835	CGATCCTGCGTGCCTCATCCAGGC	2872	CAACAAACCGCCTTGGGAAGTGAC	
2836	CCCTCAAGTGGGCGAGGGTTTTCA	2873	TTGAAGGCCACCGATACTGATCGC	
2837	TCGCCTCCGCCTCGTGTGTAGAAG	2874	TCGTAATAGAACTGCGCCCAATGC	
2838	TTCGCTTTCAGCTCATTGGAACGA	2875	GGCACGTTGCCCAAGTTGGATCCA	
2839	TGTAATCTGAACAAGCGGACCCCT	2876	ACATAGCTTGGCCGGACACCCACC	
2840	TGGAATCTTTCTTGAGCGCCGTGA	2877	CTTGCCGCCTTGCGAGTGGCTAAA	
2841	GGCTTTCATCTTTAACCGCTCGGT	2878	AGTTCCGCGTCCTACTTCAACGCT	
2842	TGATCCGAGCCATTCCTAATCACC	2879	AATGGCTCGCCAGATACCGCAGCC	
2843	TGGTAGGCGTGATGTCCTACGCAA	2880	CAAAAGGCGTGTCCGAACTTTTCA	
2844	AGGCATCGGTAAGAAGGCCCTATG	2881	CGTCCACTTAGGTGGAGATACGCC	
2845	CGCCGCGAGACGATCCTTATTATT	2882	GAGCCTCTTCGTCCTGAAGACCGA	
2846	ACATGGACGAAATTACGCCCGTCA	2883	AACATCAAGCGGCAATCTCCCTTC	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-Continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
2884	CGTCCTGACATTATTAGCGCGTGC	2921	GCGTCTTGTGATTCTGCCCTAACC	
2885	TGTGCAGACCCTAACGACCTACGG	2922	AAACAACCATCAATGTCGGGTCCA	
2886	TTAGGTCGGCCTAGACCCTCCGTA	2923	TGTAAAGACCAGTTGGCGGCTCTC	
2887	TCACATCGCTTAACTGAGCGCATT	2924	GCGTTTTGACTCGGTGGTCAGTCC	
2888	AGACCTTCCCACGCGAGATGCTAC	2925	TGTATGGAGGCACGGCAAAGTCTT	
2889	TTCTTGCCAAAATGTGTCCAACCA	2926	TTACCTAGGTTCCCGCTGACACGC	
2890	CAGTTTCATTGCAGCGAAAGCAA	2927	CGGCTCGTGGGAATCCTCTGAAGA	
2891	GTGCCGATCCCGAGACAAGTTCCG	2928	CCGGCTCGGGCATTTCTTGGACCT	
2892	CATCCGGCCTCAGTGATTCTTACC	2929	CAACGATGGAATTGTCTCCTTGGG	
2893	TGCTGGAAGCCACAAACGTTACGT	2930	CGGGCTATTATCGGGATTATGGGG	
2894	GAACGGCCAGGGGACAACTATCGT	2931	ACGTACCTGAAGATGCAACGGCGG	
2895	TCATCTAGGTCGAAGCGCAAGACA	2932	CATGGTGCAGCACGCACAAGTAAC	
2896	TTTGGTTACCAGCACCCATGTTCC	2933	CGTCGATATGTCGGGCTATTGCCT	
2897	GACAACAGTCTGTCCGCCACATCC	2934	AAATGCAGGGTTAAGAGGAGGCCC	
2898	GCCAACAGGAGATGCTTGCACCAT	2935	TGCAAGGACTGATTCTCCCGCTGT	
2899	CTAAGGACGCATTGACCCCTGAAC	2936	GTTTTCGGAACGCCGCAGAGTTCA	
2900	GGTCGCGTAGTGAGTCAGAGGCGT	2937	CCCTCGATGGTTCATTGGGAAGAC	
2901	TTACCTCATGAACCCTTCGCGGCG	2938	CCTGTTCGCTCATAATGGTGGGGT	
2902	TATACAGCATCGTCGCCGGGCATA	2939	GAAAGAACGATCGCGGAATAGCTG	
2903	GCTTAGTGGCGTCTTCGTCGTAGG	2940	TCCACCTGTGTGCCTTTATCCTCA	
2904	TGCACTCCGCAACCTTGTGAAATC	2941	TCCTCCGTGAACCGCTGTAGCGCA	
2905	AACCCGTCATGCCGACTCCATCTA	2942	GCCCCAGAGAGTCCCTGCTCCCTA	
2906	AGCACTAGTGGCGTGCGACTTTGC	2943	TTGAGATTTTTACGGTTTCCCCGC	
2907	TAAAAAGTGCCGCTAACCACGGAG	2944	CGATAGGACGTGGGCATGTCCCAG	
2908	CGCGGAATATTTGTCGTCCGATTC	2945	CCCGAACTTTGAGATCCGAGAACA	
2909	TTCTGCTATGCGTATGGGGGCCCG	2946	TCACGCAGCTAGAGTCGCGTTACC	
2910	CGAACTACTGCGTCAGCCTCTCCC	2947	AGATAACGCCCACTGACGACATGC	
2911	AGATGACGAATTAGCGGGGTTGGG	2948	ACGCTTAGAGCTCCGATGCCGAAT	
2912	AATAACAGTGGCAATGAGCGGGAA	2949	GGGCGATAACTTAAATTGTGCCGC	
2913	ATATGTTGATTCCCGTGCTGCACA	2950	AGGACGTTCATGCGTCTCTTTGCA	
2914	AGAGTGGGCACCACCAGGCAGACA	2951	CGGCTGGTAGAACTGTGCATCGTA	
2915	AGGCCTGGGTTTCTGCGTCTTAGT	2952	TTCGAAATGTACTTCCCACGCGGA	
2916	ATGACTTCAGGCACCTCAGCACCT	2953	GCAGGTTGGCTGTCTTGTGGAGTC	
2917	CGGACGTGACAAACGGACATACCC	2954	CGTTTGGTTGCTTCAAGAACCGGT	
2918	CAAGTGTTTCGGCCCAACTCTCGA	2955	CATACTTGGTTGTTGTGCCCACGC	
2919	GAACCCTTATCGGGATAGGCCCAA	2956	GGGGTCGGCTGAAGTGTTTTATCC	
2920	CAGGACGATACCAAGCAGAACGCC	2957	GTGACGGTTGATTAACGACCGTGG	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
2958	CTTATGGCAGCGCCAGGGGCACTC	2995	CAGGCGTAAACCTGAACCAAACGG	
2959	GTTAGGGGACCCACCTCGTTTGAT	2996	GCCGATCTGTGCTGAGGTTCATCA	
2960	CAATATAAATGCCGCGCATCGAGT	2997	GATATCGCGTCGCAATATCACGCG	
2961	TTCTTCATCAGCAGTCCCCGAGAA	2998	CCCTGCACGATTAAGCCACCTGTA	
2962	AGTTGCGTCCCTTGATGGCATTTT	2999	TGACATACAGATTTGTGTGGCCCC	
2963	CCGACTTTCGTCCACGATTCCTCT	3000	GTTTGCGGCCGGTATTCACGATGT	
2964	ACTTGGCCGGACGACAGCAAAGAC	3001	TTTTACCTGGCCATTGGTGAGCTC	
2965	CACCGCGGTAGATGTATCCCTTCC	3002	CTCTACTCAATCAGGGTGGGAGCG	
2966	GTTAGCTTTAGCTCGGCACGCCTG	3003	GGGTTGGAGGGAGTCTTGACCATT	
2967	GCGCATAAGAAGGTCCGCTAAAGC	3004	CGAGGTCGGTAAGGAAAAGCTTGC	
2968	ACATCACGCCTGGCGTGACCA	3005	CTTTACGCAGGCACCTCCGAGCTG	
2969	CCGGCGAAGTTTGGTGTGATTAGA	3006	CATTGTATGGCCACGTGATTGACG	
2970	TGGGAAGGCAACATGAAAGTCCTT	3007	GTACGGTGCGAGAGCGCCTAAGCG	
2971	TGCACCGCCAGATTGTGCTGAGTC	3008	TTCCATATGCCGAAATGGACACAA	
2972	ACATGTGAAGTGAGTGCCGTCCAA	3009	TACGCCTTCCGCTATAGCTCGTGA	
2973	CCTCTGGAGGGGATTAGCCACGCT	3010	CTGGCCGCTCGGCTAGCCATCAAT	
2974	CAATAGCCATGTCACTGGCAACGG	3011	CTGTACGCCACGCATGAAGGGTGA	
2975	ACCCATGGTTCCAACGTTCTTTCG	3012	CTTACGCGTCCAATGACTGCCACC	
2976	AATCTGGTCTTGGCATCCTCCAAA	3013	CACATGGTAGAACTCGATCGGCAG	
2977	GTATACCGGTGCATGCTGAAGCAA	3014	CGCACCGGAAACTAGTGGATGTGT	
2978	AGTGTTCTGGTTCGAGTCGACCCG	3015	ACTATGGCAACCGACACTTGGTCC	
2979	CGGGTATTCGACACACACGAGGAC	3016	CTAGTTTGCGCTACCCACCTGCAA	
2980	AGTGCAACAGAGCGCTTGGTCACG	3017	TAGTATCGCCCGACAATAGCCTGG	
2981	TGCACCTATAGTTTGGTGCCGGTG	3018	CCAATATTTACGGCCTGATCAGCG	
2982	TGCTCACGTACCAGGACACTCGAG	3019	ATGGCTATCCCTTACTGGCTCGCC	
2983	AGTCCACACCTCGAACGACAGGCG	3020	CAAAACTTGGCAGGCTTGGGACTT	
2984	CGCCGACCTGGTCAAAGAGCGCTA	3021	AATGACCGAGGCTGCAAGATTGAC	
2985	GCCTAAGGGCCTGTCGTTTTCCGA	3022	ATCATCTTTCGCCACCAGACATGG	
2986	TGTGCGTGCTTATGTTCCGGTCTC	3023	CGTTATTACCGATGCACACGTTGC	
2987	CAACCGTTGGCCGTAACAAAAATC	3024	CACACTGGCAATCGCCTCCCTCGT	
2988	CGAGAATCAAGGCGTACCATCTCG	3025	AGGTTGGTAGGAAATCGGAGCGCT	
2989	GCGTAGGCAGCCTCCAGGGAATGG	3026	GCTGAACCACTGTGGTCAAGATGC	
2990	GATGGTGTTTTCGCCAAGACCAAT	3027	CGTTGAGTACGACACGGTCGAGGT	
2991	CAAGCTAGGGACAGAATTGCCCAC	3028	TTTTTCCGCCGCAATGTGATCTAA	
2992	TAAATAGGCGAAACCGTTCGTGGC	3029	ACAATACCTCGACCGCTCAGCATC	
2993	TCAAGACCCGCAATGTGTTCATGT	3030	AGTATCCCTGCTGGCATACACGGG	
2994	GCGGCTGGTAGACTCTTTGCACAA	3031	TCTTGGGCTCGGTAGTTCAGCACT	

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TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
3032	CCCTATATCGAGCCCATAGGGCGA	3069	AGTCGACCCCAAGGCAACTGGGTC	
3033	CACGAGTGGCATCAACGGCCTACT	3070	GGTACTGTTAGCTCGACGATGGCC	
3034	TGCAGGGTCCGATGTGTTCAAGTA	3071	CCGCAATACTTGACGGTAACAGGG	
3035	GCTTGACCGCTGCTAACCTCGTAC	3072	AATTCCGGGTTTGAACGGTTGGAA	
3036	TTTTGCATCTCTCCACCATCCAGA	3073	GACACGCAATCGGGTCTATGCGAA	
3037	AGAATGTGCACCGGCTTCCATCTT	3074	GATTTTGGCGTCTCATTGCGTGAT	
3038	TGTTATGACCCGCTCTGTGGCGTG	3075	TGCCATAGGGAGGAAACGCAATTA	
3039	GGAGCTCCTGTTTCATCGAGGCTA	3076	GAGGTGCCCATGTTAGTGGTGTCC	
3040	CATTTTGCTGTTTGGGGGTCCCAT	3077	GCTTTAGCGGTCATACGACCACCA	
3041	CCCGCTCCTTCACGTGAGACGAGA	3078	CCGCTACCAACAATCCGATTAACG	
3042	GCGCTCAAGTCGATTGCCACAACC	3079	CATAGTGGGCTGAAACCCCAGGAA	
3043	CGGTTGACGGAGACCGCAGTACTT	3080	GAGGATCTGGCCACATCGAGAAAG	
3044	ACTCAAGACCGGTGCACCTCCAGC	3081	CTCGTTTGGTACCACGTTTTGCCG	
3045	TGGATGTCGAGCGTGTCTGAGTTT	3082	AATACACGCGGCGTAAACAGACGA	
3046	TTTCGTGTGCATGCAAGTAATGGC	3083	TGTCATGGGCCAAATGACAGTGGC	
3047	GCGGCGTTAGCTCGAGCTAACAAA	3084	ACAGCACTTCCGACCCGTGTACGA	
3048	GGGTATCCTGCCCGAGCAGTAATT	3085	CTCCGTAAAGAGCACAGCTTTGCC	
3049	GGCTCCGAATCTCTTGTCCGGTCT	3086	ACGAACAGGTAGGGATCGGTCCTC	
3050	AGGATGGCCACGCCGAATCAAAGT	3087	TGGATCCACCTTACCGCGCCATCG	
3051	GTGCGGGACGTTTACATAACGAG	3088	AGTATCAAATAGCGGCGCGCAAG	
3052	ACTTTTGACCTGAGGCCGCTTGCA	3089	GAATTACATTGTGGATGGAGGCGG	
3053	ACTCCGCTTCAATGGAGACCGTTG	3090	CTCCTCGGGGAGTCGAGGAGTACG	
3054	GATCGGAATTCGCCGCCATATTGA	3091	AGTGTCGAGCCAACTCCCACCAAT	
3055	ATGCGTGCCCATGGAATGACTTTT	3092	AAATGACATCCGTTTGGCCACAGC	
3056	CCGCATCGCACGAAGGCAGGTCAT	3093	CGAATCATATCGCCATCGAACTGG	
3057	CACCCTATGCGTCTCCAATTCCTG	3094	TATAATGCACTCGCTTGGTGCGCA	
3058	TGATATGCATCGCTGAGCCTCTGT	3095	GCCAAGCAGATGGTAATTATGGCG	
3059	AGCTTCACACGCTCACTGAACCTG	3096	CACGCGGGAAGAGCACGTAGAACT	
3060	AACCCGGAACCTCCTCTCACTCGG	3097	TACCCGAGAATTTGGAGAACAGCG	
3061	CTCGTCAAACTTGGCCGAGGAGTC	3098	TGACGGCAAACTGTGGCATCTATC	
3062	GTAGCTGGCAACAGGCAATCAGGA	3099	CACAGTGTTCCAGCCCTTGACGAT	
3063	CTTGTCACGAATATTCGCCAAGCG	3100	TACCCGCCCACACATGAAAGTTGG	
3064	CAGTATCTGAAACACGGGGTGCTG	3101	TGGCATATTTAAGATTCGGCGACG	
3065	GGCTAAAATGGGCGCCCACGTGTA	3102	ACTGAAAAAAGAACGGGTAGCGGG	
3066	ATGAGAGCCAAGCGCCTCAACTCC	3103	TCTGACCGCAATAGGTGGTCATTG	
3067	TATTGTTAGGCACCGCTTCGCGCT	3104	ACTTTTTGGCGGGCCCTCTCTCGT	
3068	GGAACTAGATTGCCAGTGCTCGCC	3105	CTGCCCAGATCATTGCGCGATCCG	

TABLE 1-continued

TABLE 1-continued

	TABLE 1-Continued		TABLE 1-Continued		
_	Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
	3106	CGGAGGTTAAATGCTTTAACCGGC	3143	CGTAGCCTTCCACCGTGTCGATAG	
	3107	AGGCGTCTCCAAACGTCCTTCTGT	3144	CGCTCTCCGTCTGAGGAAAAGGGG	
	3108	AGATGCTATCCTGAGTGGGCCTGC	3145	TCGCCCCAGCCAAGGATATATTGC	
	3109	ACAGGGTGAAGAGACCGTGGGATG	3146	TCTCTTGCAAGGAACTCTGCCGTC	
	3110	GACTGTCTAACGGACGACGACGACG	3147	GTCCTGGACAGACGGAGGGTGTTA	
	3111	AGCTGTTAGGACCCGACAACCGGT	3148	GCCAAATTAAGCGGGCTCGTAATC	
	3112	TTGCGTAGTGTGGGCATTTCCTCT	3149	CCATTTGTTGACCGATGGGAGGGG	
	3113	ATGCGCGCTTCTTTCCTTGATGTA	3150	TGGTCAAAAGAGCACGATCCAGGA	
	3114	TTAAGGGCGTCCGCGTCTATTCAG	3151	CGCTACTAAGACGCCCCTGTCCAC	
	3115	ACCTTTAAACTTGTACCGCGGCCC	3152	CATACCTCCCGCTTGGATTCACTG	
	3116	AGGGATGCAGAGGCACCACATGTT	3153	CCGCGGAAGGAATGTCATCTACAA	
	3117	CGGTTCGACGTATGAGCATCCGCA	3154	CACGGGACATTCATTCACAGGACG	
	3118	CAGGGCGATAGTCACATGGAGGTT	3155	ACTAGTGAGGCGTGAGGCGGGCGT	
	3119	GCTTGACTGCCCCGTTTCATATGT	3156	AGGAGTCACCCACTCCGCACAAAA	
	3120	CGAAGGGGTTGTGCAATTACCCGA	3157	TCATGACAGCGCACCCCATACCAT	
	3121	AAAACGCACCGCAATGACAAAATT	3158	GGTAGGGGACTATCGATCGTGCTG	
	3122	ATTCCTGGACAAGACCCTCAACCG	3159	ATGTCTCACTACCGCACGTAGCGG	
	3123	CCTACCTGCCTGCTAGCGGTGAGG	3160	TACTGCTCCGGTCTTCCGCAGCTT	
	3124	GCTCGTAAATGGGGAGGAATTGGA	3161	ACGGAGGAGCGACTCGTTCGCTGC	
	3125	ACATGAAAACAGGCTCAATTGGGG	3162	GAAGTCTGTCGCCGGTGGACGGAC	
	3126	GTTCCGCACATGGATTGAGGTCTC	3163	CCGTAACGTGTATTCGGACGAGCG	
	3127	GGCACCCAATACCACGAAGAAGAA	3164	CGTGGAAGCGACTTAACCAATCGT	
	3128	AGGGGCATTTCGAACTCCATCTTT	3165	GGCATGGGCTATGCCTCACACTAG	
	3129	CATCATCACAAAGGAACGTCGGTG	3166	GGGTCGTATTTCAGCATCGTTCGT	
	3130	TAAAGACCCACCGTCAGCAGCAGC	3167	AATGGTCGCGCAAACCGTAAGAAT	
	3131	CCCCAGGCGTAATGCACCACATAG	3168	CTGGATTCGGTACGTCCAACGTTT	
	3132	GCAGGTCGAACGCTAGTGGTTGAA	3169	CGCAAAAACACCCGTAGCCAAGAA	
	3133	GGAACTTAGGAGTTCACGTCGCCA	3170	TATGGATACGCTTTTGGACTGGGC	
	3134	GCAGATACGGCTAGCTGAGGTGGC	3171	GCTTCAAACGCGCTTCACGCTGGT	
	3135	CACAGGCCTAGAGCCTCGGCGTTC	3172	TACAGCCCGCTCTACCTCGCCACC	
	3136	GTTTTGCGCGCATGAGGTTCATTA	3173	TCAACCGATGTCAAAATGCACGTT	
	3137	TTGCGCCTGATGCCAGCAGTACTA	3174	AGCTCTCTCCGAAGTAGGGCGGTA	
	3138	GATATCAGGCTTTCCCACTGCCGC	3175	ACGCACACATGGAGACTTGGCTCC	
	3139	TGCGCGGAGACGGAGATCTATGAA	3176	TTCTTGAAAGCTAGTGGGGCGCTA	
	3140	CATTGGTGTTGGCTGAGAGTGGAC	3177	CAATCACGGCTGGGCTATTCTGTG	
	3141	GTCGGCACTTGGGCACCATTAATA	3178	GTGGCGACCCGTCGGTGAAAGAGT	
	3142	ATCGATCGGTGTCTCACCACGGAG	3179	CGTCGAATGCCGAACCAGTTAAGT	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
3180	TGCGTATTTGCATGCTCACAGCTG	3217	AAATTAATTGTGGTGGCTCCGGCG	
3181	CGCAGTTGGTTTGTGCACGGCTGC	3218	TTACAATCCTCGGGCTCACTGACA	
3182	GTTTTTCCGTGAAAACTGGCATCG	3219	GCTGAAGGACAAGGCGTGGGCAAC	
3183	ACAGGTTCCTCCACCACGATTTGA	3220	GGGATAGGAGACCCTCGCAATGGT	
3184	CTAGCGCGCTTTTAGGTCCTTGCG	3221	TTGCAGTACGTCCTTGCGCATGAA	
3185	CAAAATCAAAGGGATCAACCGGTG	3222	TTGATCACTGGATTGGGTGCGAAC	
3186	AACGTAACCCCAGTGAGTCAGGCA	3223	TCTGCAGACGTTGCGAGAGATGAT	
3187	TCAACCGGTGCACTTTAGAACGCC	3224	AGTCTAGCAGGGATCGAAGCGGAT	
3188	ATCGCAAAGTTGCAGGCGAATACT	3225	GGGGTCCCGCAACAACTAATGAAG	
3189	ATATGTCCCTGGGTGCTGCACAAC	3226	CAACCTCTTATGTGGTGTGCGCGA	
3190	TGGCACTTTGTAGTGCTGCGGTGG	3227	CTCGCTGGGTTGCTGGAGTAGCAC	
3191	ACGCACGACGTCCTTCTAAGCTCG	3228	CGTTGTATTGTGCAACGCGAAGTT	
3192	CCCACGTGCACTATAGGGATTTCG	3229	GGGCTCAAAGTGCCTGAGTCGAAA	
3193	CCGCGCTTGGTCAGTCATCCTTGC	3230	CTGCTGTGCCCTCTCAGTGAGAGC	
3194	AGCGGCTCAGGGAATAACAACAGG	3231	CGGACGTACTGTTCGGAGTCCTCA	
3195	ACAACGCGATCGGAGGCAACCAGT	3232	GTATACCACCATACCGGGACCGCA	
3196	AGCAATTGCCTCCGTAGAAACCCA	3233	CTGCTGCGAAGGGAGACACGTCCG	
3197	GAGTCGTGGCATCGCCTGCTATCG	3234	AAAGAACGTGGAGGATCCATTGGG	
3198	TCTATGCAAATACTGCGCTTGCGA	3235	TCGATTGGCTGATCTCCAGCCTAC	
3199	TCAGCTTAAGTTACGGTGTGGCCG	3236	CTGCGAATTCGAAGGTTGTTACGG	
3200	TCCAAGGTCGAACAGGGATCAGAA	3237	GCAGGAGGTCAGGAGTACGTGAG	
3201	GTTAGGCTGGCGTCAATAGCGCTT	3238	ACCAACGGAAGGGAACTTAAGGGC	
3202	GGTGTCATAAGGAAGAGGGCATCG	3239	ATGATGGAGGCTGCGTTTTGGTCG	
3203	CCGGCGGCTAGATCAATATTTCT	3240	AAGCCCAATTTACCGCTCCGAATA	
3204	CTAACGTCAAGTTTTACGCCCCGA	3241	CTAGGCTGTGCGGGACTAGAGGTG	
3205	GCAGCACAGTTTTCCGATTTGCGG	3242	TGCCATCTGACCTGGTGATTGCGT	
3206	CGCACGCAAGGGGAGGGATGACTG	3243	GTCGTCAACTTTTATCGCGCACCT	
3207	CGGGGCCGAAAAGGACGTCACAAG	3244	TTGAATGTAGGCTGCTGCAAGCGC	
3208	TTCTCCAACACGGCTAACCGGTAG	3245	CACCTATCGTGGCCTCTGTCCCAG	
3209	TTACAGCCTGGCCCGAGGTAGTTG	3246	GGAGCGCCCAGTATAATGAACGTG	
3210	TTTCGGGCAGCATGAGTTATCGAA	3247	AATGGGGTTCTTAGGGTGCCGTA	
3211	CTACTGGACGCCCTGCTTCGAAGT	3248	GCCATGAGGAAAAGCACTGGGTCT	
3212	GGTCGTCCGACGTGAAAAGACCAA	3249	TCCGGGTCGTACTGTGTATGATCG	
3213	GTTTTCGAGCTCTTTCTCCGCAGG	3250	GGAGGTTATGTGCTGCTGATGACG	
3214	GCGTGAAGGTACCCAGTGTCACAG	3251	CTTCAGCCGTGAATGGTGTGAAAG	
3215	TTTCTGAACGCTTCGACGCAACAC	3252	CTTCAAGGGCTTCGTCTGCTCGTG	
3216	TGCTAATAAGCACGCCTAGCCCGT	3253	TCAGGGGTCACGCATTGGGTTTCA	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
3254	ACGGTCCTCGCATAATGGACCACT	3291	GCAGCATCCGTTCCCCTATAGTGG	
3255	AGGCGTAAACGCCGGTCATAGTCT	3292	GTATTCCTGACCGGCTGAGTGTCG	
3256	GATCTGGTCGGAAAACAGGAGCGC	3293	GCAGCGTATGGGGTTAGCCAATGA	
3257	CCCATCGATGTTATTTCCGACGCA	3294	CGCCCTGGTGGAGTTGTATGATGA	
3258	TGTTTCTCCGCATCAGTACCGCAT	3295	AGGTAGACTGCCCGCGGCAGAGCA	
3259	CGGACCCGGATCGACAAGTAGTCA	3296	ATGCGTGAGGAACTGACTTCGGAC	
3260	AGCCAGAGCATGAACTGGAGCGTC	3297	ACGGGAGAGGACATGCATTTTCAA	
3261	TGGAGTTTACATCGGAACGCAGGG	3298	ATTCATGCAGGAAGTCCGAGGGAA	
3262	TCGACCACCGGTACGATACAATCA	3299	AGCTCTCCCGAAGTAGGGCGGTA	
3263	GCTTGTGGAATTCCGACGGTTCCA	3300	TGGCCCACATGATTGGAGCTCCAA	
3264	CACATCCACCCTACTGAGGCACAA	3301	GCCCTTTGCTTGCATTGATTGATC	
3265	GCCGGATGAATCTGCCTCGCTACA	3302	AGGAGATTCTTCGGCTCATCTCGC	
3266	GGTTGCAATTACGCCGGGATTAAA	3303	GCAGCTCCGCCAACGAACTTATAG	
3267	ATTTCCTCGCAAATCGTCTGGGTG	3304	TGGGTCAGCTTCGGCCAGGCTGAT	
3268	GCTCCTACGCCATGTGCACGTTTA	3305	ACGCTCAGCGTGCGCTAGATACGA	
3269	AGGGTTGTCGAAACATGGGGGTGA	3306	GCAACGAGAGCGAACGGTTAACTC	
3270	ACGCGACCTGCTGTCAGCGTGGTG	3307	GAACACAAACAGAGGTCGTCAGCG	
3271	CGCCTAACTAGGGGAGTGAACGGA	3308	CGTGCGTTAGCGTCGGCGTATGTT	
3272	GTTGACCTCCGGATTTGCTCACGA	3309	GTGCTAGCCGAAAGTAGCGTGCGA	
3273	TACCTCCGTCATTCACTCTTCCCG	3310	CGCGGAGGTTTGCAAGTTGTTAAC	
3274	GGCGTTCCACATGTAATTGGGTCT	3311	TACTGCCCGGCCTGAAATGACTTA	
3275	CGCATCACGATCGTTAGGAGGGAG	3312	CATGCGCACATGAGGGTCACCTTT	
3276	GGGCATTAAGCACGCACTTCGTCA	3313	CTCGGGTTCTGAAAGCGATGCTTC	
3277	TTTCCATAATTCGACACCACGCGG	3314	GGCACACGAAGGCTGATGATA	
3278	GACCATGAGATGCTTTTCTTGCGC	3315	GGAGGCCGAGTAACCTTGAGGGTC	
3279	CGCGGTCGTCCTCAGAGAATGTTG	3316	ATTCCTATCGCGCGTGCTTCTAGC	
3280	TGCTGTGACGATGGCTCCTACCCG	3317	TTGCCGGTGTGTTCGTGAGCTGTT	
3281	GGCGAATGCTTCTTCGCATCAAGT	3318	TTATGGGAATCTACAAAGGGCCGG	
3282	AAATGCACAGCGGAACTGACCACA	3319	GGGTGATCCAAAATCCACGGAGGC	
3283	TATCGACCTGGAACACGATCGGTT	3320	GCGAGATGAGCAAATTGTATCCCG	
3284	CATTGAAGTCATGAAGCCTGGTGG	3321	CCTGCACACATCATGTCTCAATGC	
3285	CTTTCAACCGTAGTGGCTTGGGCA	3322	GGCAGCGTAGGGATTTCCTAGGGG	
3286	CCGGTAAGGTCGAATTGGAGCCTA	3323	AGAGATTGCTCCTATGTCGGCAGC	
3287	GGATTGAAAAATCGCCGGAAGATC	3324	CCAATACCCTGGTGACCACTCCAA	
3288	TGAAATTGTGAGGGAGCCTTAGCG	3325	GACGTCTGTTATGTCGTCGCAAGG	
3289	AGCGGGATCCCAGAGTTTCGAAAA	3326	CCACAACGTCGAAATGACCTACCA	
3290	CGAGTGTCACTGGTCGGTTGCTCA	3327	CTTGGTGGCATGCATGCCTTGCCC	

TABLE 1-continued

TABLE 1-continued

TABLE 1-continued		TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
3328	TACGTTCGCCCGACGTGGAATAAA	3365	GTCGACCGTGTTTGTGGGGGATAT	
3329	GGAAGAGAAAACCGACAGTCGCGA	3366	AGAAGACCTTGGCAATCCGAGTCA	
3330	GACGAACAAGAATTTGGGGCAACC	3367	TTGGGTGCTTAAAATGCGGTCTGA	
3331	CGTGCCCGCGAGTTCATGGTGCTA	3368	AGCGAAGTCGTATTGACGTGCGGT	
3332	AAGAGAAACCCTTTCCGGAGCTCA	3369	ACTTTCAGCTCCCAGTAGCACGCA	
3333	TTTTAAATCTGCCGCCCTTCCATG	3370	GCGCATGGTGAGTCCGTATTGCCG	
3334	TCTGAAGCAATTTGGCCTCCTCAA	3371	GGGTCGTGTCAGAGGACAAACACC	
3335	GATGCGCAAGAGGGTATTATGGGC	3372	ACAAGAGGACCTCCGGGTGAAAAT	
3336	GTGAAAATCTCGCAACTTCCTGGC	3373	TAGCGGGGACCTATCCGCCTCAGT	
3337	ACGGGAAGCGGTGAATTGTTGGTA	3374	GCTCTATGCCATGTCCGTGGATTC	
3338	GCCCTACTATTGCCTTGGCAATGA	3375	AGCTCATAATGCGCGTTGACCCCG	
3339	GTAAATGGCAGGAAGCGGCTCTCG	3376	ACAGTGGAAACGTTTCATGCCGAG	
3340	AGGTGCCAAATAGTGGACTGCGGT	3377	GGTTTCGACGAAAAGGATGGTCGT	
3341	TCGGATGGTAGGAGGCGAGATCGG	3378	GCGGTACGTATTCTAACCCGACGG	
3342	GAGGTGAAGGAACAGCGACGCTAA	3379	GGTATTCGCCATGCTTGGTCTCTG	
3343	ACCGTCGTTACCGCTCTGGTGTCG	3380	GAGCCTCTCCGATTCTGGCCCAGA	
3344	TTCCAATGTCCGACATGCTATGCC	3381	TGGAACGTAATACGAACGCCGAAC	
3345	CGGCTTTATAGGTCCAACATGGCG	3382	GGCAGAAGTGGAACTGAGCTCGAT	
3346	CCGGCCTGGAAAGCAGAGTTATTG	3383	CGGGTAGGCCTTCAGGGTACAGGT	
3347	TTTATCGTTCAACGCTCACGTCCC	3384	AGCGATCTTGGACGCCGGCACGAT	
3348	AGACCCGCTGAACGGAGCTVGGAT	3385	GACCAGGTTGGTACAACGCCTTGG	
3349	ATCCATCAGGAGAAAGCTGGCTCA	3386	GATGTGCTACAGGACCGCCTACGC	
3350	TTGCCAATGCGTAAATCGGTTCTC	3387	TGAGGCGCACTCATTAGGAGGTGT	
3351	GCTTGGCAGAAGGCGTACACTAGG	3388	CACCTTACATCCCGAATCCGCGTA	
3352	AGGCTCCAATGCTTTAGCCGCAAA	3389	CCAAACATAAGGTGTGTCGGTCCA	
3353	GATACTAGGAGCGAGCCCCTTTGG	3390	GCGTTTGCTAATGGTTGCGATTGC	
3354	GTCGTGTGCAGCCGCATATGGAGG	3391	CCCTTGCCCTCAATCTGTATTGCA	
3355	TACCCCTGTTGCGGATAGATGTCG	3392	ATAGTCCCGTGGCGACTGTGATCC	
3356	TAGGGTAACAGAATGAGGGGCGCT	3393	GAAGTTCCCGGCCCGAGTAACATA	
3357	ATCGTGTCGGGGATCGAATTTGAG	3394	GGGAGCCACGACAGAGCTCCTAGG	
3358	ATCTCTCGTGCGGTCTTGCAGAAG	3395	CTGACTCTTACGAAGCGCACTCGC	
3359	AGAAGCCACATGTTAGTGCGGGAG	3396	AGGTATAGCGGGGCGTCTAGCAAA	
3360	ATCTGCGTTAACTGTCCCGACTGG	3397	TAAGACGCATTGCTTGGACCATCC	
3361	CGCTCACAACGAGCTTACTCATGG	3398	GCCTAGTAGGCCACGGCTTCATGC	
3362	TCTACGCTACGATCCGTTGCATCA	3399	CGTGCCCTAGCATACAACGTTGGG	
3363	TTTAACACCGAAATGGGAGCGTCC	3400	GGGAATGCGGCAGTCTGTCTACCT	
3364	ACAGGGCGTAGTAGGCCGCTTTCC	3401	GTTGAAATACTGGCCCCGCGGGAC	

TABLE 1-continued

TABLE 1-continued

	TABI	LE 1-continued	TABLE 1-Continued			
Seq. ID No.		Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')		
	3402	CGGACAGGTGAACCCAGTCACCTT	3439	AAGTTTTAACGCTCAAGGGGGCCT		
	3403	CAACAGCCCGCTCCTTGGATATAA	3440	TTGGCGGTTTCGGTACAGGATCCT		
	3404	TTAAAGGAATCAGGGGGACCCGCC	3441	TACTGCGATGATGGGGATTTGACA		
	3405	CGGGTTGTAACGCTGTTGGACGAA	3442	CGGTGAGCGAAGATCATCCCCTTA		
	3406	GGTACGCAGCGGGACCAATAGAAA	3443	ATGCAAGTCACCGACCGGCACCTC		
	3407	ACTGCAAGCCTCTTAGTTCCTGCG	3444	CAAGTGCCGCAATTGGCCTTTTAT		
	3408	TCAATACCACCCAGAAACTGGGCG	3445	CCCGTGGTGGATACCTGGGTAAGC		
	3409	GGCAGTTGACACTCATCGACCATC	3446	CCGTCAGGGTCTAAGGACCAGGGT		
	3410	TAGCACGGCCATAAGACGGTTGAA	3447	CTTTCCGTAGGCGGTGATTTCCAA		
	3411	TCCACAATGTCAGCTCACTGCAAA	3448	GCTGAAACTGAGATGGTATCCGGC		
	3412	CAGGCGGAGGGTTTTACATCCTA	3449	CCAACGAGACAGCATGAAGCTCCT		
	3413	AGGGCACTCGAAGATCCGACGGGC	3450	ATAAGTTCGTGGGCCGGCAAGGTC		
	3414	CGCAATGCCTTTTGCTGTGGTAAT	3451	GTGGCCAGGCCATAACTGGTCACT		
	3415	AGAAACGCAGACGTGGCGTTTTGT	3452	CGCTTAGCGCGAGACTCTGAGGGC		
	3416	TGAGCACGAATGTCGAACAGTCAA	3453	AAGAGCGGCGCCCTAGAACCCAAC		
	3417	CTCGTTTCCATGGGGTAACCGACT	3 4 5 4	CCACGGGAACGTCTACGAAATGAT		
	3418	CCTCATAGCTACGGGTGGACGACG	3455	AGTCGTGTATCAGGTGCCGAGAGG		
	3419	GTACGCCGTGTATCACCCCATTCA	3456	TGAAGCGGCTGGCGATAAGTAGAT		
	3420	ACCCATAGTTCGTCGATAGCGCGA	3457	CTGAGGACGTGCGGTTCATGCTGA		
	3421	TCTGCAGTGTTGCCCCTCCGACGC	3458	GAAGGCGTTCGGAAAGTTTTTCGT		
	3422	TGCACATGCAACTAATAGGTGCGC	3459	AAGAAAACCACGGCTGAGACCTGA		
	3423	CAGCGCAGTGCCTTACCAATATGA	3460	TCAGCCGCTGTTGCAGGGAGAAAA		
	3424	TTACGCGCCGAAAACACCTGAACA	3461	TTCTGGAAATGGATCGGATAGGCA		
	3425	CTCCCTCGCTTTATATAGGCGGCG	3462	GGGAAATGGTCTTGTTGGCGACCA		
	3426	GTCGGACCCCGAGAGTCCTGTTAA	3463	GGTGTCGAAGCCACGATGTATCCC		
	3427	ATCGACGAACAGGGCCTCCGGCTT	3464	CCCCGACTCCCTTCGGGCATAAGT		
	3428	TGGTTTTTCACCTCCGTCCTCAAG	3465	CCAAATGCGATAACGCAGCGTGAT		
	3429	GGAGGGGCCAACTCCTTGACTTG	3466	GCTCGCCAACGTACGAGGCTCAGA		
	3430	TCCTGTCTCGGCCTTTGGGAACTT	3467	GGCTTATCAGTCGCCACCAGAGAC		
	3431	CAAGCCATTACCCGCTAGCTGAAA	3468	GATGTGACCCATCCATTCCTGGGA		
	3432	CGCAACCGACATTATATTTCGGCC	3469	TCCTGGTTTGGTATCCCCGAATCA		
	3433	TTGAGGGCGACTGCAACACACAGG	3470	CGCCCCGTATATAGCCGGTAAGAG		
	3434	GCTCGAGTAACACGGTTGACCCGA	3471	GGTTCACTGTAACGATCGCGGCAC		
	3435	CAGCCCTAGCGCCACGGTAAAATC	3472	CCGGTATAGAGGAAACCCGGACGT		
	3436	GTCATTAGCGACTTACCCGCCGTA	3473	CCTCCCAGGAGATCCTACGCAATT		
	3437	CCCAGTGGCCGGCCCTAGATAATA	3474	TGAAACTCGTCACGCTCCTTGCAG		
	3438	CATTCCGTATGCTACTCGCGAACA	3475	TGTTGCGTAACCACCAACCCTCCT		

TABLE 1-continued

TABLE 1-continued

	TAB:	LE 1-continued	TABLE 1-continued		
Seq. ID No.		Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
	3476	GCAGCGCAACCTTGTACTTCTTGC	3513	CCCTGTGACCGTGGGAGACACACA	
	3477	CGCAAGTGGGAGCCCAAGAGTTTG	3514	GCGCATACTCTGGGTAGTCGGCAC	
	3478	TGCAGGGTAACGAGGGTAAGTGGG	3515	TCCCCTGCCCATCTCTGAGTTAGG	
	3479	GAACTGTAGGGTCTCGCCGGTCAA	3516	TGCAGCGCTAACATAGCGGGTGCA	
	3480	CGAGATGTCCAGCAGCGGTTGTTA	3517	GCAGCGTCCACAGGAAACCGCAGC	
	3481	TTGTGGTTGCTCCGGGTAAAAGGA	3518	AGCGTACCATCGATGGGGATTCGA	
	3482	TCTACGCATCCCTGGGTAATTTGC	3519	TGGCCTCGCGATCACCACGATGTT	
	3483	AGAAGCTGCGAGTCACCGTGACTC	3520	TTGGTAATCACTCGGCCAGCGCTA	
	3484	GGGCGGTGTTGAAGGGCTCTATAC	3521	CGTTAGTAACGATCGTCGGTGCAA	
	3485	TTCCACAACGGGTGAGTAGGACGG	3522	AATCGCAGATGGTTCGTGGCACAA	
	3486	GCAGCCAGACTGGCCTACCGATCG	3523	TAAAGCGTCTAGAGGCCGGCTGTG	
	3487	CCCGCCGAGTTGGTTGGCTAAACA	3524	TGGCTAAACGAAACTGGGAATCGG	
	3488	GCTAGGGTGGTCCTTTCAGTGGGT	3525	CCTATGCAGCCACTGGTGTCCTTC	
	3489	CGTGACTCTCCTTCTTTTCGGCAG	3526	ACGTGAGATCCAAGGGTGGCTCCT	
	3490	ACTGCCCATGGGCCACTAGGCTTG	3527	TAAACGCCAAAAACCACGAGCAGG	
	3491	GGCGTACGAAAAGGCCAATCACTT	3528	CCATGGAATGGAAGCATTGGACG	
	3492	ACTTGTGGTCGACAACGATGTGGC	3529	ATGATCCCTGGGCTTAGTCGCCTT	
	3493	CCACCACCCCTGACCCGAAAAAAT	3530	ACCGTATGCCTCAACAGAGTGGCT	
	3494	TGTTGTGCATCACAACATCAGGCC	3531	CCACCAAATCGCATAAGCTCCACC	
	3495	GACCACCCGGTAAAGAGGGATGGT	3532	TCTCAGTTTAATCCCGTGATCGGG	
	3496	GCCACCCTGAAGCACTCGTTATG	3533	AAAGGACTACGCCCATCGCTCACA	
	3497	GCTACCAGTTGGAAGACGGGTTGC	3534	CGGGAAGAAAGCCTAAAGCTTTG	
	3498	CAACGTTCGCATCCCACAGTTGTA	3535	TTTTGGACATTTTTCTGCATCGGG	
	3499	TATCGGGTCGTAATGGGCAAAGAG	3536	GCAGGGGTCCTTTTCCACGGTAAT	
	3500	TCGGTGTGATTGATGGATAACGCC	3537	TCAAATAGGGCGTAGGCAAGCTTG	
	3501	AGAGGTCGAGAGCCCGATAACCTG	3538	ATGAAGTTCCATCCTGTCCGGGCC	
	3502	GTAGTTAGGCGCGGCCCTGGCTCA	3539	AGAATGATTAAGCGCAAACGCAGC	
	3503	TGATTCTCGATGTCACGCCGAACA	3540	GGCAGCAGAGAGTGGCCTAGTTCC	
	3504	GATGGTTCGCCCTTGTGTCGCAGC	3541	GTGCAGAGCCGGCCTTATGTAAGA	
	3505	GCGCAGTTACGTCCATTGTCCCAC	3542	CATACGGGTATGGCGATGGTTACC	
	3506	CCGCCTGATTTAACAAGCCAAGGT	3543	AAGAACAGGAACCGCTGACAAGGA	
	3507	GACCAAGTGCAGGCGTCAGTCTGG	3544	GATGTGTCGCGTCCTTAAGGGC	
	3508	CAAAAAAGCAATTCGCCCTGGACG	3545	TATCCATGTAAGGCTCCTGAGGCG	
	3509	ACTGACCTTCTCGCTCTCTCCGTG	3546	AGTTTTTTCCTAAACGATCCGCGC	
	3510	CTCGCCGTGTATCGCTAACCCTCT	3547	CTGACCGGACGACCCAGAATGTAT	
	3511	CGGCATTTTTCACATGCTGTGTTG	3548	GCATGTGGTCAAAGCTTGTCGATG	
	3512	ACGTAACGCCTGATGGGGTACACC	3549	CAGAAGTGCATGGGTTCGGATGAA	

TABLE 1-continued

TABLE 1-continued

	TAB	LE 1-continued	TABLE 1-continued		
Seq. ID No.		Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
	3550	ATAGCGTACCGGAGGGCTTACCAG	3587	CAGGGGGCGCATATTTGACAGATT	
	3551	AAGACTTGGCGCTTGTGGGTAAGG	3588	TAACTCGCTGCCCTCAACTCAGGG	
	3552	TATTGTGGCGCCTCACGCGCAATC	3589	TCGATTGTTGGGTCTACCGTGGTT	
	3553	TCGGCCATGGGATTTCACAAAGTC	3590	GCTGGGATTAGTGCCGGGTAACCG	
	3554	TGGTCGGTGCCGTTTCACCTTTAC	3591	TGGTTGCAACATCGCGCTATTACG	
	3555	CATTTCCGCGGGCAGGAGAAAGAT	3592	GGGCGTGCTTTGAGCTGAAGCGTG	
	3556	CCTGAGTCGCGATACGACTCAACA	3593	ATGTTGAGGTTAGTCCCCGACCGT	
	3557	AGGTGTACCGCCGTCGGGTTATAC	3594	GACCGCGTAGTTAGCAATGTTGCG	
	3558	TCCTTGTACGAGCCAAGCCTGGGT	3595	CCAACCCACTGACATCGATGGAAA	
	3559	AGAAGCCCGAAGTCCCGTGTAGAC	3596	TGCTGCTATTGTCGCACCGATATG	
	3560	AGAGGGGCCCTTAGGCAAATACGT	3597	TACAAAGAATCGGGACCTGCGACT	
	3561	ATGCGGCAACATCCGATCGTAGAT	3598	GCGCCTCATCCCGCATCGAATTAT	
	3562	CGCAGTGGGCAGTAAAGACAGAGG	3599	CGAGGGATTTTGACCAGTGGATGA	
	3563	TCGGGTAGTGCAAACCTCAATCGT	3600	TGATAGGCATACGCGGAGAAGTCC	
	3564	TCTTCACTGTGGTGGACTTGGGG	3601	CGAGTTGTCAACGGCCATCGAATT	
	3565	GTCCCAGGGCGATTGGTACTAAGG	3602	CCCGCACCGGATTATTAACGAACC	
	3566	GGTAGATCCAGCCATTGGGACCTC	3603	TCGTCCTTGGGTCCCATGTAGAAA	
	3567	GGGGATTGTGCGCTCCAAGGACCC	3604	TCACGAAGCATCTTTGCGACGTAA	
	3568	CTCTGTCCTAGACTGAGCCGTCGC	3605	TGTAAGTTGCCAACTTTGCGGGTT	
	3569	CGATGAACAAATGAGTGCGTGTGA	3606	GCACACCACCGGCAGATATCAAGA	
	3570	GAGGTCGAGCTGCCTGAGAGGAGT	3607	GTGTGGTTTGTGPATGCGTGGTGA	
	3571	CAGTGGGACTGCTAACGTGGGTCA	3608	CAGCTGCGGCCCCACCTTCGATAC	
	3572	GAGTCGCTCGAGGAACTACGGCCG	3609	CAGCGAAGGACGACTACTGTGCAC	
	3573	CGGCTACGGAATGATGCAGGATGG	3610	CAGCAGTTCGTTGCTTCCTGATTG	
	3574	TCGCTCTCGCTATGGCAATTCTGG	3611	AAACAATGGAGTGTACCTCCCGCA	
	3575	TGAATCACGGCCCTCTCTGGTACA	3612	ACTATACGAGCATCATGAGCCGGC	
	3576	CAGGTGCCATCGAGCGCTTTAGTG	3613	CTTGATAAGGTGGGATTCCGGGCA	
	3577	TGGGAAAATCGAAATCGTCAGGAA	3614	TTTAGTAGAACGCTGCGCGCGGTG	
	3578	CGGGGAGGAAGATGTTCCAGCGGT	3615	AACTGACGTTGAATAAAACCGGCG	
	3579	TGTGGACCGGTGGTCACGTCTTTT	3616	GCTTTGTTCTACCGCGGATCATCA	
	3580	GCACGTCTCGCAATCTGCGATCAG	3617	TGATATGCAGCGGCTCGGCCTTAT	
	3581	CCTAATGCCGTATCAGCGACCAGA	3618	CGGGAGTGCGTTTATGTCCATGAT	
	3582	ATAACGCGGGTGAAGGATTCGTCT	3619	CAAATACCGGGAACGGATCGAAGC	
	3583	TTCAACCTTGTGGGGCGTCCCACT	3620	GATCAAGCCGAATGCTTTGCAAAG	
	3584	CTACTTCCAAATCTCCGCGTCGGT	3621	AGAGAGGATGCGCTCCGGTTAGAG	
	3585	AGCGAACGCACTGCCAGTGGATAC	3622	CTTAGTCAGCATACCCGCGGGCAG	
	3586	GAAAGTGGCGGCGAGGAAAAACAC	3623	GTGTCTCGGGGCGCAGGACCTGTA	

TABLE 1-continued

TABLE 1-continued

	TAB:	LE 1-continued	TABLE 1-continued		
Seq. ID No.		Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
	3624	AACGCTCCACTGCCGTGATTCACT	3661	AGCATGGTAACCCTGAGCCAGCAG	
	3625	GATCGTTGAGTCATCCCGTGGAGT	3662	GGAATCCTTGTGGGAACAGCCGAT	
	3626	CCTGGCCGGGTGCAATACTACAGT	3663	CTGATGTGGGAAAGAGGGTGGGAC	
	3627	CGTAGCCCGAACGTAAGGGTCAGC	3664	ACTTTTTGCAATCCCGGCGTTGTA	
	3628	CTGTGGCTTCAAGAGGATCCGTTG	3665	GCGATGACGTGACGAGTTCTCACC	
	3629	CTTGGGTCGGTGTAATGTCCTCGA	3666	CCAGGTATTGAGCCCCGCCATATA	
	3630	GCCGTTGTGCGCTATTCTTACGGA	3667	TTGGACGTCCTCCGAATATTGGCA	
	3631	TCGCACGATGGCTAGAACGAGTAA	3668	GGTAAGTGCGGGAAGTACGCTGAC	
	3632	ATTTGTTGCAATGGGATGGCTCTG	3669	CCGCCTGAACCGTCGTAGGGATTA	
	3633	CGAATATCCGCTCGAACCTGACAA	3670	CGTTTTTGAGTAAGGATTGGGCGA	
	3634	AAGTGGCGTGCGTCATAGCGCGAC	3671	TGTGGTATTGAGGCATAGGTGGCA	
	3635	TGATGTCCCTCCACACCGTGAACT	3672	TCCGGAAGGAAGGCGCGATATGGC	
	3636	CAAATGAAGTCGGGGCCAATATTG	3673	GTTGAGCGAATCGGACGGCTTTAC	
	3637	GATGCATAGCGTGATTCCGGTGTA	3674	TGAGTCTCCGAACGACAAGCGATC	
	3638	GTGACCGTAGAAGCTCACCAGGGC	3675	AGTGAAGAGGGAGAGTCCAACCCG	
	3639	ATAAGGACATATTCGGCCTGGGGA	3676	GTGAAGCCTGACGAATCCAACGTG	
	3640	AGATCTCACAACCGGAACCGGACG	3677	GTGCAGGCCTGTATCCCCATGACT	
	3641	GTTGCGTTTGGGGGCGTCATACAA	3678	GTGGGTTTCCTACACACCGGATGA	
	3642	TGTGAGGTTTTCCTAAGGCGAACG	3679	GCGCCGTCGACTCTCTTCAGCTGC	
	3643	CATCTTGGTTTGCGAACGAACTCA	3680	CTAGGCCTGCCATCACTGAGCAAT	
	3644	TTCCTGTCACAGATTCGTGGCCTT	3681	TTGGTGATGACTCATGGCCAGACC	
	3645	AACTTACCGATCCCTGAACGTGCA	3682	TATCTCCCGCGGGGTATATTACCG	
	3646	CCTATTCTGGACATGCGGCCACAT	3683	CCGAGGGACACGTATCCCTGTTCG	
	3647	GTCGATGGGGAGCTCCAGTTGCAT	3684	TATCCCGCAGCACGCATTCGATCT	
	3648	CGACCGTGAGGGTCCATACGTAGA	3685	TGATGATAGAGCAGGGTGCCGTCA	
	3649	TCTCGTTTGCACGCAACTGGGCCA	3686	GTAGGAGCACACATTCGGATTCGG	
	3650	ACTCCGCCGAATGAAGGAATAGCT	3687	CCCTTACTACGCCCAGCCCTTTTG	
	3651	CCTCGACCTGGCGTGATGGAAGGC	3688	GTACCAGGGGGTGTGCTCCAAGGG	
	3652	TAACAGCCGTTTTGCGGTTCACAA	3689	TGACCAGGCGGACCAGACGGTTTT	
	3653	GCCTCCTGCAGTACGGTGTCTGTT	3690	CGTAAGCGGCGGTAGGTGTGCTAC	
	3654	GGCAGTCGGTCCCACTTAGTTCGA	3691	CGCGGGAGGGATCAGCAGTTTTG	
	3655	TAATCCACGGCTTTGGTGGAAGTC	3692	AAAGCGTATCCAGAAAGGCCATGG	
	3656	CGGTGCAAGATCCTGGTTGTGTGA	3693	AAGAAGAGACGCATGCTTGGACGT	
	3657	TTTCACCACTACCTTAGGTCGGCG	3694	TGGCCATTTGCGGGAGGTGGCTTA	
	3658	CATCCCGTACCGGGAGGACAAGTC	3695	AACGCCGAATTGAGGAGGCGGTTA	
	3659	ACGAGGTAAAGGGATCCGTGCTGG	3696	GCCTCATTACGACATTGGCAGCAT	
	3660	CTAATAGTTTGGCAGAGGGGCGCT	3697	TCGAACGCGATTTTGGAAATGCCC	

TABLE 1-continued

TABLE 1-continued

	TAB	LE 1-continued	TABLE 1-continued			
Seq. ID No.		Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')		
	3698	AGGAATTCTAGCCGAAAGCCCTGC	3735	GCGGAACGCTAGCCCCTTATGGTT		
	3699	TCCGCTGGTTGGGTGCTCTGGTTG	3736	TGCGAGGCTCCTGGAGCAATCCAA		
	3700	GTCGCGCTCCGTCCGATAGTATGA	3737	ACAGAAGGGCGATCGCTCTGGCTG		
	3701	TGTGCAAGGACGGATGATTGCACT	3738	GGTTGGCAAGGGGCCAGCTCCTAC		
	3702	GGACAAGCGGCAACCTGGGAGAAG	3739	ATCGCTTCGCTCTATGGAGTCCGA		
	3703	ATGCGGTGGCTACGGACTAATCCA	3740	CGTCCCGATAGGCCGCCTTGATCT		
	3704	TGCACGCAGGTGGAAAGCAGGCTT	3741	GAATTCTGAGGCGGCATTGTCCAC		
	3705	AGATTGTGGGAGTTGTCACGCTCC	3742	CAGCCCATCAGTATCGGCTGCGTA		
	3706	AACAGCAGTGAGGGCTGAAGCTTG	3743	TGGAGAGTCGGATCCGTAGCGTCA		
	3707	CTGCCTGTTTCCTTCACGCTCCAT	3744	TGGATCCAGTGCGAGTCTTGGCCG		
	3708	CCAATCCACTTGAGTCAACTTGCG	3745	ATGCGGTCGTGCTTGGAATCCTCT		
	3709	CATTCTACCGCCCAACTTTTGCAA	3746	ATCGCACTGCCGCGTCATAACAGC		
	3710	CGGAGAACCATGCTGAGCAGTCCA	3747	CACGTCTCCGCCGGAACACAACTG		
	3711	GACTGTTCCTCCAGAAAGGCGCAT	3748	AAGACAGTGGGTGAACGCACGGTA		
	3712	AAATAATTGCTCCACGCGAAGCGC	3749	ACGCGCATAGGTGGTCAAACATCG		
	3713	GGGCCTGGAAGACCAAATAC	3750	CCCGGCGGTAGAAATTGACAACCT		
	3714	ACGACGCGAGCACGTAGATATCAA	3751	AAGGGATACTCAGGCGCCTGTTTT		
	3715	TACGGGATCCTCGTGGCTACATCT	3752	CTTCTCTTGTGCGGGCTCCCGT		
	3716	CAAAGTCTCCCCGACCGAGTTGAC	3753	TTGAAGGGACCTGCCAAATGGCGA		
	3717	CCCGAGGCGAAGATCTCTAGGCAC	3754	ACGCATGACGACGTCCAGTACGGG		
	3718	CAAAATTCTCGCCACGAGACCCTA	3755	AAATGGATGTTACGCCGGCAAGCT		
	3719	CTGTGCGCATTCCAAACACATCAC	3756	TCGTGCGAGGCCTCTTCGGCATAC		
	3720	CATGGAAATGCCAGCTGCCTCCAT	3757	TACATCGCGTCGAGTCATTCTTGG		
	3721	CGCGAAACCACAGTCCTCGTCGGG	3758	TCACACCACATAATGGCACCACGT		
	3722	GTCCGCAGCTGTCCCGACATTGGT	3759	CAGGTTCACGGTTGAGGAGTGCGA		
	3723	GTCTCATTGGGACGATCGTCTCGA	3760	GGTGTTACACCGCTTCGTTGTCCT		
	3724	AGAGCGTTGCATGCTTGGCTGCGG	3761	ACAATAATAAGGGAGCATCGGCCG		
	3725	CTTCCGCCCCTGTTCGCAATGAGG	3762	TCGGGTCCTATGATCCAGTCCCAA		
	3726	TTGCGGTTCATACCGAAGCCAACA	3763	ACCCATTCCTCCTGCGGCGATCAA		
	3727	TGCGCGAGAATCGTTCGTACGACG	3764	TCGCAGGTGTAGACGGACGAAAAG		
	3728	TGTATACCGTAGGCGTCCGTGGGG	3765	CTCTTGCGTAGTAATCGGCCCGCA		
	3729	TGCGGGGTATAGGGCTTCCTTATG	3766	TTCCGTGTCACGCGAGCCTGCTTT		
	3730	ATCCCAGCCCAAGCAGCAGACGCA	3767	ACTCTAAGTAGGGCTGGGTCGCGA		
	3731	GTTCTTGGCCACAGGAATGGCCGT	3768	TTGGTGGCTGTAAAGGTGCTTGGC		
	3732	CACATGGGCATTAATTGCTACGGC	3769	CCGAATTACCCATTCATACGGCAC		
	3733	ATAAGTCGGTCTGCCTGGCAATGA	3770	GATGGATAGGTTCGCTTCCCGCAA		
	3734	ACCTCGAGGCTGAGAACGTCAAAA	3771	ATGACGGAAAGAATGTGATTCGGC		

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TABLE 1-continued

TABLE 1-continued

TAE	BLE 1-continued	TABLE 1-Continued			
Seq. ID No. Decoder (5'-3')		Seq. ID No.	Decoder (5'-3')		
3772	ACGGTTCGGCTTCTGTTAGTCACG	3809	TGTTGGCACGACTCCGTCCATGAA		
3773	GGATCCCGTAATTGAGGCGGCCAC	3810	TGCCTACCCGGTGATTGCGACATC		
3774	ACCCGTTAAGTCGACGCCTGCGGG	3811	CAACGGTCGGATCTGAGGAGATCT		
3775	TTCGATGTGAACGGTTGGCCAACC	3812	CGTTACGAAGCGAAGTTCCCGAGT		
3776	TCGATCGGGAGTCTACCGCCATGT	3813	AGTGACGGCCAAAGTCGCCATTCT		
3777	AGCAACGAGTTTATGAGCGCAGGA	3814	ATTCAGCTGGGCATAGGCGATGGG		
3778	TGGGAAACGAATGGGTGGCGGTTG	3815	TAGGACAGCGTGGCTGGCTACACA		
3779	TCTGTGTTGCCCCACCTACAGCAA	3816	AATTTGTCCAGCTCTGCACGACCG		
3780	CCTGCATTGGATGTACCCGCGGGT	3817	TGAGTGGGCTGTGATCCGTTCCAC		
3781	GAACGAGGTCCGGGTTTGCATCTC	3818	TGTGGTGACACGCCAGAGCTGGTT		
3782	GGCGCCGAAGCAGAACGACCATAT	3819	CCTCACAGGTGTGAGAGGAGCCGC		
3783	AGGCATCACGCATCAGGTACTTGG	3820	AGTCCCGCTTCTGCAAATTCCGAA		
3784	TTTACAAAAGCATCGGCCCTGGGA	3821	TCTGCGCCTACCCGTAAGCTGAAC		
3785	CCCAGGCGGTCAACCAATTGTAGA	3822	GCCTCCTGAGTTGATTCATGCATG		
3786	CTGCAGCACGTGCCTGAAATTCGT	3823	CCTAACGGTTGGTTCGCCGTTTTT		
3787	CCGTTTTGCTCCAGCTATGAGCGT	3824	TCGCAAACCCACGAATGAGTCCCG		
3788	ATTTGTGCCGCATTGGGGTTATTC	3825	AGTGCTAAGGTGGGCGAGCAGAGG		
3789	TAAGCAGAAAGCCGCAACTCCGGT	3826	CTGGAGACTGCGATGGCAGGGTTG		
3790	GCGACTGATATAGTGCTCGGACCG	3827	AAGGGATAGTGATGGCGATGGACG		
3791	AACTCTATTCTGACACCGCCCGAA	3828	CTATCCACGGTGATGTCCGCCATT		
3792	GTGCGCTCCAAGAAGAAACACACC	3829	CGGACTAGAACTTGCCAAGCACGA		
3793	ACGACCAGCGGTCTGAGATCTAGG	3830	AGAGCCGGATGGCATTGCATGAAC		
3794	ATCCCCTCCTCAGGTCGACGCTGT	3831	AGTTGGCTAGCGGTCGAATGAGCA		
3795	TGACATACGCGTCACCCAGCACAG	3832	GCATGCGGTCACCGCTTCATCTAA		
3796	TAACCGCGACTCTGACTCCCTTGT	3833	GTGAGATTCCAAGCTCGCCGGTGA		
3797	AAGCGGTTTGATCTGTGCAATCGG	3834	GCCATCCACCGCACAATGAACGCT		
3798	CTGTCAACTCGGTCGTCCGCACAG	3835	GGGTGGTCCTCACTGTGGTTGGCA		
3799	AACTTTGCCGTTTAGGGCAGGTGA	3836	AGGCGGCTACGACGAGCGTCGTTA		
3800	GCTGAAGAACTCCCAATTCGCTGG	3837	GCCAAGTGATCGTGCTTCCGCGTA		
3801	AAGATGCGATGGGTCAGTCCTCGT	3838	TAGCCGTTTATTCCCTTGATGCGC		
3802	ACCCACCTCTGAAGGTTGAGACGG	3839	ACTATGTGGGACGAGCGTCTGCGA		
3803	AGGCTACGCACCCTCGAGAGTGAC	3840	GCACCTTCGAGAACCCATCAGATG		
3804	CGGTCACGAACGTGGTCCAGTTTT	3841	ATTTTCTGTACCGATGCTCACCGG		
3805	CAAAGCAACGCGCCCACTTAAAA	3842	CACTGGAGCAATAAATGGCCAGGC		
3806	ACGAGGAAGGAACTGATCCCCAGT	3843	GGGTTCACGTATCTCATGGATGCG		
3807	TTCGCCACTATGGGCTCAGCATTA	3844	GCACGCTCCCAGTATGCTCCTTCA		
3808	CGCTCGGCAGAGGAG[]CCACTCAC	3845	GAAGGGACTTAGTCCGCGGCCCTC		

TABLE 1-continued

TABLE 1-continued

	TAB:	LE 1-continued	TABLE 1-continued		
Seq. ID No.		Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
	3846	TTCGTTACCCTAAGGGCGTTTGCA	3883	GGCGATCGTTCAGGAATCGCGTCA	
	3847	GTTCCAGGTCACGACGAGCTGCGC	3884	CTGGCTAGACCTCCGACACAGGCT	
	3848	TCGTACGTAGTCACACCGCGACTT	3885	CGGGTTAAACGCCAACTGGCCTAG	
	3849	GGGCTGGAGTAGCGGTCTGCTATG	3886	ATCGCAGCCTGGCCGCCTAGTTTT	
	3850	TAGCGGCACTCGTGTTGCGAGTGG	3887	GGCGTAGCCTAGCAAATTATGCCA	
	3851	ACGTTGGGTTCTGACACGGCGATT	3888	ATGACGCGACGGAGACAATACGGC	
	3852	TGTTGCTGCGCCCCAAGTGATCTT	3889	GTTGCATCACGAAAATGCCGTCTT	
	3853	CCCAGGTCGTTACGGTGCATCACA	3890	GAGTCATGCGTTCCTCGCTTTACC	
	3854	CCTAGTGCACAGGCAAATCGGGCT	3891	TCTGAACCGGTTATCCCCAACCTC	
	3855	GGCGTTCTCCAAGATAAGGCCAAA	3892	TGCCTCTGGTAGGCGCCCAGTTAC	
	3856	ACTTCGATACCGTGGACCTCGCCA	3893	CTGACGGTTTTCATTCGGCGTGCC	
	3857	CTGAGCGCGCTAAACGTCCCTAGC	3894	TGAACACGAGCAACACTCCAACGC	
	3858	ATCAGATAAACGATCCGACGCGTC	3895	CGGCGCGAAAGACTTGAACTTG	
	3859	CATGGCTGAATTTGTCGACCCTCT	3896	GCTACGAGTACCCGTCGGAAACGC	
	3860	CGAAAGCGAGCAAATAGAATCCCC	3897	ATACCCAACAGCATGGAGCGACCA	
	3861	AGATTGCCCTGCGGCAGGTTGAAT	3898	ATCGCATCGCATCGTATTCACGGG	
	3862	AAGAGGCGGCCGATCAGTTAGAAA	3899	CGGCCTAGAGGTGCGAAAGCTATC	
	3863	CTGATGCCTGTAAGGAGGCGCTCG	3900	TAACGCTTTTCCGAGGCCGA1TCT	
	3864	AATCGCGAGGTTCGGCAGACAAAG	3901	TCTGTCCTAGCACGCCGACCTGCT	
	3865	CGTTGGGACACGGACCGTTCACTC	3902	CTCATCGTTCAGTCGGTCGTCGTA	
	3866	AGATGTGTGCACTCGCGGTCATTT	3903	TCGTCGAGCAGATAGCGGGGTAGG	
	3867	CAACTCGAGTGGCGGTAACATCTG	3904	TCGACCACAGTCAGGACACTACCG	
	3868	ACCAAGGTTGCGATTACGGGAAGC	3905	TGCGATTCTATGATGTCCGAACGC	
	3869	CGAAGCGGTAGACGGCTCGCGTTA	3906	CAAATGCAATGGCAAGCACTCACC	
	3870	TCTCGCGAACAGGAGGGAAGGCGT	3907	TCTAATCCATCGTTTTTTGGGCGA	
	3871	GTCCCGATTTGCGCTGTGAGGAAA	3908	TCTCAACTCCGGTACGACGAAACA	
	3872	TACCACGCGTCGGCACGGAAATGG	3909	CTGAAGAGGGTAGCCTGGGAGCGG	
	3873	AAATGCTACCCGATTGCGCGGGAT	3910	GGCACAATTAAAACGCGCCGCGTT	
	3874	TCGATTCAGGTTTGTGCTGCGGAG	3911	CAAAGGAGGTCAAAGGCCAGAAA	
	3875	CCATCTCATCCCACTATGGCATGC	3912	TTTGCGGCCGTGACGAGCAAAAAT	
	3876	CTGGCCCGTGTTTGGTTGAGTCGA	3913	AGGAATGTGCGTGGCACCTGTGGA	
	3877	GACACACGTTGCAGGGCTTCCC	3914	TCGTGATGACTGCCTTCCGAATCA	
	3878	TCGAATCGAGTCGATCGTGAAGGT	3915	CACGTCGACATGTTTGGTACCTCG	
	3879	GAAAGCACTCGATCGCGTTGGATT	3916	TTGCGGTAGTTTGGTTACCACCGT	
	3880	AATTACGCGAACATGGGGCGTCAA	3917	GCAGTGGCGACAAATACAGCTGAG	
	3881	GTGCTAACACTGTGGTCGTTCCCA	3918	ACGGCATGATGGAGGGATAAACGT	
	3882	GGTAAGCGCCAGCCAGGAGTTGTC	3919	TGGGATAATCCGCAAGCGCATAGC	

TABLE 1-continued

TABLE 1-continued

 TABI	LE 1-continued	TABLE 1-continued		
Seq. ID No.	Decoder (5'-3')	Seq. ID No.	Decoder (5'-3')	
3920	CCTAGCTCTGCTGCGTCTTTGCGC	3957	TGTCTATTCGCCAGCGTGAGCATC	
3921	TCCTGGAACTGCTGAAGGCGACTT	3958	TGTTGTTGGCACGCCTCTACGGCA	
3922	CGAAGGCGGCATGGTGTAGTCTCC	3959	GTGCCTCAACCGTATCGTGGCGGT	
3923	AACATTGTTCCCATCCCAGAGCAC	3960	TCCTCGAAGTAGCGTGACCGPACC	
3924	CCAGGCAAGAAACAACCACGCGCT	3961	AAACAATTTCCTGCACTCTCGGCC	
3925	AAATCCACAGGCGCGCCAAAGCTG	3962	CACAAACTCGTCGAGGCACACAGT	
3926	GCTCACCGCAGACTCCGCGCGATA	3963	GACGAAACGCTCGGCAGAAAGCCT	
3927	TAGGTGGCGAGAGAGCGCCCACAA	3964	TCAACTCACACGGGACAGCAGTTC	
3928	GGCGTTGGTGTCGGGACCATGA	3965	TCACGTGGATGGGCTTAGCTGGGC	
3929	TCTGAATGCTTCCGTGCTTTCGTG	3966	AGGTGTTTGTTCCGACTGGCCACA	
3930	ACGCTCTGGACCTCGCTCATTCGA	3967	TCAACCCTCTATTCCCGAGCATTG	
3931	TCCTTTATGCGCAGCGCTCGTGTT	3968	ACCTCACACAAGCGTTCTCGTCGA	
3932	TTGCCGTCCTGCAGCAGGTAGCTC	3969	AACAGCATGCGGTCGCTGGCTTTC	
3933	GGTCTAGTGGCAGCAAGGAGCGAT	3970	CACGGACACGTGTTACATCCGATG	
3934	GGTAACGCGACCAGCTTAGACACC	3971	CTGGGAGCCTGCTGATACATGGTG	
3935	GTGGCGATTGGCTTCCTATGCATA	3972	CGTCCTATGGGCCATGGCCAGGAT	
3936	TCAAAATACGGCCAGGAAGGGCAA	3973	GTCCCCAAATCTCGCTTTACAGGC	
3937	TGCCATGCAGTCAGGTACGATGGT	3974	TCACAAACCTGTGCGTGCATTGTC	
3938	ACAGGTTACGTCGTGTTTCCCGT	3975	CACACTCGTGGCCTGCGTTGGGAA	
3939	CTCATGACGAACGAGCGGTCTGCA	3976	GCCTGCACTTACGGCTATCTCGCC	
3940	GTCGTGCGAGAGGCCAAGACCTTA	3977	TTGGCGTGGCGATTACCTGTTATT	
3941	GCTGGCTGACGCTGTTGTCAGAGG	3978	TTTGCGGCTGAAGTTTACAGGGTG	
3942	GCTACAGTGCTGCGTCCCGTGCCT	3979	CACTTAAGGGGCTGACCGAGCAAC	
3943	TTTACGAGCACCAAGCTGGCGTAG	3980	AGAAAACGTCAATCCGCCACCTTT	
3944	ACGAGTTGACGGTCGTAGGGACCG	3981	AACAAAACGGCGCTCCAACAAACG	
3945	TCGGATGGTAGGAGGCGAGATCGG	3982	GCCTCAATATCTGGTTGCCGCCTG	
3946	ATTATGCAGATCCTGTGCATCCGC	3983	TTCCACAGTCAATGATGGGCGTGC	
3947	AGGGATGGAGCAAGGAAGCATT	3984	GATTCCCAGTCTACCCGCGAGCAT	
3948	ACCCCAGGACCCGTATTCCCTAGC	3985	AGGCCAATTACGACCCTGTCACGG	
3949	GCACCATCCTGGGGCTTCTCAATG	3986	CATGCGAACGTTCCGAGGAGACGG	
3950	TACAATCCGTGGACGTTTGCTCAG	3987	CACACGCGATGGGTTGTGTGACGC	
3951	GGTAGGCGAATCCGACTGGCATAG	3988	TCCGGTATTGCGCAGGAACCATAG	
3952	AGGACCGAACCCATGTGCAGCATC	3989	AAGATTAGGTGTGCCCGCCTCAGG	
3953	ATACACCGCACAGAAGCACAGCTG	3990	TCGTTACGCCCCGACTCGACGATG	
3954	TCCTTGGCGGCCGTGTGTTTATTG	3991	ACTAAAATCGCCAGGTTGCTCCCT	
3955	CTCCACGCGAAGGGCGCTTGTAAC	3992	AGGATGGCCACGCCGAATCAAAGT	
3956	TGGCCCTGCCATCCTCGGATTCAG	3993	TGATGAAGCAGCTCATCGCTGGCG	

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TABLE 1-continued

TABLE 1-continued

Seq. ID No.	Seq. ID No. Decoder (5'-3')		Decoder (5'-3')
3994	CCCCGATGGGTCTTTGTTGGACTC	3998	CCAGTGTTCGTTCATCGGTGGCGT
3995	ACACGAGGGCTGCTGGTGAGGGCT	3999	CCGACCGCTACATAGGTGTGCGAA
3996	TGGTCACCAATTTGATGATCCGAG	4000	TGTTGAAGCCGTTCCCAGATGACA
3997	AAGGCCGCTTGCATGCGACAAATT		
		[0207]	

# TABLE 2

Seq.	ID	No.	Decoder	Sequence	(5'-3'	) Probe	e Sequence	(5'-	3 '	)
	1		TTCGCCGT	CGTGTAGG	CTTTTCA	A TTGA	AAGCCTACAG	CGACG	GC	GAA
	2		TTCGAAGO	GCACGTCC	CTTTTCA	A TTGA	AAGGGACGT	GCGCT	TC	GAA
	3		AACGCGTG	GGGAATGG	GACATCA	A TTGAT	GTCCCATTC	CCCAC	GCC	GTT
	4		CCGTCGC	TACCGGCT	ACGATCA	A TTGAT	CGTAGCCGG	<b>FATG</b> C	GA	CGG
	5		ATGGCCGT	GCTGGGGA	CAAGTCA	A TTGAC	TTGTCCCCA	GCACG	GC	CAT
	6		TTGCAACG	GGCTGGTC	AACGTCA	A TTGAC	GTTGACCAG	CCCGT	TG	CAA
	7		CGCATAGO	TTGCCGAT	TCGTCA	A TTGAC	GAAATCGGC	AACCT	'ATC	GCG
	8		CCGTTTGC	GGTCGTCC	TGCTCA	A TTGAC	CAAGGACGA	CCGCA	AA	CGG
	9		TTCGCTTT	CGTGGCTG	CACTTCA	A TTGA	GTGCAGCCAG	CGAAA	.GC(	GAA
	10		GTCCAACG	GCGCAACTC	CGATTCA	A TTGA	TCGGAGTTG	CGCGT	TG(	GAC
	11						SATGACGGAC			
	12		CATCGTCC	CTTTCGAT	GGATCA	A TTGAT	CCCATCGAA	AGGGA	CGI	ATG
	13						CACGTCGTCA			
	14						AGCCTGTTG			
	15						CAGCACGGGA			
	16						TGCGGTACT			
	17						CTTTCGGGC			
	18						TCGCAGCTT			
	19						AGGGATTCC			
	20						TGCCCTGAA			
	21						GCGGGTTCA			
	22						CATATTGAA			
	23						CAAGGTCCC!			
	24						CACTGCCGG			
	25						CCCGTCCTG			
	26						GGATTGGCG			
	27						GGTCGGCTC			
	28						CGGTGAATC			
	29						CTGATTAGC			
	30						GCATATGCT			
	31						CAGCACTGA!			
	32						GGGACGCCT			
	33						CGCCCTTGC			
	34						CATGCGCAA!			
	35						CCCGCAGAC'			
	36						CGATCAATC			
	37						CGGGAACGA			
	38						AGGCCCTTCG			
	39						GGAAGTCCG			
	40			GAGCTGCGC GCGTAGGCGA			GCGCGCAGC'			
	41 42						ACTCGCGTA			
	42						TCATTCTGC( TGCGCGTAG'			
	43						CGGGAGTCC			
	45						CTGCCAATC			
	46			CGGTTGAG			TGCCTCAAC			
	47						AGCATGGTG			
	48						AAAGTTGCA			
	49						AAAGTTGCAC			
	50						GTGAGGTTG			
	51						GTGAGGTTG/			
	52						CCCTCAGCG			
	53						GCCACAAGT			
	54						GGACCATAT			
	55		GTCTGCCG	GTGTGACC	GCTTCAT	T AATG	AGCGGTCAC	ACCGG	CAC	GAC

TABLE 2-continued

			TABLE 2-conti	inued
Seq.	ID	No.	Decoder Sequence (5'-3')	Probe Sequence (5'-3')
	56		CATCGCAGAGCATAAACACCCTCA	${\tt TGAGGGTGTTTATGCTCTGCGATG}$
	57			TCCGCCTCTGCCATAGATACCAAC
	58			AATGGAACCTCAGCGGCACCTCGT
	59 60			AATGTGCCTGGGTCCACTCATTCC AGACGACACGGACGCATATTGACA
	61			TGCCTCGTACCCTGAGGCTCATCA
	62			TCATTCTGTAGGAACACCGCGGTG
	63		${\tt TTGTTGCCAATGGTGTCCGCTCGG}$	CCGAGCGGACACCATTGGCAACAA
	64			AGGAAAGGGGCAGACGCAGGTTAA
	65			CGTCACTAAGGCAGGAACGCGCCT
	66 67			TTGAAGCTTCGTGCCATCGCCCTA CATCGCCGACTTTGGCTCTATGCA
	68			TCCGTGTGGCCACCTGCCTCTCAA
	69			GCTCGTTTTTTCTCACAATGCGGA
	70		GGCGGTTTCCGTAGCTATAGGTGC	GCACCTATAGCTACGGAAACCGCC
	71			GCCCGTGGCTACGAAATTTTCACC
	72			GTGATTGTCTTCATCCTCCGTCGG
	73 74			TTTTGGCGAATTGGGCCAAACTGG CTGTGCGCACGGCCTAATAGATCC
	75			TGAAAGTCCAAACGGTGACATCCG
	76			TTAGGGACGAGCAGGATTTGCGAT
	77		CAGGGCATGCAATAATCGAGGTTC	GAACCTCGATTATTGCATGCCCTG
	78			${\tt CTTGGGCCCATATATCAACGCATG}$
	79			GTGGTTGGTCACAAGCTGCAGCTG
	80			GGTCGCCGGTCGCCAGACATACAA
	81 82			CCATACCTATCAACGGGCGCCATC TAGCAGATTGCCGGCGATTCTCAT
	83			CACGAGCCTGCGGTCAGTGCAAAT
	84			ACGGGAACTTAACCGTTCTCCCTG
	85		AGGCCGGCGATCGAGGAGTTTGGT	ACCAAACTCCTCGATCGCCGGCCT
	86			GGTCGCTATCAGAGACCACCGTGT
	87			TGATGGAAGTCCTCGGCGTTGCAC
	88 89			ATCGGAATGGCTATCAGGCACCGA GCCAATTGGCTGTGTGGTATTTCA
	90			TCGCGGCAGTCATGTACACGATGC
	91			TTCACGCGCGCCGTTAGAACACTG
	92			AGAGTAGGTGCAACGTTGCAAGCG
	93			CGCGGCGAGCCCACTAGTTTTTCG
	94			CGACTCCGGCAGTTCCCCTGAAAG
	95 96			CGTGCCTTTACAAGAAGGCCACAA AGACAACGGGTCGCCGTTCGTGGA
	97			CTCGTTAGGTTTCGTGCAAGGTCG
	98			TCAGGCTGGCTCGTGAAGCTGCAC
	99		CGCTTTCGTGCGAATAGACGATGA	TCATCGTCTATTCGCACGAAAGCG
	100			GACCACTAGGAGCCTGTAAGCGCA
	101			TATGCGATCGCGACTAAGCGCGTG
	102 103			TCGAAGGCTAGCTCCCTCCG AGGCGTCATCAACAGGCCGGATGC
	104			CTCGGCAATAAGATCGATTGGCCT
	105			TGGGCGTATGCAATCATTGGAAGG
:	106		AACACTTGATCAGGCGGGTCGTCT	AGACGACCCGCCTGATCAAGTGTT
	107			CTGTCCTTTACGGCCTTGATTCCA
	108			CACTGGTGGACAGGTTACGGGAGC
	109 110			TCAGGGTAGCGGCCATTCACCACT TGGCCGTTTTAGCTCGCTTCAACA
	111			ATTGCTGTCAATTCTGGAGCGCTG
	112			TAGCCAAATGAATGCACCACCTT
	113		CGTTAAACCGCAATCCGTTCGGCT	AGCCGAACGGATTGCGGTTTAACG
	114			CCACCCTTACGCCGGTATCTCGTG
	115			ACCCATTCCACACGTTTGCCGTAG
	116			GTAGTTCGCCCGTCATCGCCCTAC
	117 118			TGCGAATGTGTGCGGAGGTCGATT GAATCTCCGCCGCCATGCTGACTC
	119			CCCGTGTTGCCAGCGTCTTTATCT
	120			ACAAGTGGTTCGCGTTGAGGTACC
	121			ATCGCTCTTGGGTAGCCATCGCTT
	122			GGCGCCTGGTTCTGCATAAGCTCT
	123			TATCCAACCCTGCGTGAGACCGAT
	124 125			ATGTTTCTTCTGGCGGGCAACCTA CTACAGGCTTTTGCAACAGCACCG
	126			GTGTCCTGCCGCAAACTTTCATCA
	127			CTATCGCTGCATCCTGCACTCAAC
	128			AACCCTGGTGGACCGCGCAATGTT
:	129		GGGCAGTTAGAGAGGGCCAGAAGT	ACTTCTGGCCCTCTCTAACTGCCC

TABLE 2-continued

Seq.	ID	No.Decoder Sequence (5'-3')	Probe Sequence (5'-3')
	130 131		ACACGTTCACGGGGACCAGCTCGA TTTTCACTAAGCGGCCCCCAAGAC
	132		TGGACATGAGAGCAAGCCAACAGT
	133		TATCTTCGCCTTCCGAATGGTCCT
	134		TCCTTATAGCGGATGCCTCCCAAG
	135		CTGTAGCGGTGCGTTCCGTTTATT
	136 137		TGCTTATGGGGACCGCACGTACAA GTCTGGGAAACTCAGTTTGGTGCG
	138		TTCCCAATAGGGGAACGATCAGGT
	139		GCTCAGTCCCCTCGCCTCTGTTCC
	140	CCCTGCCTTGGCGTGTCGGCTTAT	ATAAGCCGACACGCCAAGGCAGGG
	141		CTTCCGGAGTTGGCGTGTCAGAGT
	142		GGCACGCCGAATGAAAACCGTCAG
	143 144		GGCCAGCTCCAATGAACCACCGCA TTGCGAGTCACTAGTTGGCCATGC
	145		CAGGTGAGATTCGCTTTACGGCCT
	146		CGCGGATTCTCGGCATAATATTCG
	147		TCATGTGGTTGGGAGCTCGTCTGT
	148		CAGACAATCCAGCACAAACCGTCC
	149		CGCCCAACCAACTCAATAGCCTTT
	150 151		GGCCCGATCTCCGAATAGGCCATC TGGGATGAAGCTGCCTACTGGATC
	152		AGAAGCATACCCGCGCGAGTTATT
	153		TGCTTTCCGAGACAAACCTCCTCC
	154	CTTTGGTATGGCACATGCTGCCCG	CGGGCAGCATGTGCCATACCAAAG
	155		AGTTCCCGTTGCTCGAGCCTTTCT
	156		ACTTGCGGACCAGTGCGGTAGATT
	157 158		CCTCCAAAAACTGTGGCCGCCACG ACGTGCGTATGGATTGAAGTGCAA
	159		TAAAATGGTCTGGGGCTTTGGGCC
	160		ATTGTCCGGAGACAAGACAGGCG
	161	TGAGGCAACAGGGGCCAAAAACTA	TAGTTTTTGGCCCCTGTTGCCTCA
	162		GACGAGCCGAGGACTACTTCCGCT
	163		CCACTATCTCTAAGCCTTGGGGCC
	164 165		GAATCGCGGTTAAACTTCACGTGC CCGTCAAGGAACGTTTCTGCCGCT
	166		CGTGCAATCTCGTCTGCTCGACGA
	167		AAGCAGTCAGTTACGCGGCAAAGA
	168	TTTATGTGCCAAGGGGTTAACCGA	TCGGTTAACCCCTTGGCACATAAA
	169		GGACTGCCGTGAACCACAGTAACA
	170		CAATAAAAGGTCTAGCGAGGCGCG
	171 172	CGCGCAGATTATAGACCCGAATGT	AGTTGGGAGCTCTCACGCATTTGT ACATTCGGGTCTATAATCTGCGCG
	173	CAAATAACGCCGCTGAATCGGCGT	
	174		AACATCATCACCGATGCACGAAGG
	175	TGAACACGAGCAACACTCCAACGC	GCGTTGGAGTGTTGCTCGTGTTCA
	176		ACGACCGCTACGAAGGATCTGCTG
	177 178		ATGAGGCACAACTCACCAGGTTCC
	179	CCCAACGTCACTGAAGCTCACAGT	TAAGCCCGCGATTGTCGCTTATGA ACTGTGAGCTTCAGTGACGTTGGG
	180		CCGTCTGAGTCGCGGGCTCTGACA
	181	TACACGAAGCCTCTCCGTGGTCCA	TGGACCACGGAGAGGCTTCGTGTA
	182		CCCAGTTCGCCGAGGACTTCTGAG
	183		TCGCCGCGGAGTAGATAAAAGGAT
	184 185		GGTTTATCCTGTTGCTGCACGCCT TGTGCCAGAGACTCCCTCGAGAGT
	186		AACAGGTCTCGATGGACCTGGCAA
	187		ACACGGACCCGCAGTTATAGTGGA
	188	GCCCAGTCGGCTCTAACAAGTTCG	${\tt CGAACTTGTTAGAGCCGACTGGGC}$
	189		ACCTGACGCCGATTATCCGTTCCG
	190		TCCTCCCGCCAGGCGCTTATTTTA
	191 192	GCGCACTCGTGAAACCTTTCTCGC	GCGAGAAAGGTTTCACGAGTGCGC GCACTTGCCAGTACCTGGCAAACT
	193		ATGCCGCTGGACATCCCTCGTTGT
	194		ACTGTACCTAGCGGGTGCTGCGAA
	195		GGCAGAGTCGCAAAAATCGGGTTA
	196		CAAGCCTACGCTTGCAATGCGACG
	197		TTCCTCTGATGGTGACGTCAGCTC
	198 199		ACTTAAGCGCGACCCCCAGCCTCC AGCCAGCTAGTGCGGTTCCCACAA
	200		AAGAGGGTGAACACAGTGCGAGGG
	201		CGTTGTGCGGATTCGAGTCAATGA
	202	ACAGGGGTTGGCCTTCGTACGTAC	GTACGTACGAAGGCCAACCCCTGT
	203	AGGCCGTGCAACATCACACAGGAT	ATCCTGTGTGATGTTGCACGGCCT

TABLE 2-continued

		TABLE 2-conti	inued
Seq. ID	No.	Decoder Sequence (5'-3')	Probe Sequence (5'-3')
204		$\tt GGGCCGTGGTCACGTAATATTGGC$	GCCAATATTACGTGACCACGGCCC
205			GGCCTTGTCGTTTCATGTCCGCGC
206 207			AATCCGACACCGGCACCCAATAAG ATCGGATTTTTTGGTAACCGCCCC
207			GGCAGTTACGGAGCACGCTTTAGC
209			ACGACGAACCGAGATGCATGAGAT
210		ACGAAAAAGTGTGCGGATCCCCT	AGGGGATCCGCACACTTTTTTCGT
211			${\tt TAAACATGCGTGCGGTGTACTTGG}$
212			TAGATGCGACACTCCACGCACGAT
213 214			TCAAAGTTCGGGGCGGTATCTGGA GCCACTTCACGTGCTGCCAGCAGA
214			TGACTGACGCAGAGCAATTTCAA
216			GCTGCCTGAACATCTCGCCTGACT
217		ACAAGCCGACGTTAAGCCCGCCCA	${\tt TGGGCGGGCTTAACGTCGGCTTGT}$
218			TGCAGGTTACTGGCCTCATTAGGG
219			CATTGGAGGGGATGTGTCTCAC
220 221			GACCACTGAACTCTGCATCCGTCG TTGTAATACCGCCAGGCATGCGGG
222			TTGCTAACGGCGCCGCTTTGCTAA
223			ATTATTACGCTGACCCGTGTCGGG
224		${\tt GCGACGGCCCTGAGGTATGTCGTC}$	GACGACATACCTCAGGGCCGTCGC
225			CAAGCGCAAGGGAACACACTTTTG
226			CAATAACCGGGCTGTGCTTCGAGA
227 228			AGTTCCATGGCCAACGGTTAGCAT ACCGCTGGGCTAACACTCCGCAAG
229			ACTCCTCCGAGCGCCTAGGGAGCA
230			CCATCGCTTACTCAAAGGCATTGG
231			$\tt GGCGTCATTGGGACGTTATCTGCT$
232			ATGGGCGCAACACGTAATGGTCAA
233			CAGACGAATTCCGCAAATACGCGA
234 235			CTGCGGGACATTGTTGACACGCAG CTGTGGACCTTGCGTGGCACCAGA
236			CCGCAATTAAGTGACCTCCCGGAG
237			GCCTCCTCCGGGCAATCACGAAAA
238			${\tt CCGGTAGCCCCAGCTACATCCCGA}$
239			CAAGGACGTGTTTGCGTTGGCTCG
240 241			ACTACCGCCCCACAAAGGCTTTGC CGAAGACCTCATTTCCGGTCGAAT
241			GAACAGAGCAACTCAGCAAGCGAA
243			ACTCGGGAATGGGGTCTTCACGCG
244		${\tt AACCGTATTCGCGGTCACTTGTGG}$	${\tt CCACAAGTGACCGCGAATACGGTT}$
245			ATACGCCTCGAAACGGTTGGCCCC
246 247			AAGCCGTTTGGACTGCCAGCCGAA GAACCGTGCATTCTAACCACACCC
247			CCGTTTGTCTAGTTCGGTCCTCGC
249			CAGCAACTTCGGTCACGCGTGCGT
250			TCCCCCTTTCAAAGCGACCTTTTA
251			TTGTCCCAGCAGTTAGCGATCGCA
252			TGAGGCCGCTCCGCTTATACCTCC
253 254			ACGAGGTGCACGACATGTCAGCAT CGTTGAACGGACGCTTTAACCACA
255			ACGCAGCTTACGCCGGTGTGAACG
256			CACAGAAGTTCTCGCCGGGATAGG
257			${\tt TCCCTCCGCTGCGTGAGTGCAGAC}$
258			AATCTGCCGAGCACCAACTCGTGC
259			GACGAACGTGTGTCGTGCGACGTT GACCATGCTAGGATAAGCGCGCAT
260 261			CCTCATGTCGAGACGAAAACGTGA
262			GCCGTATCCTAAGGATGAGGCACA
263			TAAAGCGGTTGACCCACACCACCT
264			GAGCTTGCAGTCCCTTCGATCCAG
265			TCCATGCGTACGCGAGTTGATCTA
266 267			CTGCACTCTCTTCTCCGCAGGATC CGGTTCGGGGCATCTCCACACGTA
267			CTACGCCCACGATTGACATAGCGC
269			GGTGTCGACGCTAGAAACCTCGCT
270			ATTCCACAACGGCAAAACCTGGGT
271			${\tt GAGACTACGCAGCCGTTAACAGGG}$
272			GCAATTGGCGGGTGAAATCGGCCT
273			TCAAAGGGCAAGGAGTGAGGGCTC
274 275			TGACTGCGAGGCGGATGTCCACCC ATCGTAGCACGGTTCTCAGCCATC
276			TTCTGGCAGCACTCCTAACGTCGA
277			CTATGCAAGGTCCAGACCCATTCG

Seq. ID	No.Decoder Sequence (5'-3')	Probe Sequence (5'-3')
278	GTGCACCAGACATTCGAACTCGGA	TCCGAGTTCGAATGTCTGGTGCAC
279	AGAGGCCCCGTATATCCCATCCAT	ATGGATGGGATATACGGGGCCTCT
280	AACGCCTGTTCAGAGCATCAGCGG	CCGCTGATGCTCTGAACAGGCGTT
281	AAGGCTCAACACGCCTATGTGCGC	GCGCACATAGGCGTGTTGAGCCTT
282	AGTCCGTGTTGCCAGATTGGCTCG	CGAGCCAATCTGGCAACACGGACT
283	ATGTCCCATGTAAAGACGCGTGTG	CACACGCGTCTTTACATGGGACAT
284	ATGGAGTCTGCTCACGCCCAAAGG	
285	CGGCCTCCAACAAGGAGCACTAAC	
286		GCTCGCAATGTTGCCACGGCTCTG
287		CCGGTGCGCACCTCATTCAAATGA
288	GACGTACCGGAAGCGCCGTATAAA	
289		GAATCCGGATCCCATTGCTCGCAT
290		CACTGGTCAGGGAGGCCTCACTCT
291		GCGGCAAATCTACTTACGGTGCG
292		GCGCACGACGTGCTCAAAGGTTCA
293		CTTCGAGGTAACCAAAAAGGCGGA
294		GATGTGTTAGTGCCGTTGGCGTTC
294		CTGGGACGTCTTGGCTGCTGTCGG
295		CGCAGAGCCCCAGGTTTTTTATG
296		TAAGTCCGGTCTGCACAGTTGGCA
	GGCGAAAGAGCGAAACCGGCTCGT	
298		CGTGTTCGCTAAAATACGCATCCC
299		TCGCGTACTGGTCGCTGAATCCCA
300		
301		CGAATAGGCCGGGCGAATATCGGG
302		TTGGTTGCGTGAGGCATCTTCTCG
303	GGCTAGACGATGATGACGCTA	TAGCGTCATCCACGGGTCAAGGTT
304		AAAATCGCATCGTCTAGCC
305 306	GCTTCTCTCGACGATGCGATTTT	
307		AAACCGTTCGAAGAACATGGAGGG
307		AGCAAGAGCATTGCCGCCCATCAA
309		GGGGAATTTGGCGCCTCAA
310		AAGTTGACCGTCTGGCTGTGCTGA
311		TAGTTTGCCACCGAGGAGTGGAGT
312		CGTCTCCGTCCAGGCATGCCCAGA
313		TGTTTCGTCGTACCGGAGTTGAGA
314		CACGTTGCGCCTTTGACCACGCAA
315		ATCATGAGCCGCGGATCGCTGTCT
316	CGCGTCTCTAACTGAGAGCAGCCA	
317		CTGAATGTCCGTACATGTGCGCCT
318	GATGAGTGGCACGTCGGTGTGTAA	TTACACACCGACGTGCCACTCATC
319	TGATCCATATTGTCGGACGTTGCG	CGCAACGTCCGACAATATGGATCA
320	ACCTGCCGGGAGTTCATAGGCTAG	CTAGCCTATGAACTCCCGGCAGGT
321	AGCATTGGCGTTTTTCCGCAACGA	TCGTTGCGGAAAAACGCCAATGCT
322	GGTAATATTCAGCGCGACCGCTCA	TGAGCGGTCGCGCTGAATAYTACC
323	ATAGCGTACGACGAGGTGACGCGC	GCGCGTCACCTCGTCGTACGCTAT
324	TAGGTCACGATGCGTTTGACGCTA	TAGCGTCAAACGCATCGTGACCTA
325	ACTGCCCGTACCTCTGGTTCTGGC	GCCAGAACCAGAGGTACGGGCAGT
326	CCTTTGGCCTGAAGTTGTCGTAGC	GCTACGACAACTTCAGGCCAAAGG
327	GTGCCCCACGAGCGTATCGTTGTA	TACAACGATACGCTCGTGGGGCAC
328	AGGCGCTACGTGGGCCTGGAGCAA	TTGCTCCAGGCCCACGTAGCGCCT
329	GGGTGCTACCATTGCATTAGTCCG	CGGACTAATGCAATGGTAGCACCC
330	ACCACGCGCGTACGTGTAACCGAG	CTCGGTTACACGTACGCGCGTGGT
331	CCATGATGCATTGGGTGCATTTAG	CTAAATGCACCCAATGCATCATGG
332	GGTCCGGCCCTACGAAACGTTCGA	TCGAACGTTTCGTAGGGCCGGACC
333	CCGTGTGGCTGGAGATTCGTGTGA	TCACACGAATCTCCAGCCACACGG
334	GTTAGGGCGACGCATATTGGCACA	TGTGCCAATATGCGTCGCCCTAAC
335	GGGTCAGTCAGGTGCGTTAGGATC	GATCCTAACGCACCTGACTGACCC
336	GCCGTGAAGTCGAATGCAGATCGA	TCGATCTGCATTCGACTTCACGGC
337	GCCACCACCCAGTGCATTCAGGTA	TACCTGAATGCACTGGGTGGTGGC
338	GAGCTTAGTTTGCGGTCATCGGGC	GCCCGATGACCGCAAACTAAGCTC
339		GTTACTCCCTAATGGCGGCAAACA
340		CTAAACCGGCACATCCAGCGGAGC
341		TAACAGGGATCTCGCATGCTACCG
342		TCGCAGGCAACTGGTAGAGCGTAG
343		CTTGGCAAATACAGCAGGAGGCAC
344		CTACTCGTCCAAGTCGAGTCGCAA
345		TGGCTGGAGTAAACAGCTCCCAGA
346		ATGGTAAAGGGAGTTCCGCGTGCA
347		GTGCTTTCGATTCATTTGCTGCCA
348		CTTCGCTGTACCGCGTCACCAGTT
349		CGACGGCGTCCAGCGTAATCGTCT
350 351		AACCCTTTCCATGAAGGAGGGCAT TTCTGGCGCATACGCTCCGAGAAT
331	MITCICGGAGCGIAIGCGCCAGAA	1101GGGGGATACGCTCCGAGAAT

Seq. ID	No.Decoder Sequence (5'-3')	Probe Sequence (5'-3')
352		GTTCGCGTACCCAAACTCCGCTAT
353 354		CCTCGCCAAGCGGTATGCGTAGGT GCTCGCTTGGCCATTCAGGTAATC
355		CCTAAGCGCCGTGATGCTAACAGG
356		AGCGTTGTCGAGCGCATCATTCCG
357		TTGCCTTAACCAACGCCTCTCTCA
358	AAGCAGGCGAAGGGATACTCCTCG	CGAGGAGTATCCCTTCGCCTGCTT
359	TCACGACAGACGGGCCGAGATTAC	GTAATCTCGGCCCGTCTGTCGTGA
360	AAGCAATTTGGCCTCGTTTTGTGA	TCACAAAACGAGGCCAAATTGCTT
361		ATATGCGATCCTACCGCAACCAGC
362		GTCGGGGACAGAACGGATTCACAA
363		GCCATCTCGCCTCAGAGGAGCCCA
364		GTTGCCGGTCGATTCACTCTATCC
365 366		AATTACTCGTGCACGTTCGGTGCA CGTCCAACACCCGAGAATACTGGC
367	TCGCTACCTAAGACCGGGCCATAC	GTATGGCCGGTCTTAGGTAGCGA
368	TGGCATTGACGAGCAGCAGTCAGT	ACTGACTGCTGCTCGTCAATGCCA
369		ATACTCCAAGGGCGCTGGGACGCG
370		ACGAAGTCGCCCGGTAGGCTTCAT
371		CATGGTTCCAGGCCATCTGTCTGG
372	TGGCGTGGGACCATCTCAAAGCTA	TAGCTTTGAGATGGTCCCACGCCA
373	CCGCATGGGAACACGTGTCAAGGT	ACCTTGACACGTGTTCCCATGCGG
374	GCCCACTCGTCAGCTGGACGTAAT	ATTACGTCCAGCTGACGAGTGGGC
375		CGCTTTCTGGATCACGACCGTAAT
376	TGCGAGGTGAGCACCTACGAGAGA	
377	GGGCCGCATTCTTGATGTCCATTC	
378 379		CTAGGCGAGAGCCCACATCCGAGG
379		ATAGCGCTCACGCCAACATGCCTA AGGCGGACATCCTCGTTCGTATCG
381		TAGCGCACCGTGCTAACCGGCGTA
382		GCGACACGGCCCGGACATCGTATG
383		ATAACGCGCCATACAACTGCGGAT
384		CCATCCCATCTTTGTCCCTTACCC
385		GCGGATTCACCAAAACACTCCAAT
386	GAACCGAGCCAACGTATGGACACG	CGTGTCCATACGTTGGCTCGGTTC
387	GCCGTCAAGCTTAAGGTTTTGGGC	${\tt GCCCAAAACCTTAAGCTTGACGGC}$
388		CATATCACCCACCCAAAAGCAGGT
389		TATACGTTTGCTGCGCCCACGATT
390		GCTTATACTGAGCAATCCGGCGAC
391		TCTGAGGAGGAAGCATCGACGGGT
392 393		ATCTCTTGTATCGCCCACCCGGAT TTTTCAAAGCTGACTCATGCGGAA
394		ATCGGCTTGCCAGTGGGACTTTGC
395		ATGTGTACGATGAAGCCGAGGTCG
396		CTCACGCACAACTGCGCTCATGAG
397		CTCCGGCCGTGGATCCTTCATCTG
398	TCAAAGGCTCTTGGATACAGCCGT	ACGGCTGTATCCAAGAGCCTTTGA
399		GAGCCCTGATTGGAAATTAGCGGA
400		CATTAAGGCAAAAGCGCCGTGCGT
401		GTCCTGCTCCTTGTGACGTTGTCA
402		TCTGGATACCGCGCCCCAACTAAG
403		GTTCCGACTCCACGGCATTAGAGC
404 405		TGCGGTCAGTCAATTTGTAATCGG GACACGGGAGGCTCACGTACGTCT
405		TGCGTTGGATCGTATCGCTCCATT
407		TACGCCTATCAGTACAGCGCCTCC
408		TCCCGTGTGGTCAATTCAAAAACA
409		CTTCATTGAGCGCATCCAGACATG
410	GCCCGCTAATCCGACACCCAGTTT	AAACTGGGTGTCGGATTAGCGGGC
411	CCATTGACAGGAGAGCCATGAGCC	GGCTCATGGCTCTCCTGTCAATGG
412	GAATCACCGAATCACCGACTCGTT	AACGAGTCGGTGATTC
413		CGACGTAAGCTACTGCGGCTGGTT
414		AACGCCCGCGTGTCCCTCAGAAAA
415		GGAGGATCGATCAAACGGAGCACC
416		TGGCTCAGAGTATGGCCTAAGCGG
417		AGGCAAGGCGTCGGTATGTCTTA
418 419		GTCTCAATGACTGGCGTCGGGAAC AGCCCGACCTCCGCGAAACTTTTA
419		GCCGAACTCAGCTCGGAAACTTTTA
421		TTTAAGTCCGTAGCCGCTACGCCG
422		ACCTTGCCGCATGGGCATCCAAGC
423		TTTTCGAAACTCTGGGATCCCGCT
424		GAGGATGACCTCGCTCTCAAGGTC
425		GAATATGGTCAAAACGGCCGATGC

Seq. ID	No.Decoder Sequence (5'-3')	Probe Sequence (5'-3')
426 427	CATAGCGCTGCACGTTTCGACCGC ACCCGACAACCACCAATTCAAAAA	GCGGTCGAAACGTGCAGCGCTATG
427	GCGAACACCACCAATTCAAAAA	
429		TCGGAGTCTCTCTACACTCGGCGG
430	GACATCGGGAGCCGGAAACATGAG	${\tt CTCATGTTTCCGGCTCCCGATGTC}$
431		${\tt ACGCCTGTCGCCGAGTCTACACGA}$
432	ATGCGCATATACTGACTGCGCAGG	
433 434	ACAAGCGAACCCGAGTTTTGATGA GCATGAGACTCCGCGAAGACATGT	
435		GTGATCGTGACGCGACATGTAGGA
436	GACCGATCGCGAAGTCGTACACAT	
437	GTCGCCAGGACTGGGCCGATGTGA	
438	ACCGATAAGACTTGCATCCGAACG	
439		CCGGCACTTCGGACTGGTTATGGA TTAAATACGAGATGCAGGGCGCGT
440 441	AGGCGCCTGCATCTCGTATTTAA AGACCGCATCAATTGGCGCGTACC	
442	AGAGGCTTGGCAAGTAGGGACCCT	
443	GCAATGGACGCCAGACGATACCGG	
444	GCTGGACTTAGTCGTGTTCGGCGG	
445		AGGGAGCAATCCGGCACGATGCCT
446		CTTTGTTCAACGTCGACATGCGCA
447 448	ACCCATCGCCGGAAAGCGATGTTG	GTATGGCATCGGATGTGACCCGAA
449	AAGCGCTGACTCGGCTAAGAATCA	
450	ACTTCCAAGTCCTTGACCGTCCGA	
451	TCTCAATATTCCCGTAGTCGCCCA	TGGGCGACTACGGGAATATTGAGA
452		${\tt GCGCCAGGAAAAAGAGGAACTGTT}$
453	CGTCCTCCATGTTGTCACGAACAG	
454 455		AGCAAAGACAGGTAGGTCTGCGCA AAGGAGGACTGCGAAGCCGTCCAT
455		TACGTGGCCCATAGAAAGCGTTCA
457		GGTTATCGCTCGCGGCAGGGTTCA
458	GTTCTTGCGCGATGAATCAGGACC	GGTCCTGATTCATCGCGCAAGAAC
459	AGGGTACGTGTCGCAGCTTCGCGT	
460	ACCCTTGCTCCGCCATGTCTCTCA	
461 462	GGGACAAGGATTGAAGCTGGCGTC	CAATGGTACTCGGGAGCAACGACA
462	GTTGTCCGAGACGTTTGTGTCAGC	
464	GCTGGTGAACACTCACGAACCGCT	
465	GCAGACAGGGCAAATCGGTGCAAA	${\tt TTTGCACCGATTTGCCCTGTCTGC}$
466		${\tt AAAGTCGCCACTCGTTGTGATGGG}$
467	GCTTCTACAGCTGGCGTGCTAGCG	
468 469	GAATGTGTGCCGACCATTCTAGCC	CCACAGAGCTCTAACTTCCGCTGG
470		CCGACATGGAGTGGTCGGTAAAAA
471	GCGGCTATGTGATGACGGCCTAGC	
472	AGTACACGGGCGTGTTAGCGCTCC	
473		GTGGGAGTGCGCCACACACAGGA
474 475	CCAACTAACCAATCGCGCGGATGA AGTGAGTGACCAAGGCAGGAGCAA	
475		CCGCAATAAACTCCGCGAAAGATG
477	CTTCGTCCGGTTAGTGCGACAGCA	
478		${\tt ATTTCGGGCCCACGTTTTCGTGAG}$
479		CAATGCTAGAGTTCAGCTGCTGCG
480		GCACCATTTGGGCGTATGTCTCCT
481 482		CAAACTCCCGCACGAGTTCTCAAT TGCTCCTCCTGGGCCTACAAAGAG
483		TAGACCAATTATCGACCCTGCGGC
484		CCCAATAGTCTCAGGGCGGCGTTT
485	CTGAGTTGCCTGGAACGTTGGACT	${\tt AGTCCAACGTTCCAGGCAACTCAG}$
486		ATCCCATACTCTGCAACCCATCCG
487		ACCGCACTAACCCCCAAAGGTCAG
488 489		CGCTGGGGTAAGGTTCTCATTTCC TGATGAGTTGACGGACGATGCGTT
490		AACAATGGCCGAAGTCTCTCTCA
491		CCTGACAAGATCCAATGAGCGCAA
492		${\tt AATGTTGCCGTGCTTTAACGCGCT}$
493		ACAGCCGCCCACAGTTTACTGGCT
494		CAGCTGCTGGTTGCACATCAGTCG
495 496		CACTCGCTCGTCGTATGAGCAACC GGTACGGGTTCCGTGGATTTGCGC
497		AGAAGCCAGGGGAATAAACTGCGT
498		CTACTACGGAGGCGCGGAGGTTCT
499	AAAGGAGCTTTCGCCCAACGTACC	${\tt GGTACGTTGGGCGAAAGCTCCTTT}$

TABLE 2-continued

		TABLE 2-CONT	Indea
Seq. ID	No.	Decoder Sequence (5'-3')	Probe Sequence (5'-3')
500			GAGCTGTGGAGTGGCACAATCACT
501			TTCAGCTCAACCCTCGACGATCGC
502 503			CGAGGACCATAATGGCTGTCTCCC GTTCTGCCGGAGTGACAGCGTCTC
503		CCACCGGTCGCTTAAGATGCACTT	AAGTGCATCTTAAGCGACCGGTGG
505		CGGCATAACGTCCAGTCCTGGGAC	
506		AAGCGGAACGGGTTATACCGAGGT	ACCTCGGTATAACCCGTTCCGCTT
507		TGCACACTAGGTCCGTCGCTTGAT	ATCAAGCGACGGACCTAGTGTGCA
508			AACTGAGTTTGAACGCGGTTCCCT
509			AACACGAGCGGGTGGTTGTAATTC
510 511		TTCAGTGCTCACGAAGCATGGATT TTAGTTTGGCGTTGGGACTTCACC	AATCCATGCTTCGTGAGCACTGAA GGTGAAGTCCCAACGCCAAACTAA
512			TATGAGGCTCGTCGAGGTCGCATT
513			TGTGCGCCACGTTAACGGTTTCGG
514		TAAAGTAACAAGGCGACCTCCCGC	GCGGGAGGTCGCCTTGTTACTTTA
515			CCCACCCGCGACTAAAATCATTA
516		GGCTACTCTAAGTGCCCGCTCAGG	CCTGAGCGGGCACTTAGAGTAGCC
517			COTGAGATATTGAGTCGTCCGCCA
518 519			GACGGTCTATTACGCCTAACGCCC CTAGAGCCGCCGTCTAAAGGTGGC
520		GAGATGTGTAAACGTGCAGGCACC	
521			ACACGCTTGGAGGGCCACGAGCTA
522		GTGTCGGCGCTATTTGGCCTTACC	GGTAAGGCCAAATAGCGCCGACAC
523			AATGGCAACCAGTTGCTTCCCTGG
524			AGCGGTTCTGGCTTAGTTTCGGAA
525 526			GAACTCTCGGGTTACCGGGTTTGC ACGTTCGTGCATGACGCCATTTGC
527			CCCTAAACTGGGCGCGAAAGTACT
528			AAGCCGGGATGCCTCGCAGATCTT
529		GCAAGTGTATCGCACAGTGCGATT	AATCGCACTGTGCGATACACTTGC
530			CAGAATGAATTGAGGCCTTGTCGG
531			CGCGCCTTAAAGTTGAGACGAGAC
532			ACGCTGCAAAACGGATCTCTGGAT
533 534			GGGTGAAACTTCCCTCCTGGTGAC ATTCCGTTGATCCGCCTGACGGAA
535			GCCTGTGTAATGCGTGTCCGGCAT
536			TCTATGAAAGCGCCAAGCGGCCCA
537		CCTAGCGCGAGCTTTACTGACCAG	CTGGTCAGTAAAGCTCGCGCTAGG
538			TCTCGAGACCATATTCCTGGCCAA
539			ATGCATAGCAAGTCGGCCGCAGAC
540 541		ACTTGCTCATTCTCAAGCCGACG ACGTCAGCGATTGTGGCGAAATAT	CGTCGGCTTGAGAATGAGCAAGTT ATATTTCGCCACAATCGCTGACGT
542		ACGCCTGCGTCAGCACATGCATC	GATGCATGTGCTGACGCAGGCCGT
543		ATACCTCCGCAGAACCATTCCGTT	AACGGAATGGTTCTGCGGAGGTAT
544		AGTTCGCGGTCCCACGATTCACTT	AAGTGAATCGTGGGACCGCGAACT
545		TGCTCAATTTGTGCAGAAAACGCC	GGCGTTTTCTGCACAAATTGAGCA
546		TTATCGCGAGAGACGACCGTGTCC	GGACACGGTCGTCTCTCGCGATAA
547 548			CGCTTCCACTACTCACGTCGCGTC AGGAAAGCCCAATGCCCCTACCAT
549		CCAAATATAGCCGCGCGGAGACAT	ATGTCTCCGCGCGGCTATATTTGG
550		GCAAACCCTGATTGAATCGTGCCC	GGGCACGATTCAATCAGGGTTTGC
551		TAGCGTCTTGCGTGAAACCATGGG	${\tt CCCATGGTTTCACGCAAGACGCTA}$
552			AAGAGTCCAGCGCTGTCGGGGTGG
553			CGTAAAGCAGCCTTCAGTGCTCGT
554			CGCGAGCTAGACGACGCTGATATG
555 556			ATTAGTCTAGCCGGTCCGGGATCA TGATTACCCTGTAGTGTCGGGGCC
557			CATTCATAATCTCGCCCTGGAGCC
558			TAATTTCCGCCCATCGGATTTTG
559			TAGCTTGCTCCCTATGCGCCTGTG
560			${\tt AGTAGCCCATCGGGGCAATAGCTA}$
561			CGACTTGCTATGGACCGCGTACCA
562			GAACAGTTTCCGAGCCACAGCGTC
563 564			CAGTTACCACGCGGCGAACCCAGG TATAGCTGTTGGGCTACGCGGGAA
564 565			TATAGCTGTTGGGCTACGCGGAA TGTTATGCGGCAGCAATCCGCGAA
566			TGCCTCAACTTCGGTGCCATTTTT
567			CTGGATTTCAACTCGCGCGGAATG
568			${\tt TTAACCGTGCCAAAAAACGTGCGT}$
569			ACCAGAGAAACGACGTCATGGACA
570			TCTGGCATACGAGTCCGACTGAGA
571 572			GATGCTTGATGTGTGCGTTTGGAG TCACGAACACCCCGCTTGGTTGAA
572 573			TCACGAACACCCCGCTTGGTTGAA TCGAGGTCACCACCCTCCGACACC
3,3			

TABLE 2-continued			
Seq. ID	No.	Decoder Sequence (5'-3')	Probe Sequence (5'-3')
574		AGCGCTTTTGGTCATGATTTGCAA	TTGCAAATCATGACCAAAAGCGCT
575			TCCTGGGCAGACGTAAGTCCTCGG
576			GGGCGCATAAGAACTGGATTGGGC
577 578			TCATAACTTGCGTGGGTTAACCCG CACGCGTGTATTGAGCGCTAATCA
579			CAGTCGAACCAAAGGTCTGCCCTT
580			AATGACATGTGAATCTTGTGGCGC
581		GCCATGTTCAAGGGCCTTTCGAAG	${\tt CTTCGAAAGGCCCTTGAACATGGC}$
582			CCGGCACCTAGACAAAACACCGCG
583			GGATGGAGTGCCACCACAATGTTG
584 585			GATTTAACAAACCGGCGCGTATCG GGAGCAGTCCGCACGTTTATAGCC
586			AACCGCGCAATAGTGATTTACCCA
587			TAGCTTGCGCGGGCCGATGAAGAC
588		GCGACACCCTGTACTCTGATGC	GCATCAGAGTACAGGGTGTGTCGC
589			GCTTGGTCTTGCGGACCCTGCTAC
590			ATGGCAGTTACCCTGCGTTGGCGA
591 592			TCGTGCCGCTCGAAGCTTCGGAGT TACGAGTCAGTCTAGTGGGCGGGA
593			TATTGGTGAGCGACCCCAGAAGGT
594			CTCTTCACTCTGCCGTGGGATGAT
595		CGCTGGACTGGCCTATCCGAGTCG	CGACTCGGATAGGCCAGTCCAGCG
596			${\tt TTTGCGACAGTGTTGCTGAGACCG}$
597			GGCCATTACATCGGAGAACGTTCG
598			TCAGAGGGGCTTGTCGCACGGTAT GGTGTTCCGTCTCGGGAATGAGCT
599 600			ATGATTTGCAACGCCGCATGAAA
601			TGGGAATTGAACGTCCGTTCGAGT
602			GGGAGTCTCACCCACACCATGCAG
603		CCGCGAGTGTGGATGGCGTGTTGA	${\tt TCAACACGCCATCCACACTCGCGG}$
604			CACCCGGCTTAGGACCGACACATT
605			CGCAAGCTGTGCAGGCTCGTCTTA
606 607			GACATCGTCTTATCCTCCCACGCC GTGGTGCGTTCCTAACATGGAGCA
608			CAGTCGTCAGTCCGACCAACACCG
609			CCCAGATCTGATAGATACGCGCGG
610			CTCGCTCCAGGTGGAGCATGCTTT
611			${\tt CCGGATCTACCCAGCGATGCAAGT}$
612			TCTGACCAATCCACTGCGTAAGCA
613 614			ATTCGGCGATTTGTTCATCTGCAT GACGAATACATGGCCCAGAATTGC
615			CCATGTCGACGCGTAAGGAACCCT
616			TCTGAGGCTCGCGATTAGCTCCAC
617		${\tt TCGTAGTCTCACCGGCAATGATCC}$	$\tt GGATCATTGCCGGTGAGACTACGA$
618			CGAAGCATTGGCGCACTGCTATAA
619			TTGAGCGACGGACAGCACTGTTCG
620 621			ATAGCGTCTAACAGTCCACGCGGA ACAGTTACCGACAGCGGGCTAATG
622			CATTGCGCGTCTGAGTTTCTTTCC
623			ACGATTCTCCTGTCCAGCGAGTCG
624		CATGATCCTCTGTTTCACCCGCGG	CCGCGGGTGAAACAGAGGATCATG
625			CCGAAGCTTTTAGAGCGCTACGCC
626			GTATACGGGCCTGATGGCATCACT
627 628			GATAGCGCTGTTGCCCTTTCCATA GTGTGGATCCTCCATCAACCACAG
629			GTGTCAGCGCAAATTCCAGCGAGT
630			CTGTAACCGCGTGGTTCGGGCCTG
631			TAGTATTTATGCGCCCATTGCGCC
632			TAGGGCATGTAGCGCGAATTGACC
633			GCGGAAGGGCTCCAGTCCACCATC
634			TCTCCCCTATTGCGCTATGCGCGG
635 636			TTCGGGTGCCGGACAGCCAGAAGA TAAGGGCCCGTGAATTGCGAACGC
637			CGATACTCTCCAAGGCCGAAACGA
638			GCCTCTCGCCTTGCACTTGCACCT
639			AAACGTCAGCCATCGAAACTGGCG
640			${\tt GATATCTGGGATCGGCGGTAAAGC}$
641			ACATTTCGCCTCTTCGTCAAGCAC
642			TGAGGACATGAAGCGCACGGACTG
643 644			CGCGAGGGTAGGCTCTTACGCGTA ACACATGTCCCCACAAGACTCGCC
645			ATAGACACGCTCGCTTCGCTTTGG
646			GTTCGGTGAAGAGCAACCTACGGC
647			${\tt AGCCTCACGGCACATCGCGGATTT}$

	TABLE 2-CORC	eu
Seq. ID	No.Decoder Sequence (5'-3')	Probe Sequence (5'-3')
648	GGCTTCGCACCCGTACCAATTTAG	CTAAATTGGTACGGGTGCGAAGCC
649	TGTAGAGTCCCACGTAGCCGGCAT	ATGCCGGCTACGTGGGACTCTACA
650	CACTAGTCTGGGGCAAGGTGCATT	AATGCACCTTGCCCCAGACTAGTG
651	TGTACTCGGCAGGCGCAATAGATT	AATCTATTGCGCCTGCCGAGTACA
652	AACGGGTATCGGAAGCGTAAAAGC	GCTTTTACGCTTCCGATACCCGTT
653	CGGACTGCCCGTTTGCAAGTTGAG	CTCAACTTGCAAACGGGCAGTCCG
654	ATCGTTCAGCACTGGAGCCCGTAA	TTACGGGCTCCAGTGCTGAACGAT
655	ATGCATCGAACTAGTCGTGACGGC	GCCGTCACGACTAGTTCGATGCAT
656	TTCCAGGCATTAAGGAGAGGGAGC	GCTCCCTCTCCTTAATGCCTGGAA
657	GTGCGACATCTACTCCACGATCCC	GGGATCGTGGAGTAGATGTCGCAC
658	CTCATCGTCCTAACACGAGAGCCC	GGGCTCTCGTGTTAGGACGATGAG
659	AATGGCACTTCGGCGGTGATGCAA	TTGCATCACCGCCGAAGTGCCATT
660	CCGTGGGAGGGAATCCAACCGAGG	CCTCGGTTGGATTCCCTCCCACGG
661	AAATTCTCGTTGGTGACGGCTCAT	ATGAGCCGTCACCAACGAGAATTT
662	TTGCTCTTATCCTTGTCCTGGGCG	CGCCCAGGACAAGGATAAGAGCAA
663	TTAAGGATCAGGCGGAGCTTGCAG	CTGCAAGCTCCGCCTGATCCTTAA
664	CGCGACTAAGGTGCTGCAACTCGA	${\tt TCGAGTTGCAGCACCTTAGTCGCG}$
665	GCTCGATTTCACGGCCCGTTGTTC	${\tt GAACAACGGGCCGTGAAATCGAGC}$
666	AGCAGAGTGCGTTGCAGAGGCTAA	TTAGCCTCTGCAACGCACTCTGCT
667	TGGAGGTGAGGACGTGCACTA	TAGTGCACGTCGTCCTCACCTCCA
668	AACCGTTTAGGGTACATTCGCGGT	ACCGCGAATGTACCCTAAACGGTT
669	TATGATCGCTCGGCTCACAGTTTG	CAAACTGTGAGCCGAGCGATCATA
670	GACTTTTTGCGGAAACGTCATGGT	${\tt ACCATGACGTTTCCGCAAAAAGTC}$
671	TGTCGGTTATTCCACCTGCAAGGA	TCCTTGCAGGTGGAATAACCGACA
672	CTATGGTTTGCACTGCGCCGTCGA	TCGACGGCGCAGTGCAAACCATAG
673	AGCAGGGAAATTCAATCGTTCGCA	${\tt TGCGAACGATTGAATTTCCCTGCT}$
674	CCTAACCGAGCGCTTAGCATTTCC	${\tt GGAAATGCTAAGCGCTCGGTTAGG}$
675	CCCGACCCTAACTCGCATTGAATA	${\tt TATTCAATGCGAGTTAGGGTCGGG}$
676	TTGCTTAATGGTGACGCCACGGAT	ATCCGTGGCGTCACCATTAAGCAA
677	GATGCTCGCCGTGTTTAGTTCACG	CGTGAACTAAACACGGCGAGCATC
678	TCGGATGACGAGTTTCCATGACGG	CCGTCATGGAAACTCGTCATCCGA
679	ATGCGGTCTACTTTCTCGATCGGG	CCCGATCGAGAAAGTAGACCGCAT
680	TTGCGAGGCTAAGCACACGGTAAA	TTTACCGTGTGCTTAGCCTCGCAA
681	AACTTAATTACCGCCTCTGGCGCC	${\tt GGCGCCAGAGGCGGTAATTAAGTT}$
682	GTGACCGCGAACTTGTTCCGACAG	${\tt CTGTCGGAACAAGTTCGCGGTCAC}$
683	TGCGGATTACCGATTCGCTCTTAA	TTAAGAGCGAATCGGTAATCCGCA
684	TGATAGGGGGCCACGTTGATCAGA	TCTGATCAACGTGGCCCCCTATCA
685	TCGCTCCGTAGCGATTCATCGTAG	CTACGATGAATCGCTACGGAGCGA
686	TGTCAGCTGGTAGCCTCCGTTTGA	TCAAACGGAGGCTACCAGCTGACA
687	AGCGTCGCATGACGCTTACGGCAC	GTGCCGTAAGCGTCATGCGACGCT
688		TCAGGCAGTCACAGCGCTGAGTGA
689	GTTTGCGCTATAGTGGGGGACCGT	ACGGTCCCCCACTATAGCGCAAAC
690	GTCGCATTCTGCACTGGCTTCGCC	GGCGAAGCCAGTGCAGAATGCGAC
691	TGATTAGGTGCGGTCCCGTAGTCC	GGACTACGGGACCGCACCTAATCA
692	AAGGGACCTTGGGTGACGGCGAGA	TCTCGCCGTCACCCAAGGTCCCTT
693	TCAAATGGCCACCGCGTGTCATTC	GAATGACACGCGGTGGCCATTTGA
694	CTCCGACGACCAATAAATAGCCGC	GCGGCTATTTATTGGTCGTCGGAG
695	GGCTATTCCCGTAGAGAGCGTCCA	TGGACGCTCTCTACGGGAATAGCC
696	TGGATAACCTCTCGGTCCATCCAC	GTGGATGGACCGAGAGGTTATCCA
697	GACCGCTGTACGGGAGTGTGCCTT	AAGGCACACTCCCGTACAGCGGTC
698	GCCACAGAGTTTTAGCAGGGACCC	GGGTCCCTGCTAAAACTCTGTGGC
699	CCCACGCTTTCCGACCACTGACCT	AGGTCAGTGGTCGGAAAGCGTGGG
700	CATTGACACAATGCGGGGACTGAT	ATCAGTCCCCGCATTGTGTCAATG
701		GCTTTGGAACCCTGTCGAGTGGCT
702		TGGAGAGTCGCTTTGCTCATCCTG
703		GCTTAGGCCCCAGACCATACCTTG
704		CCGAAAGAGTTTAGGCCGAACACC
705		GAATTGCCACAGGGTCCGACTAAA
706		GTTCAGGCTGGTCGGAAACGTGTG
707		GTACGAGGAAGCCAGTTCGTCCAG
708		GGTCAGTTTTCGGCGGATTGTGAA
709		TGTCGTGATCGCGGATATCCTGTT
710		ACTCGGCGCAATGGATCCGACGTA
711		GGCGATCAAACCGAGAGATCCATG
712		CCGAGCGTATATACGCGCCTGGCT
713		AACATGGCACGACACGTGCCAAAT
714		GCACCTCAAAGTGGTGCAACGCGG
715		GAGCGCCATGCTTGTCACGTCCAA
716		CCCCCATTTACTTGCGCGATTCAG
717		GCGCGCAATCTGGTGGACCTTATC
718		GCCGTCCCGGTTGGCAATTGTTAG
719		TAACCTGCAAGCACCCAGGTTACC
720		CCCAATGCGAATGGTGGCTCCGAT
721	GTGAACTGGCTTGCCCCAGGATTA	TAATCCTGGGGCAAGCCAGTTCAC

TABLE 2-continued

Seq. ID	No.Decoder Sequence (5'-3')	Probe Sequence (5'-3')
722 723	AGGCGATAGCATGGTCCCATATGA AACGGTATCGTGGCTAATGCACGA	
723	AGTAGTGGTCCTCCAGATCGCCAA	
725		CTAACCTCCCGTCCAATTCAACGG
726	GCATAAGTGCGGCATCGCGAAGGG	
727		GCATGTAGCAGCTGCATCTTGTCG
728	TCGCAGTGATTCCCGACCGATAAG	CTTATCGGTCGGGAATCACTGCGA
729	CAAGGCGAGTCCACTCGAGGGGAC	GTCCCCTCGAGTGGACTCGCCTTG
730	GCAACTTGCACGGCATAAGTGGCC	$\tt GGCCACTTATGCCGTGCAAGTTGC$
731		${\tt GACGTCGCGAACGTCAAGCTCGGA}$
732	AGCGCTGGGCTGTGCCATCTC	
733		GCGAGGGTTACTCAGCGACATGAA
734 735		CTGACAATGGGCATTAGCGGTTCG
735		CGGCGATTTGTCCCACCTTCCGTG AAGGCGCGTTTGTCTCCATCTGTG
737		GGGTTATGGAGCGAGTTGCGAAAA
738	ACGTTACGTTTCCGGCGCCTCTAA	
739		GATTGAAACCCACGCAATCCGATA
740		GTGCGTCGCAGACAATTGTGGAAG
741		GCCGGACAGCCATACCTTTGTGCA
742	TCCGATGCCAGTCCCATCTTAAGA	TCTTAAGATGGGACTGGCATCGGA
743		${\tt TCACCTCGATTCGCACGGTTTCAG}$
744		${\tt ATTTTTTCGACACGCGGAACACCG}$
745		TGGCGATTCAAAAGGCCTGCTAGA
746	GAGTCACCTCTGAGACGGACGCCA	
747		ATGCTGCTGCAGGATGACAGAAGA
748	GCGGATGAAACCTGAAAGGGGCCT	
749 750	GGGGCCCCAAACTGGTATCAAGCC GCATTGGCTTCGGATTCTCCTACA	
750		CAAGACCTCACAGTTGGGCCGCCT
751	ACACCATGTGCTCCGCGCTGCAGT	
753	ACGATGAACATGAATCGGGAGTCG	
754		CGGAGCGCTGCTACAGGGATGCAG
755	GTGCCGTATTTCGACCTGTGCGTT	AACGCACAGGTCGAAATACGGCAC
756	GCAGTGCGCACTTCAGTTCAAAAG	CTTTTGAACTGAAGTGCGCACTGC
757	GCGATTTTAAGCGATGCCTTGACG	${\tt CGTCAAGGCATCGCTTAAAATCGC}$
758	TAGGTGACCTAGGCTTGCTTGCGG	${\tt CCGCAAGCAAGCCTAGGTCACCTA}$
759		GCGCCGCACAGGCAAGGTATCCAG
760		GCATAGACGACGAGCCGTAAGGGG
761	GCGCTTGCCCGATGCGATGCATTA	
762 763	TTTCTGTAAGCGGCCTGGGGTTCA GGCTGAGGTGAGCGGTAAGGATGA	TGAACCCCAGGCCGCTTACAGAAA
763		CAAATTAGATCGGGGAGGCCAAGA
765	GGAGGTAACGCCGTGTACGTAGGA	
766	GTAATCCATTTGTGGCTGCGTCAA	
767		CAGGCGTCTGCTGGAATGGGTTTG
768	TAGGAGGAATTTGGCATGCGGGCG	CGCCCGCATGCCAAATTCCTCCTA
769	ATAGGTAGGATGTGCCCGGCGTTG	CAACGCCGGGCACATCCTACCTAT
770	GCAAGTGCTTAGCTCGTCAGCCTC	
771		GTTAACGAGATGCGACACAGCCAG
772		AGTGATTGCGCGAGACGACGTTAG
773		GCTCGGGGACAACGTTTATGAAAA
774 775		GGAGCGGAGGTTCGTCCTCCTGCT TTGGATTGCACGATGGTGCTTGAA
775		CCACTAGCGATCACTGGCGACGCT
777		AAGCCCACGGAGGCAGGGAATGTA
778		AACCGCTACTGAATACGCGAAGCG
779		TATAATGAGTGTCGACGCGTCCGA
780		AGCTGGAGCGCTGGCCTGAGA
781	TTGAATTGCCAAGCCCTGAAAGCC	GGCTTTCAGGGCTTGGCAATTCAA
782	AGTTTTCGCCTTGATGCGTCGGTG	CACCGACGCATCAAGGCGAAAACT
783	GTTTCATAGGCCACGCGTGCTAAA	${\tt TTTAGCACGCGTGGCCTATGAAAC}$
784		TTGGGCAGACGAAGTCTTCGCTCC
785		AGGCTGCATTCACCCTCGGCCAAT
786		ATGGAAAAGCATTCGGATGGATCA
787		TCATGGGCCAAGACAACTGTGTGC
788		GTTGTTTTTTCCACTGCCCGCCAG
789 790		CGGAGCAGTCTTACGCATGGAGAT TCCACGAACTGCGACGAGAGAGA
790 791		TCCACGAACTGCGACGAGAGAGAGA TGCTCGGCAAGAGTGAATACGCTA
791		CCATCGCGCCGTGGCTTTTGATTG
793		AGATCTGCTGAATTCCGTGACGCT
794		CCTTGGGCGCATTAACAGGGAGTC
795		TTGAATCTGAACCGGCAGTGCCTA

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Seq. ID	No.Decoder Sequence (5'-3')	Probe Sequence (5'-3')
796	AACAGGGTGATAACGGTGGCCAAT	ATTGGCCACCGTTATCACCCTGTT
797		ACGCACTTACACATGGTACGCACG
798		TGGGCTGCCGAAGTAGAATTGGTC
799		CAGCCAAAAGCAAATCGGTCCGAT
800		CGAATAAGCGTGTGCTTCGGCGGA
		ACACTGCTCACAATGCGTACCGTT
801		
802		GATTCAGGGGAACAGTAGTCGCCA
803		TAAGGCATACGGCTGTCCCCTCTG
804		TCGCAGATTCCGATAAAACCACCG
805		ATATGTCGTGAGGTCGGAGGCCAA
806		TCGGCGCCAGATGCTAGCGAAACG
807		CATCCACCGCTCCACCGCTTAGT
808		GCGGCCCGTAAACGCAGCCAATAT
809		GTATCGGGATTGCCACCATAGCGG
810		TATGCCGCCTGAGCCACATGCAAC
811		AAGCCCTGGGTCACTCCCCAGAAT
812	CTCTCCAAGGAGACGAGCCAATGT	ACATTGGCTCGTCTCCTTGGAGAG
813	GAAAGGACGGGATTTGGGGGCTAA	TTAGCCCCCAAATCCCGTCCTTTC
814	TATGTAGTACCTTGGCTCGCGCCA	TGGCGCGAGCCAAGGTACTACATA
815	TCCCTTTCGATGAGCGGCTGTACT	AGTACAGCCGCTCATCGAAAGGGA
816	TAGATCGGGCAGAGCCCGTATCTT	AAGATACGGGCTCTGCCCGATCTA
817	GGAATGCTTTAGGCTGCCGAGCTG	CAGCTCGGCAGCCTAAAGCATTCC
818	ATGGTAGCAACATTCAACGCCAGG	CCTGGCGTTGAATGTTGCTACCAT
819	CTATGAAACGTGTGGCCCAGCAAC	GTTGCTGGGCCACACGTTTCATAG
820	ATGTTGCTAGTGCCTTTCGGGCCT	AGGCCCGAAAGGCACTAGCAACAT
821	CCAATGTGCGCAGACTCAGTCATT	AATGACTGAGTCTGCGCACATTGG
822	GATAGTGCTCGCAAACGGGCCTTC	GAAGGCCCGTTTGCGAGCACTATC
823	GCACCCTGTTGCCTCATTGAGCGT	ACGCTCAATGAGGCAACAGGGTGC
824	GGCGTGAATAGAGTGACCAGGCGG	CCGCCTGGTCACTCTATTCACGCC
825	ACGTGCCAGCTGCGGGCACTTTAT	
826	AGTGGAATAGTCGCGTCGTGCCGC	GCGGCACGACGCGACTATTCCACT
827		CCAATCCAGCGGTAATAGGCGAGT
828		ACGGGATCATCTCAATCCGGTCTC
829		ACTGGTTCGGTGGTAAACTGCCAG
830		TCACATGCGAAATCGGCAATGTAA
831		TGCTGAGGCGACCCTTCAGTTTTA
832		AATGTTGCAAAGGCATGCGAAGCC
833		GCCCTCAGAGAGACCTTCGGTCTT
834		TACTGCTGAGCTGGAGCCATAGGC
835		TTGTCCACCGAACGCTATGATACG
836		AGACAGGCAGAGTGCGAGCGCATG
837	TGGGCAATTCGGAAACGTCGGTCT	AGACCGACGTTTCCGAATTGCCCA
838	TTGCGGAGATGCGACGGTACATTG	CAATGTACCGTCGCATCTCCGCAA
839	ACTTTCGCACGTCGATCTGGACTG	CAGTCCAGATCGACGTGCGAAAGT
840	CTAACTGCCGCGGCAAACTGATTA	TAATCAGTTTGCCGCGGCAGTTAG
841	GGCCGCGGATTTTATTCCTTGGAT	ATCCAAGGAATAAAATCCGCGGCC
842	GAATTTGGAACGGTGTTCCGATGA	TCATCGGAACACCGTTCCAAATTC
843		TCCTGATGCCGTAGATGGATGGAC
844		TACGCACATGTGCCAGGTCGTTTA
845		CCTAGGATTGGCTCTTGGATGGTG
846		GCGGCGGACTGATCGTATATGAGT
847	GTGCCAACCGACGATCAACCGAAC	
848	TGGGGTTCGTACAGGTCGGTTCAT	ATGAACCGACCTGTACGAACCCCA
849		CCCGCAGGCCTCGCCTCTACTGTT
850		AAGATCCATCTCGGATTCGATGCA
851		GACAGAGCGGACATAACGTGACGC
852		GTGATATTGCGCTACGCATGTCCC
853		CCACTTTGGATGTGTGACGTGTG
854		TGGCCGTATTTAGCACCTGAGCAT
855		CCAGTCAGCGCGCTAAACATTTTT
		TCGTTGGGAACGGAAACGGACTAT
856 857		CTGGTCTGCAACCCAGAAGATCGA
858 959		GACATGAGGATCGGCTGCGCCGCAAC
859		AGATCCTTTTCGACACCCCGCAAC
860		CTGGCATCCACCCGAGGAAGAGAT
861		CGCGAAAAGCTGAAACGCACATCA
862		GGCCGGATGTTCTCACCCCTTAAC
863		GGACGAGACGCAGGGAGACGACTT
864		CATTGTTGCGCCTTATTAGGTCGG
865		GGCATTGGTACGGTGCCAATGATG
866		CGTTGCTGCACTTCCCTTTCTCCA
867		TGGCAGGCATGACAAGGAGTACCA
868		CCGCGCTGCAAGAGAACCTGTGCC
869	GAATCTGGGCATTGCTACGAGACC	GGTCTCGTAGCAATGCCCAGATTC

Seq. II	No.Decoder Sequence (5'-3')	Probe Sequence (5'-3')
870 871		GTGGTAGTGGACGCTCCCATTTCG ATGCAAGCACGCGAGCTCATATGT
872		
873	GAGGGTCCCTGCTCAGAGTTGGTT	AACCAACTCTGAGCAGGGACCCTC
874		ATTCCATAAGGGGCGATCGCATTT
875		GCCATCCGCAATCCATTCGGGTAG
876		ACGCGCAGAGACCTGCCAGTCCCT
871 878		CTGCATTCGTGGAATGGATCGTTA CAAGGCGTAATCGTACGTGCGGCC
879		AGCCAACAACTGATGCATTCCCCA
880	) TATCTGGGAGTAGCAGGCAGGGCC	GGCCCTGCCTGCTACTCCCAGATA
883		GCGACCTGAGCGTGAAACCTTCGG
882		CTGAAGGATGTCCCAGCTGGGTTC
883 884		GTCCGGGTTATTTGCTCGCATGCA CTGAAAAGCGTTTGGCGGACAATT
885		
886		TCATGGGCTACGTAGAGCACGCGA
887		GCGAATTACGTTATCGCGGAAGCC
888		GGGCTTCGGCCCTAGTCGGCTACA
889 890		AATATTCAGCCAGGGCGTTCGCTT AAATCTGCAGCACGTCGCGTGACA
891		CGCCTGTCGACACACGGACACGG
892		CACATATAGGCGCAACGTGTGGGG
893	GGCGGGCACAACTCAACACAGATG	CATCTGTGTTGAGTTGTGCCCGCC
894		TAATCACCGGTGATCCCGCAGTCG
895		GACTCCGTACCGGTCATGTCCCGA
896 897		CCCGATCAACGGCCACTCGAGGTA TGGTTCGGCTAGCCCCATGAATTA
898		TCGAACGGAATCGGCTTAGAGTGT
899		TTTGTGCGTGTCACTCACGCCCAC
900	) ACGACTCCTCGGGCAAAGTACGTA	TACGTACTTTGCCCGAGGAGTCGT
90		GAAAACAGTAGCGCCATGACCACA
902 903		GGAACCCGCTCTGGCTAGCGAAAG
90.		TTGTCACACGCTAACACGCCCTGT GTGGCCCGATACGCCGGAAGTACC
905		CCCAGAAGGGTGAACAAAACCCAC
906	ACGCAATTCCGCATTACTTACCCG	CGGGTAAGTAATGCGGAATTGCGT
90		TTGTGCTTGACCGCAGTCGAGGCG
908		TGGCCCTCTCTGGATCCATTTCAC
909 910		TAACGGAGCCCTGCAGCGTTTATA CCCGTTACAAGCCGCCTGAATAAC
91:		AACTGAACGCGCACGCTAGAACCC
912	2 TTGGGCTCGAGCGGTACACCACTA	TAGTGGTGTACCGCTCGAGCCCAA
913		CGCATACCGTTGTCCTGAAGACGG
914		GTGCCGCAATCTGTCAAAGGGTCC
915 916		AGCGCCGCCTGGCGATAAAATTTA AGTTCAAGCGATCTTGCGTTCGGC
917		CCGTCTTAGGGCACCAATGGCCTA
918		ACGCAGCCTGTAAGCTGTGGTTTG
919		TGCTACCGTGCCAGTCTCCGTTTA
920		CGATTCCAAGTGTGATGCGCGCTA
92: 92:		CGAAACGGCTCGTTTGTGTCAGCA GTGGACAGTCAATGCCGTYAAGCG
923		TATCCGTAATACACGGCCGTGGAA
924		AGTCTTCCTCGGCAACGGCATAAA
925	AGTGCCGAGATAGGGGACTGGGCG	CGCCCAGTCCCCTATCTCGGCACT
926		TCGTCCCGAGGGCGTGGAGACTAG
927		CATCATCCATCTTCCGAATGGCGG
928 929		CTTCGCAATCGACTTTCACCGTCA TCGGAACCGGGTGGTGACGCATAT
930		TGGCAGCAACCCCTTCACTGATGG
93		GTCATCGCAAGCCAAGCACATATG
932		AGCAGTTCAGGCTTCCAAAGCAGA
933		ATTTCCGCCTTCTTGACCAAATCG
934 935		TAACGAGGCGGGAAGGCCTCTGAT CTGCGATGTGGCAACGACAACAAT
935		AGACTCGCGTCCAGACACATTTCA
937		TACCCTTTAAGGAGCATCGCCCGC
938		ACGGTCGACGCATGGAGATTGCGG
939		CAAGTTCCAGGTGATTACGCGGCA
940		TCACACTACCGCTGGCTACTGGAA
941 942		TGCCGAACAATAGGCGGAATTCAG AGAACATCGCCTCGAGGTTCAAGC
943		TGGCGGGTCGTACTTCCACGCTTG
		<del>-</del> -

TABLE 2-continued

		- 1	- 1
Seq. ID	No.	Decoder Sequence (5'-3')	Probe Sequence (5'-3')
944		CTCTCC ACTCC ATCCCACCCCTAC	CTAGGGCTCGGATCCAGTGCACAC
945			AACCTCGCAATGCTAGCCCAGGGA
946			CGGCAAACAAGCGTCTTTGGTTCT
947		CGTCACATGCAAACGTTCCCTCCC	GGGAGGGAACGTTTGCATGTGACG
948			AGCGACTCAATACACATGCGGTCA
949			ATGACGGATACTCATTGGGCCCGC
950			AACCAGGGGCGTTCACAGTCACTA
951			GATATACGCGCGGCAGACGGTGCC
952 953			TTGACGGGAAAAAGACTGCATCGA AAAAATGGCGAAACCCCACGGGGT
953			GACAAGTCACAACTGCGCGTGTAG
955			GGCTCCAGAGATGAGGTCGCTGCG
956			ACCGATTTTAGGAGTGCTGGGTCG
957		ACGCGCCGCTCATCACTACAATCT	AGATTGTAGTGATGAGCGGCGCGT
958		CGCAACTTCCTGTGGCAAAGCCAG	CTGGCTTTGCCACAGGAAGTTGCG
959			TCAGTTGCCTTATGTGCCCAACGA
960			ACGGAGAATGGCAATTACAAGCGG
961			CACAGCCCAGGACTCCCTGGTTAC
962			GTGACTGCCCCCAGATCTTGCGCT
963 964			CCATGCTGATGAGCAGATGTACGC ACGGTTTCTTTCCTGCCACAGAGG
965			TCCGATGCAGGTCCATTGCATAGG
966			TATCCTTATTCGCCATCCACCGAG
967			TGCGTCACGCCATCACGAGTGAGG
968			GGCGTATGGCGTTCTGTGAGCGTA
969		CCGGAGAAGTTACGCGGATCGGAC	GTCCGATCCGCGTAACTTCTCCGG
970		GCGCCCTCACTGCATTTTTGGTAT	ATACCAAAAATGCAGTGAGGGCGC
971			TTGCGCTGTTCGCGTGCTGAAAGT
972			TGCTCATGCATCAAGGGCGTTTAG
973			TAGCGACGATCGTAAAAGGCAAGC
974			GATGCCGAGTGCGTACGATGTCTG
975 976			AAGAGCATAGGAGCCGCGCGCTA TGGCATGGGGACCAAAAGGGCATC
977			GAGGCATCGTGGCAAGGCAGCTCA
978			CAAACTATGGCACGTATACGGCGG
979			GTTGGATGAGCGCGGAGAGCACTA
980		CCCTAGATAAGTTGGGGTGGGACG	CGTCCCACCCCAACTTATCTAGGG
981		${\tt TGAAGGGCCACCTGATATGGTTTC}$	GAAACCATATCAGGTGGCCCTTCA
982			TCGGGTTAACCAGTCGGAGGCGGC
983			TGATCCGCTGTTAGTAGCCGTGCG
984			CGATGCTCGTTGGAATTGGTCCGG
985 986			GGATGTGAACGGTGGACCTCAATG CTCGGCTGGGACATGCTGCGTCCT
987			CGTTGGTAGTATGGCCCGCGATTA
988			GCTTGCCGACCGGAGAAATTTGCG
989			CACGCAAGGCATTAGTCGAGCCAC
990		TGTGGGCGTGTTCCGGCTCACTGT	ACAGTGAGCCGGAACACGCCCACA
991		${\tt GTTCTTCCTTTTCTGCGGTGGGAA}$	${\tt TTCCCACCGCAGAAAAGGAAGAAC}$
992		ACCTCGAGTCAGATTGTGCGCCTT	${\tt AAGGCGCACAATCTGACTCGAGGT}$
993			CGGAACAAACCGTCTGTCCACTTG
994			CCTCGTCGGCGCGACTCAACTGGA
995			GCAAATAAGGGCTGACCTGTTGCG
996 997			TACCGACATTGCAGGAGTCACGGC TGTTTCAGACCAGCTTGCGCTGAT
998			CATGGCCTCTCGTTCTGGCCAGGG
999			CAACCCTGACGAGTCCTTGATCGT
1000			TAACGGTGGTCTTGGTGCCATGAA
1001			CGTCGCAATCCATCTCCTTGCTGT
1002		CGTAAATATCTGCGGCGGTGTGAA	TTCACACCGCCGCAGATATTTACG
1003			GCCAACAGACGAACACGTGTTTCC
1004			TGGCCTATCCGAATCCTAACATCG
1005			ACCATCCACTTGTCCTTGTCCGAT
1006			TAACTCGAACTTTGTCCTCCGGGC TCCATGTGCCCATTTGTCGGATTT
1007 1008			TCACTCATCCGCATCCCCTAACTG
1008			CAATGTCGGAATCTCCACCTGCCG
1010			AGATGAGTGAACCTGGCTGCCCTA
1011			GCGTGCCTACTGCTAATACGGTGC
1012			TCCCTTCGCACACCTGTAATGCGT
1013			CCCTGTGGAACACGTGCAGTCACG
1014			${\tt CGCGATTTTAGGCGGTAGTTCAGC}$
1015			TAACTCGATCCTCCCTGGCGTGCT
1016			GCATGACCCATTCCTTGCCCTCAT
1017		GGGTCTCTCGTAATCAAAGGCCGA	TCGGCCTTTGATTACGAGAGACCC

TABLE 2-continued

	TABLE 2-conti	inued
Seq. ID	No.Decoder Sequence (5'-3')	Probe Sequence (5'-3')
1018	TATCTTGCGCAACGCCTCCATTTA	${\tt TAAATGGAGGCGTTGCGCAAGATA}$
1019	GGTTACACCTACGGAATCCAGCGG	
1020 1021		CTATTGACCGGACCAACTCGGTGT CGGTGGCTAGCGTTTAATCTGGGA
1021		CTTCCGACGGCCAGTTTCACCAA
1023	CCAGGGAGTTGACAATGAGGCTG	
1024	TCTGCGTTATTGGACCGTTTGTCG	CGACAAACGGTCCAATAACGCAGA
1025		${\tt TGTACGCCGGTTTAGCATCCCATA}$
1026	CACAGACGTCTGTCGGGCTTGTGT	
1027 1028	AGAATGCCGTTCGCCTACTCCCGT CGACGGATAATGCAGGCCTCATGA	
1028	ACCCTCTAAAGCAATAGGTCGGCG	
1030	CACTCACGGCAGAAGCCTGCTTGT	
1031	ATCAGCCCACATATTCTCGGCCGT	ACGGCCGAGAATATGTGGGCTGAT
1032	CAAATCTGGGGTCGTCCTAAACGC	
1033		GTATTTAACCTGCCATGGGCGACA
1034 1035	GGGGGCCCATCAATTCATTATCGA GTCGAGCAGCTTTAGTATCGCGGG	
1035		TTGTGAGCCTTCGGTGCTTAGCGG
1037		CGGGATCACCGTTCGCTAATTCTA
1038	CACATGACATTTGGCAAAGGTCCA	${\tt TGGACCTTTGCCAAATGTCATGTG}$
1039	TCAACGCACTGGCGATGACTAGAT	
1040	CGGGAAATGTCTTTAGCCGTCGAA	
1041 1042	ATCAGAGCAAATCTGCAGCGGGGA GGCCTGTTTCTGTCCAACTGGGCT	
1042	ATTTCACCTCGCTGATCGCTTCCG	
1044	AGTGACGCCGAGTCGCGAGGGTTA	
1045	AGTTGTCTCATCCTGTCCGGGACC	${\tt GGTCCCGGACAGGATGAGACAACT}$
1046	CTTCTTTGTGCACACTTGCCAGGG	
1047	CACCTCATCGGAGCATAGCAACCC	
1048 1049	ATGCGATCCATGACAAGGGTTGCT	TAAGCCGCACATCATCTCCACGGG
1050	CCCAATAGACGCCACAGCCAGTGA	
1051	AACGACCACGACCCTCGCCGAGTA	
1052	GGTGCTTTGTCTGAGGCGAGTGAA	${\tt TTCACTCGCCTCAGACAAAGCACC}$
1053		AAATTCGGAGAGCAGCGCCGACAG
1054	CTCGCCGGAGTGTTGTAAGCATTG	
1055 1056	ATTTGCCACCGGCGACAAAAAGAT	CACCGGCCACCTCTCATGATTGCT
1057	CCGCCGTGTTGGCATGTCTTTTG	
1058		CGTGTGTCAGTCAGCACTTCCGAT
1059	CCTCAGACCCTATCTGGGTTGACG	
1060	CTGTGTGGTCTGGTCCGGCTGTTC	
1061 1062	GTCCCCATTATCGGTGAGTGCAAC ACAGGCACGTAAGTGCTCAATCGG	
1062	ACCAAGATAGCGGGAGTGCCCCTA	
1064	GGTTTACGCCATGACATCCCGTCA	
1065	GTGCAGGCCTTTGTGTGTGAATCG	${\tt CGATTCACACACAAAGGCCTGCAC}$
1066	CTTCGAGGGTAGGGCTTCGAAACG	
1067 1068		CCGTGGTAAACCCAAGTGTCGACT
1069	ACATAAATCTCGCCCGCTGCACTC GTTTGGTTTTCCACGGAGGTTTGA	
1070		CCGGGACACTAATCTGGTTCCTGC
1071		GCTTTAGCTCCGCGCTCTAGCAAA
1072		GAGCATGTCAGCGATGCCACATAG
1073		AGAGCAGCTGCAAACCGACTTAGG
1074 1075		CCTTCCGTTCCTGTGGACGAACGC AGACAATTTCTCGGGCGCGGGTTA
1075		TTGGCAACAGCTCTGAGCACCATA
1077		GCCCTGACGTTAGTGGGTCGATGA
1078	TGCTCAAGCTACGCGTCACTTCCC	${\tt GGGAAGTGACGCGTAGCTTGAGCA}$
1079		${\tt TTTCCCTCCTCAGACCTTCCCGCT}$
1080		GCCACTGCGGTGGTGCTACATCGG
1081 1082		CGCGCCGTGTGATTCCCAGAACTT TTAACGCCGCACGTAAGGCTGGTG
1082		GCATTCGGAAGAGGAGGCGAAACG
1084		GCGCGCTGCTCTATTGGCCTCCTC
1085	AGTAATCTTGCGGCACACAAGCGG	${\tt CCGCTTGTGTGCCGCAAGATTACT}$
1086		TATCCTACGCGCGGTTTGTCCTCA
1087		GAGATGGGCACTGCGTCTCTACGA
1088 1089		CACCGCACTCGGGGTGTAGCTTCG CCAGCCATGGGAAGATCACATCAT
1099		CTAGGCGAACGCGATACGTGTACA
1091		TGCGTACATGCGTAAAAGCACACC

TABLE 2-continued

Seq. I	ID N	o.Decoder	Sequence	(5'-3')	Probe	Sequence (5'-3')
	92					GCATCCACGTATCCCGCCT
	94					GGAGGGCTGTGCCTAATTT AATGGCTCACCAAACTTAT
	95	CCTATTTC	GGCGGACCI	CGATGCC	GGCAT	CGAGGTCCGCCGAAATAGG
	96					CAAGTGCATATTCCGGTAA
	97		ACGGTCCCT TGCTGTATT			AAAGGGACCGTCCGAGAGG FTAATACAGCATTCGCTTG
	99					GTTCTGGCATGGGAAATGC
11	00	GTTTTGGC	TAACCGTCC	TGCCTTG	CAAGG	CAGGACGGTTAGCCAAAAC
	.01		TCCGGGCGA			ATTCGCCCGGACAAAACCT
	.02		GAGTGCGTC			CGGACGCACTCGTGGACAT CACAGATGGGAACGGTATT
	.05		TGCCTCATC			CGATGAGGCACCTTGTGT
	06					TTTGTAGGATTTTGCCGGC
	.07 .08		ATGTGCCGG			GACCGGCACATGGGATAAG FGCTATGCATTATGGCCGC
	.09					CATACTGCGATGCACCGTA
	10		GTCGAGGAT			FGATCCTCGACATCTGGTG
	11		GCCCAAAGA			CCTCTTTGGGCGTAGGAGC
	.12		GGCAGCAGC GCACGCAGT			CTGCTGCTGCCCATATTCT CTACTGCGTGCGACTGCAG
	14					AGATTCCGGTCAGGGACAT
11	15	TTCGCCAC	GAGGCATTA	GTCCGAC		ACTAATGCCTCGTGGCGAA
	16		CCCGAGAAT			GTATTCTCGGGAACGACGT
	.17 .18					CGTCAAAGCGCCAGCGGAT CCGGTAAGAATTTGGTTCA
	19					ACACACCAGCCTACGCGTG
	20					GCCAGATCGCGGGATCGA
	21					CACGGTGGTTGAGTGTTCC
	.22					GTGGCCAGTTGGTGTGA GCCTGGTGTCCTAAGCACA
	24					ATCGGTCGGGTTAAATGTC
	.25					GCCTACTGGCTCGGTGCC
	.26 .27					ACCAACATGCACGCTTGAG ATTGGATGGTGGCCTTCCT
	.28					CATAACCTTGGCGTTCGTA
11	29	CGCACCAG	AGTTATGCA	GGCTCAA	TTGAG	CCTGCATAACTCTGGTGCG
	30					CCTTCCTCGTCCAAGCTGG
	.31 .32					GTCATTTGAAAGGCGTGAC ACTCGGGCTGGGTCTAGCA
	.33					GACCCAAGTGCCACAATA
	34					ACTTCCGGTCTCACACGTG
	.35 .36		GATGCTACA			GCTGTAGCATCAGGCTGCC CTGAAGGATGGACGGACCG
	.37					CGTAGGGTCCGCGAATAG
	38					rcgtgctgactgcacaggt
	39					FGGACCACCTGTGGTTCTC
	40		GAGAAATCC GTGCAAACC			GTGGATTTCTCTAGCGAGG ACGGTTTGCACCGATGTTA
	42		GACATGGCA			AATGCCATGTCTTCTGGGT
	43					GTGTTAGAGCAGCGCTTTT
	44		TCCATTTCC TGGTGGGCT			IGGGAAATGGACAGACTTG AAAGCCCACCATGTGTCGG
	46					CGCAAAAAGCTGGTCTGT
	47					GAAGTGAAATGGATCGCCG
	48					CCTGTGTCATGATAACGTC
	.49 .50					GATCCGATCCAACTCTGCC GAATTCGGTGGCATTGAGG
	51					GACTAATCACGCTAACTCC
	52					FCCGTGACACGTCGAGTTC
	.53					ACCAGAAATGTCGCTTGTG
	.54 .55					GCGAATTCACGCATTCTGG AATTCGCAGGGCTCCCTTG
	.56					AGTCGTCCGAAGCAAGAAT
	.57					CTGGAAATCAAAGTGGCA
	.58 .59					CACTTATCTGCCGACCATC FTGGTCAACCCGTGTGAAC
	.60					GAATGGGGCAATTGAATC
11	61	TACCGGAA	ACTGAGCCT	CGTGCTA	TAGCA	CGAGGCTCAGTTTCCGGTA
	.62					TGCCCCTGAGTAAAGATCC
	.63 .64					ACAGAACAAAGCACTCGCG IGTACGCCATCGCGACGAC
	.65					CACTTCGGGAGATTCCCGT
11	66	GGTCGAAA	TGAGCCAGC	AGCAGAT	ATCTG	CTGCTGGCTCATTTCGACC

		TABLE 2-Conti	inuea
Seq. ID	No.	Decoder Sequence (5'-3')	Probe Sequence (5'-3')
116	7	CCATTGGAATACTGCGTGCGGCTT	AAGCCGCACGCAGTATTCCAATGG
1168			CATTGTGCCCTCGCGAAGTCTTCC
1169			AGTTCGGACCTTCGAAGTCACCCT
1170 1171			GTGATTCGACCACCAGAGGGACGA CTCACGCCCAGCATAATTTGCACA
1172			TGGGCACACATGACAGTTGGCGAC
1173			TCGTTTCGTCTTGAGGGTTCGAGG
1174			GGCAACAAAGGTCACGTGATGAAG
1175			${\tt AAGCCATCCTGCTGGGAATGAAGG}$
1176			TAAGACGCTCCATTGAGGTCCCCG
1177			TCGACGTAACAAGCGCTAGAGGCG CCGTCCCTGTTTTGAGTCTGGCAG
1178 1179			GGTTCCCTCACACGGTGTAAGGAG
1180			TGCGCGAGGCGATATGGCATGAAA
1183			CGCATACAGGGCAGACAGTCAGAC
1182			${\tt CGCGTTAACGCCGTTCCATTAACC}$
1183			AGCTTGAGATTCCGCAGTGCGAAG
1184			TCCAGGACTCCTACGCCTCTGGCA
1185 1186			TGAGTTAATACTGGCTCGCCCGTC CCGCCAAGACTGACTTTGGAGGTC
1187			GACGTGTTCGGTCATGCTCTAACG
1188			GGCGTACCCAATTTTTGAGCCCAC
1189			AGAGGAACGCGTGATCTCTGCCCC
1190	)	TTTCGCCCTACGAAGCGAAGTTTC	${\tt GAAACTTCGCTTCGTAGGGCGAAA}$
119			CGCGTAGCTTAACATCACCCCGTA
1192			ACACGGCGATCTCAGACTCACAGG
1193			CGAATGCCTGTTCCAGCTTCAGT
1194 1195			TGGACTCCCATGTGAACCAGTGCT GCGCAGGGAGTGTGATCTTCCTTA
1196			CGGCTTCAATTTTAGCGTGTGGTG
119			ACGATACATGATCCTGGCGACAGC
1198	3	TTCGTTCGTGCACTGGATTCTTGA	TCAAGAATCCAGTGCACGAACGAA
1199			${\tt CACTGCAAGCACAAGGAGAGCTGA}$
1200			TTCCCACGAAGTTCACCTCGTCGT
120			TAAACCAAGGCCCGCGGCAATGCT
1202 1203			TTGAGGAGTCACATCTGCCCTCTG CGCGTTTGAGAGGCTGAAATATCG
120			TTCGAATCGCCAACATTTCTGGCA
1205			GAATTGTGAACACCGGGTGGCCTA
1206	5	GAGAGTCAGACCGAGGGACACGAG	$\tt CTCGTGTCCCTCGGTCTGACTCTC$
120			GTTGCGTGGTTCCAGGATCGCCTC
1208			TGAGTCAGTAGCCCGCCTCTCTGG
1209 1210			ACTGCCGTACGATGGGACTGTGTG TAGAGGCACGCTTCCGCAACGTAA
121			GGGACACGATTGCAGCGTGTACAT
1212			ACCTGGGCGCTTCCGACGACGAGT
1213	3	ATGCGAGAGCAGAATTGAGCCGGT	${\tt ACCGGCTCAATTCTGCTCTCGCAT}$
1214			GCACGCGTGAATACGAACCAACTT
1215			TAGCAATCTTCGGCGATAAGCCCA
1216 1217			TAAAATTCTGGGTCTTCGCCGTTG GTCCCTAGACTTTCGCCGTACGCT
1218			TAATCAAGGGGACGCTGGATGCAT
1219			CAGAAGCCTGCGACTGATGACGGT
1220		TCTTGACGGCTGGGCATGNTTGGA	TCCAATCATGCCCAGCCGTCAAGA
122			${\tt CCAGGTCCTGGGTCCGAATGTTAA}$
1222			AACACGCAAGGGAGTTCGACACCA
1223			GTTTGCGCGCAGGCGACTGGAGTA
1224 1225			GCTTGGCATGCTTACGGCATTGCG TACTGTTCGTATTTCGCGCGGACT
122			TGTGATACAGTGCGCGTGCAACAT
122			GCACGCCGCGGGTAGTTAGGCGAT
1228			TACCGAGCTTGTGTTCCCTGGCCA
1229			${\tt TGATCTCAGACGCGACCCATGTTT}$
1230			${\tt CTAAAAGGGAATCGCAGCTCTCGC}$
123			TCCGCTCGTCTCTTGTTTGGCCGG
1232			TGTCAAGCGAGACTGTGCCCCATT AGTGTGTCCTGAAGGCCCGAGACA
1233 1234			GCCGAACCACTTAATGAAGGTGGA
123			ATGACAGGTGGATGATTCCGPAGC
123			CCGACGACGATAGCCCATCGGCTC
123			TCCTCTGTGCGTGCGTAATTCGTG
1238			${\tt CCTAGTTGAGGGGAGCGTCACAGC}$
1239			AACGTAGCCCGCGTTTTCAGAGCG
1240	י	GAGTGCTGGACACCGTAGCCAGGA	TCCTGGCTACGGTGTCCAGCACTC

TABLE 2-continued

	TABLE 2-conti	.nued
Seq. ID 1	No. Decoder Sequence (5'-3')	Probe Sequence (5'-3')
1241	CCAACCCCAGTGTAGGCGCAAATG	${\tt CATTTGCGCCTACACTGGGGTTGG}$
1242	GAAGTAGGGGATGTTGGCCGGCGG	
1243	CAACGTGGGCACCTGTTTTAGCAG	
1244 1245	CTAGCTGCGATCCGAACCTCTACG CATTGAACCATCAGCCAAGCTGCG	
1246	AGACTGGCAATTTTTCGAGGCCAA	
1247	CTGGCCGTCCATGAGTTGGTCCAG	
1248	CATGCTGAAACACGGGATTGCCAT	${\tt ATGGCAATCCCGTGTTTCAGCATG}$
1249	CGATATGTAAGACAGCCGTCGCAA	
1250	AGCGTAACCTACTGGGAAGGCACC	
1251 1252	GTTCGAACCCCGCGATGTTAAATG GTTGTTAGGAGGCTCGAGGCTGCT	
1253	ACTGGTGCTACGCGGGATATTTGA	
1254	CTGGGAGCTATCCTCAGCCGAATC	GATTCGGCTGAGGATAGCTCCCAG
1255	GAACTCGCCGCTGCCGAAGGGTAG	
1256	TTCGATCGAGGAGCAAGGAGAGTC	
1257 1258	GGGGAAAATTGAGGCCTTAGCCAT CTAAGGTCAAAGCGCTGTCGCCAG	
1259		GAACCTGGTCGAGCACCGCTACGG
1260		TCACTACATTCGGATTCGTCCCCA
1261	GTCATGTAATTGCATCCCACGGGT	${\tt ACCCGTGGGATGCAATTACATGAC}$
1262	CTTTGCGCGGTGGTCAATAAAAAG	
1263	CTCGGGGATGCCCTCTTGGCATTA	
1264 1265	CGAAACGTGGTGCAGAAACCTGAA GGAGTTCACGAGTCGAGCAGTCGC	
1266	AGCCGTTTTCAAAGATCTCGACGA	
1267		TGCATTGCAGACAATGTCCAGCCA
1268	ATCGGCTGCCTCAGTCCCTAATTT	
1269	CCAGCATGGAGTTAAGTGAGCGCG	
1270 1271	TTCATATTTACGAATGCCGGGTGC CGAAATCGCACAGGAATTCGCGTC	GCACCCGATTCGTAAATATGAA
1271	GGCAATTTCGGGACACTCGTTTCA	
1273		TCGGGTTATACCCCCAATCACAAA
1274	CCCAGCTAATCCAGCTTGGGCTGT	ACAGCCCAAGCTGGATTAGCTGGG
1275	AAAATCGTTTGGCTGTAACGTCGC	
1276	AGGAGATTCATCGACTTCCGGGAA	
1277 1278	GCACGGGGTCTCAATGCTTAGGGT GCGCAACAAGTAGCCTACCGAGGC	
1279		TGTGTAGACGGCATCAGCCTGCTA
1280	GCAAGCGGCGATCGTACAACTTGT	
1281	GCACCTCTGGTAAGCCTGAAAGGG	
1282	CGAGGGCGGTGAGTGCATACCGTG	
1283 1284	GGATTAACCGGAACTGCCCTTCTG GATATTGGGTCCGGCGCGCATTAC	
1285	GGCCTTTAATCTCCGGTCGCAATG	
1286	AACCTTAGTGCGGCTAGGTGGGGT	
1287	CACGCTGACGCCAGTGTGGTGAGG	${\tt CCTCACCACACTGGCGTCAGCGTG}$
1288	GGTTCCCTTGACCCACCGAATTGA	
1289	TTCTGACAACATCGACCCTGGCTC	
1290 1291	GCGAGCGAAGATAATCCCCAAACT GTACTCTGTGCAACGGTCCCGAGT	
1292	ACACGCCAGGAACAGTGTCTGTGA	
1293	AAGGGAATTTAGCGCGCGTGACTT	AAGTCACGCGCGCTAAATTCCCTT
1294		${\tt TCCCCACTTAAAACGCGTACGTCA}$
1295		CATTCATGGCCTCGTCCCTCTAAG
1296 1297		ACGACCTTTTTTGCGGAGTCGTCC TGAGGCTTTGGATGTTGGGATTGA
1298	GCACTGGTCTACCAAGCTTGTCCC	
1299		TGCTCGGTCTCGTTTCCGACAAGT
1300		$\tt CTTTCGCCTTTAGGCCTTTCCTGA$
1301	GGAATGTAGTCAAGGAGGACGGGG	
1302 1303		CTCGCCAATTCATTTACCACGTGC CGCGACGCATAACCCCTGATGATC
1303		CCGCGGCATCAGAATGAGTGAG
1305		GGGTGACGTTCGAGAGATCACCCC
1306		${\tt TCGAGGTACGCTAGCAGCAACCTT}$
1307		CTCCTGCCTGTTGGGCGATCTATA
1308		TGCCCACTCCCAACAGGTCCAAAC
1309 1310		CCTTGAGACCGGGTTTTCCCCAAT GTCCCGTGAGCACTTTATCGTCGA
1311		TCCGCCTGCATTGAATTCTATCG
1312		GAAACCAGCCGCCGTAGCGAACCG
1313		${\tt CTAGCGCGACTAACCGAAACCTGG}$
1314	ACGACCTTACACTCGGATCCGACG	CGTCGGATCCGAGTGTAAGGTCGT

			TABLE 2-Conti	Inuea
Seq.	ID	No.	Decoder Sequence (5'-3')	Probe Sequence (5'-3')
	1315		TCGCGTTAAATGGACCAAGGGGCC	GGCCCCTTGGTCCATTTAACGCGA
	1316		CCAGAAAGAAAATGGCGCCCGGAT	${\tt ATCCGGGCGCCATTTTCTTGG}$
	1317			GTGCCTAGCAGGCGGCGATGTATC
	1318			CATCCGGTTTCCGAGTGTGATCTC
	1319			AATGCCAGCCTTTTTCCGCGAAGT
	L320 L321			ACTTTGTGTGCTCGTGCAGCTCGG GCCTCACTATGCCGCCTTGTGGAA
	1321			GGTTTTTCCGGATTCCAGTTTGCT
	1323			GTAAATGCATGCTGCGACATAGCG
	1324			AAAGAACCGACGTTGGGCGTGACT
:	1325		AGTGGGCGCACTTGGCCTTAAATA	${\tt TATTTAAGGGGAAGTGCGCCCACT}$
	1326			${\tt AGTCAAACGGCCGAAGTTGCAAGT}$
	1327			CGTACGGCATGAACCTGATGTTTG
	1328			TTGCCATTGTAGGGTGGTCACGCT
	L329 L330			GAGACATCTCTGCCGGATGCCTGC TTTGGTCTGGCCTCTTAGCCGCTC
	1331			TAGCGGGAAACACCCTGTTCTGTG
	1332			CTTGTGTTGGGCCTTCTGCAAAGT
	1333			GTCGCCCACAAAGTACCAGGAAGG
	1334		CTACATGCTCACCCCACCAGAGTG	${\tt CACTCTGGTGGGGTGAGCATGTAG}$
	1335		ATTTTCAGAATAGCCCCGCCTCGA	${\tt TCGAGGCGGGGCTATTCTGAAAAT}$
	1336			CAGAGGGCGTCAACGTAGCAATTG
	1337			CGGCCACCGAGGATTAGGCGACAG
	1338			TCCAATGTACGGAGCCAACACAA
	L339 L340			GATTCAACCACCTTCCCGTCACGT TCTGTTTCGTGCAACGCAAGAACT
	1341			CAGACATAAAGACGCGCGGCGAGC
	1342			AAAGGCTTGCCTCGCGATGTTCAT
	1343			CCTTAATGTTGGTGGGCGCGGTTG
	1344		TGATCGAGGACGGCTTGGTAGCCT	AGGCTACCAAGCCGTCCTCGATCA
	1345			${\tt GTTGCTCTCGGAAGGCATGCCTCC}$
	1346			TAGCAATTGCGTTGAGGATCGGTG
	1347			ACATGGATTTCCCAATTCATGGCC
	1348			GCCCGCTGGTTACGCCTGGAACAG
	L349 L350			TCTTCTGATGGCGAGCCAGACATA CTCGATGCTTGTGCTGGTCACTCC
	1351			TCATGCGAGTTACTTCCAGTCCGA
	1352			GGCTTCAATCGTGCTTGACCCTAC
:	1353		CACCGGCGGTTCGACTAACGTGAC	GTCACGTTAGTCGAACCGCCGGTG
	1354			${\tt GTTCAAATGCACTGCGCGTCATTC}$
	1355			CTCTATCCGCGGTTAGACGAGCAC
	1356			GCGCGTCAATTAACCCAGGTCCGC
	L 357 L 358			TAGCCCGGTGCGCAACATCAAAAA AATCGAGCAGATGCGCTGACGCAA
	1359			AAAGGAACGAACTGGCGTGCTCAT
	1360			TGCGGGGCGATTCTTTACCGTTGA
:	1361		CGCGATTGACTGAACCACACCTCT	AGAGGTGTGGTTCAGTCAATCGCG
	1362		GCGTGAAAGATGACGGCCGGTATA	${\tt TATACCGGCCGTCATCTTTCACGC}$
	1363			CTAGCCGATCGAGGTGGAATCATG
	1364			TTTTGCACGGTTGCTTTGTCGTAG
	L365 L366			GGACCATCAAGATGAACACGGCAT GGATCTCCAAAGTCCCTCCACGAA
	1367			CGACGGTGTACGTTACGGCGCTTC
	1368			TAGCCTTATAGCCAAGCGCACGCT
	1369			TTGAGCGGCGTTACTCCTGACTGT
	1370		TTTAGCCGCTGCGACTGTAGGAAA	TTTCCTACAGTCGCAGCGGCTAAA
	1371			${\tt TTTGCGGGTTGATTGCGACACAGT}$
	1372			CCTCTAAGTTCCGCATTGGCTGCA
	1373			GAACTGCAAGACCGGGATAGCGGG
	L374 L375			CAGCACTGCATATGTTGCGCCCTC CGTTGCGTCATCGATGTCCGTACG
	L375 L376			GCCTTATGCGTTTCTCGGGAGACT
	1377			TGCAGCCGCGTTCATCCACTTCCT
	1378			CCTGATGACGAGGGTGAGCAACCC
:	1379			TTACCGCCGGAACTCGCATTCCTA
	1380			${\tt TATCCGCAGCTTGGAAGTGAGGAG}$
	1381			CGGGAGCATGCTAGGTGCTATTGA
	1382			CGACCTGTGAAAGCGCAGGAATCA
	L383 L384			GCGTGATTTCCATCCCGCACATAC GCCCTCGTATCGACAGTTGCCGTA
	L 385			GCGAGGAGTGCTGGATAGGGAACC
	1386			GGTACATACCTGTGGCGCGCTTAT
	1387			TGCTCGAGTCTGTTGGCGACTTTC
:	1388		${\tt CGCTAATGCCTCATAGGCGTGTGC}$	${\tt GCACACGCCTATGAGGCATTAGCG}$

		TABLE 2-COIN		
Seq. II	No.	Decoder Sequence (5'-3'	) Pr	obe Sequence (5'-3')
138	9	ATCCCCGCCGCACGAAGTACCAA	G CT	IGGTACTTCGTGCGGCGGGAT
139	0	GACGCTGCTGATGGCTTTATCGA	T AT	CGATAAAGCCATCAGCAGCGTC
139		CTCTCCCCGTCGCTTCAGAGATT		
139		TCATGTGGGCCGTCGTATCAGTT		
139		GGCCTGAAGGTGAATGGTTACGT		
139		AGCCTCCAAAGCCGGTAGAGTTC		
139 139		TTGTCGTAGGCGCTCACCTTAGG GCCTGAGTCCGGGTCGGGAAAGA		
139		GGCACTATACCGGTTCTGGACGC		
139		CCGTGTATACGGAAAGGTACGCC		
139		CCCAAGGCAAGTGTGCATCAGTC		
140	0	GGAGTGCATCATGGCCAAATCTG		
140	1	CCATGTTACGTCTGCGCACCACA	G CT	STGGTGCGCAGACGTAACATGG
140	2	GGCGTTGAGCTTAAAAGCAGCGA		
140		TTGGCACTCTGCAAGATACGTGG		
140		GATCTGCACTGCAAGGTCTTGGG		
140		CGATCAACTTGCGGCCATTCCTG		
140		CGGCTGGGGTCACAGAAACGAGT		
140 140		GCGGCTAGTTGTACCTAGCGGCT TCGTCACTGTTAGAGAGGCCTCC		GCCGCTAGGTACAACTAGCCGC
140		AGTGTCGTGAGCCCTAGCGGCGC		CGCCGCTAGGGCTCACGACACT
141		AGGACGCAGGGATTCAAGTGCAA		IGCACTTGAATCCCTGCGTCCT
141		ACCGATGCGCGGTCGGTCTCATA		ATGAGACCGACCGCGCATCGGT
141		GGCAGAGGGTTAGGGGGTTTTTT		AAAAACCCCCTAACCCTCTGCC
141	3	GGCAAAGGGTGTTTATGGGAGAC	C GG'	TCTCCCATAAACACCCTTTGCC
141	4	ACAAGGCTTCGGCTGGCAGAATA	C GT	ATTCTGCCAGCCGAAGCCTTGT
141	5	CATATCCGTTCCTATCGCCAGAC	G CG'	TCTGGCGATAGGAACGGATATG
141		AAGCCTTTGTGGCCAAGGCCGCG		GCGGCCTTGGCCACAAAGGCTT
141		CCGAACCATGGCTTTATCCAGTG		ACTGGATAAAGCCATGGTTCGG
141		GTTCAGCAGTAGCTCCCTCCTCG		GAGGAGGGAGCTACTGCTGAAC
141		GCGCAGTGACACCATGATGCTTT		AAGCATCATGGTGTCACTGCGC
142 142		ACGATCCATTTTGCCAGCATGCA TCCCTTCATTTCGGGTTTTTAGC		CTAAAAACCCGAAATGAAGGGA
142		TCTTCTTGCCCACATTCCCTTTT		AAAGGGAATGTGGGCAAGAAGA
142		TGCCTTTTGATTGGTGGTCACGG		CGTGACCACCAATCAAAAGGCA
142		GACCCTCACGGTCATCAGAGGGA		CCCTCTGATGACCGTGAGGGTC
142		CCGTTCAACACAGTGATACACGC		CGTGTATCACTGTGTTGAACGG
142	6	CACCAGGGGATAGGTGCGGTACG	C GC	GTACCGCACCTATCCCCTGGTG
142	7	GGTCGGAACTGATCTGTGCGATC	C GG	ATCGCACAGATCAGTTCCGACC
142	8	TGCTCCTTCCTAGGGTCATCCGT	G CA	CGGATGACCCTAGGAAGGAGCA
142		GTGGACTTTGACGCCGGCTACCG		GGTAGCCGGCGTCAAAGTCCAC
143		CTGATCTGTCGGCGGTTACTTGC		CAAGTAACCGCCGACAGATCAG
143		AGAGGAGCGGAAAAAACCGGACG		GTCCGGTTTTTTCCGCTCCTCT
143 143		GCGACGAAGAGATCCAGCAAGCT GGGACTTCCAGCTGAGGGACGAA		GCTTGCTGGATCTCTTCGTCGC ICGTCCCTCAGCTGGAAGTCCC
143		GGCGCACTCCAATACCCACTGTT		ACAGTGGGTATTGGAGTGCGCC
143		GCGCTTGGAGACTGTCAGGACGT		
143		CAAACCGCTGGTTTCTCCACCTG		AGGTGGAGAAACCAGCGGTTTG
143	7	GCGATTGCTTGGGATCGGTGACT	A TA	GTCACCGATCCCAAGCAATCGC
143	8	CTCAGCGACATTTTTCTGGTGGC	G CG	CCACCAGAAAAATGTCGCTGAG
143	9	CAGCGGCGTCGTTTACTCAGGAC		ICCTGAGTAAACGACGCCGCTG
144		GACAGCCGTGAACGCTCAGCCGT		CGGCTGAGCGTTCACGGCTGTC
144		GGGCCGTAGAGGCATCGGGTAAA		
144		CGCCGCTCACCTGCTTAAAGCAT		
144		TGCCAAATCGCAACTCTTGAGAC		
144 144		CCCCGATCGGGTGTAATTCTCCC CAAGGTCCAGGTGACGCAACCAC		
144		CGAGCCTTCAGTGGTATGCATGC		
144		CAGCAGCGTGCCCATCTCGACTT		
144		CGGACCAAGATGGCAGTAATCCA		
144	9	CTACCACGCTCTGCGCGGGCTGT	A TA	CAGCCCGCGCAGAGCGTGGTAG
145	0	ACGTGGTTAGGCATGAGCTGCGT	C GA	CGCAGCTCATGCCTAACCACGT
145	1	CGACATATCCGACATGACCGGAT	G CA	ICCGGTCATGTCGGATATGTCG
145		GCGCCCAGGCTGTGTTAGAAAAT		
145		AGCTGGGACTCCGGACCTTGAGT		
145		CGGTCGTAACCGCTGCTACAACT		
145		TCGTTCCTCTGGAACAATTCAGC		
145 145		CGGCATCTCCGGACAAAGGTTAA TATCTTGTCGAGCGCCACTCGGA		
145		TGCAAGGGAGAAAGCCCCATGAG		
145		ACTGCATAGCCCAGATCCGCTTG		
146		TGTGATTCAGTCGAAGCAAGGCC		
146		CATCCATCTACAATTCGGGCCAG		
146	2	ATGAGCCGTTCAGAAAGCCAAAG		

			TABLE 2-conti	Indea
Seq.	ID	No.	Decoder Sequence (5'-3')	Probe Sequence (5'-3')
	1463		ACACTGGAATTGCTAGACCCCGCG	${\tt CGCGGGGTCTAGCAATTCCAGTGT}$
	1464			GCGGAGTTGTCCCACGCAGCTCAG
	1465			GGGTACATCGCGCCCTAGTAGCTG
	1466 1467			GGGGCCTTCTCGTCCCATCATTAT GCACCATGTCGTAACACTCGGTCG
	1468			ACTAGTGGAGCGGCGGTACTGCA
	1469			GTACGTTGACAGGCGCGCTAGCAT
:	1470			ATTTGATCAGCCGGCAGTGAGTCT
	1471			${\tt GGAATCCCTATCTTCGCACCAGGC}$
	1472			AGTGCTCGGATCCGCCAACTTTCC
	1473			CCTCGTCACACACTTGCTCACTGCC
	1474 1475			TCGTAGTCCGCCGGGAGGACCTCA TGCGGAACCACGATCTAAGGCGAG
	1476			CTGGCTGCGATGATATTCCTCGAC
	1477		GCGAATGCAACGAGACAAGAAGGA	TCCTTCTTGTCTCGTTGCATTCGC
:	1478		$\tt TTCGCCACCAAGTCGGCATTTGTT$	${\tt AACAAATGCCGACTTGGTGGCGAA}$
	1479			GAATCCGGCAAGTGTCAGCCACCG
	1480			CTCCGACCATCTGATTGCTCCTTG
	1481 1482			CACAGCTAGAACGGACCGGGTCAC TTTGTGCAGTTATGTGGGCGAGAG
	1482			TCCAGTGCTTGCTTAGGCAGGTTT
	1484			GCATGCGCGGGGTACAATATGGAA
	1485			CGCAGTATCGTGATATCGCAAGCA
:	1486		${\tt TTAGTGTTCGAGCCTTGAGCCGGC}$	${\tt GCCGGCTCAAGGCTCGAACACTAA}$
	1487			TCCCAGACGGACTCGCGCAACAAG
	1488			GAAGAGCACCAGCAGCAGCTGAC
	1489 1490			GTGTTGCCTACACCTCGAGGGATG
	1490 1491			CTGAATCCCGTCGGAGTGCATCTG ATGCCACAGCTTCGCGAGGCTCAG
	1492			GCTCTATCTGCGGCGTGGCATAGC
	1493			TGAACGGACGGTATGGTTGGTGTT
:	1494			CCCAGACATGCTTTAGCTCTGGGC
	1495		${\tt AATGCTGCAATGCTAGCGTCGCTA}$	${\tt TAGCGACGCTAGCATTGCAGCATT}$
	1496			TCCGGATTGGATACTGCGTCCGGA
	1497			GCACCTTGGTGCCACATGGTCTTA
	1498 1499			TAGTGGGCGCGTGTGTGTGGCTGT TACAAGGCGCCGTGCTCGGTTCTA
	1500			AGTGGTCCTGCCAGCTTACTCGAA
	1501			GGATTGTCTGCGAACCTGCGAAAG
:	1502		${\tt TACGTCCTGTGCTGTTGACACCGG}$	${\tt CCGGTGTCAACAGCACAGGACGTA}$
	1503			TCTCCCCGAAACATTGACCCGAAC
	1504			TCACAAAACCCCTTCACAACAGGG
	1505 1506			TTATCTGGGGTTCACCAATCTGCC GATTTGGCTTGAACACACCGAGGG
	1507			TTAAGCTGTTCAAATGTTCGCGGG
	1508			CGTGCCAGGGAGCAACTGACACGG
	1509		TCCGTCTCAGCCGCCTCCCTATCC	GGATAGGGAGGCGGCTGAGACGGA
:	1510		${\tt ATAGCTGGGTCACCACAGGCGGTC}$	${\tt GACCGCCTGTGGTGACCCAGCTAT}$
	1511			CGCTGTGCTACACCGCTTGCCTAT
	1512			ACGCAAATCCAGACCGGCTTCTAA
	1513 1514			CGAGGATCCTGGTAAAGGTCGGCA TGCCAGCTTGGTTATAGTGTGGGC
	1515			TTGAGATCCGTACTAGTGGCGCAA
	1516			GGACGGGTCAGCATAAACTGCAAG
	1517		TGCCTCCAAATTACTTACCGCCGT	ACGGCGGTAAGTAATTTGGAGGCA
	1518		${\tt CCCGTATGCGGAAGCTATGGGCTA}$	${\tt TAGCCCATAGCTTCCGCATACGGG}$
	1519			CAACTGAAGTGTGGGGTTGAACGA
	1520			AACCTTGAAATGTCCCCCACATTG
	1521 1522		GGTGGCTTCGTGACAATATCGGCC	CGGTCAGCCATTTGTGCGACGCTA GGCCGATATTGTCACGAAGCCACC
	1523			GAGAGCCAATTTCGGACGCCGCTG
	1524			TGCAATCAAAAACGAGAGCAAGCC
	1525		ATGCGAGGAGGACACGACCGTTCC	GGAACGGTCGTGTCCTCCTCGCAT
	1526		${\tt CCTGTTCACTACGACCCACGGGAA}$	
	1527		GTGCCACGGAGTGCGACTGTTGCT	
	1528		ACACATCCAAGTCTGACGATGGCC	GGCCATCGTCAGACTTGGATGTGT
	1529 1530		AACTGAATGTAGGTGGGCCCCTGT	CACGGAGGCTTTCCTTTCGGGCTG ACAGGGGCCCACCTACATTCAGTT
	1530		ATTTTCGACGATAAGCTGGCCGGT	ACCGCCAGCTTATCGTCGAAAAT
	1532			AAGCAGATTTCGGGTTCTCCCTCA
	1533			CAAGCAATTGGGGATGTAGTCGCC
	1534			${\tt AAAAGTATGGAAGGCCGCGTCTGC}$
	1535			TGCAGCTACACGTCATGTGGTTGT
:	1536		CTGCTGGGCGCGCAAAGCTTGTTG	CAACAAGCTTTGCGCGCCCAGCAG

TABLE 2-continued

	TABLE 2-conti	inued
Seq. ID No.	Decoder Sequence (5'-3')	Probe Sequence (5'-3')
1537	AAGCCTTCTTTGGCTTGCTCCGCT	AGCGGAGCAAGCCAAAGAAGGCTT
1538		${\tt ATGCCTTGCTCCAGGCAGCAGGTA}$
1539		ACACTCACTCATGGCTGCGGCGTC
1540		GGTGAGCAAAATAAGCGGCCAACT
1541		TGAGGATCTGTCGAAGGCGCCTGG
1542 1543		AAACTGGCTAGCTGGAGGGGACAC GACGTGTCACCTTGGCTTGTTGTC
1544		TTTGCCGAGTCACGAGCGGTGTAG
1545		GTACAACGTGCTTTGATGGCACCA
1546		TATGCGTTTCGCAACACGCATTGT
1547	${\tt TTGTCCAGCCATTGTATTTTGCGC}$	${\tt GCGCAAAATACAATGGCTGGACAA}$
1548		TCGGAGGAGTCCGCTATCTCTCGT
1549		AAGAGCTCGCCTGACGACAAAGCT
1550 1551		ACAACAAACTGCACGCCGACTGTC TACGTGAGTTGGCCGTCGCTAGCT
1552		ACCAGTAACGCCCCGAACAGGAG
1553		CTATGTGGCACTGCGTCGGTCAGT
1554	AGGTAGGGTCTGGTTTGACTCGCA	TGCGAGTCAAACCAGACCCTACCT
1555		ATTGGCAACGCGCTAAAATGGAGG
1556		CCAAGAGTGCGCGGATCCTAAGAA
1557		CTGCGCACGGTAGACACCTTCGAC
1558 1559		CGAGTGATTGGGCCGCCGAGTGAC AAGGGTCAAGACGGGTGACCGAGA
1560		GTTCAGGATGAGTTCGTCGAGGGC
1561		ATCGCCGTGTCAGAGTACGCCGGA
1562	AGCCAAATGCTTTCGTGGTTCGGA	TCCGAACCACGAAAGCATTTGGCT
1563		TCACAGCAACATGCGGCGTGGAGT
1564		ATACAGATGCCACCGACTCGAAGC
1565		GCAGCAAGTCGATGGCCCAAGACC TTGCCCTTAGTGCAGTCCGATACC
1566 1567		CAAATCATCCGGAACGCATGGGCT
1568		GAGCCCATCACTTTTAACCCTGGC
1569	GACGACGTGCTGGCTACGAAGGGG	CCCCTTCGTAGCCAGCACGTCGTC
1570		GATCACGATGCACGGTCAATAGGA
1571		TTTAGTTGTGGAGTCGAGGCGGGT
1572 1573		TACTGGCAGGTCGTGATCCACATC ACGCATTATGGGTGGCAATGGCAC
1574		CTCCTGACTGGGTGCACAGGCTAA
1575		GTGAGATCAGCCTCTCCCATCGGA
1576	${\tt CACTACTGAAGTGGCCTGGCGCTG}$	${\tt CAGCGCCAGGCCACTTCAGTAGTG}$
1577		ATCTATCACATCGCTATGGCCGCA
1578 1579		CGTGCATCTCCGTTAAGCGCAATC AATGCTTGGCGTTGTCAAACGTGA
1580		AATGCCGCCTTTAGCAAACAATGC
1581		CAGCGTTGCACGCGTAGAGCGACT
1582	TAGCTCCATGGAGGTCCGAAAGGG	CCCTTTCGGACCTCCATGGAGCTA
1583		GAAGCCAGTGAGGTCCAACCGGTC
1584		ATACGCACATTGACTGTCCGGCTT
1585 1586		CACGGTGAAGAACTCAGCGAGGCA TGAGCCCAAAAGCAAGGTCTACGA
1587		ATGCTTTGTAGGGCGCATAGCGGT
1588		CTGCCCCAAGCTACGGTGACGCTA
1589	CTCTCAGCAACTGATGGCACCGGA	TCCGGTGCCATCAGTTGCTGAGAG
1590	${\tt AAAGGAAATGTGGTGCTGGTCGGC}$	${\tt GCCGACCAGCACCACATTTCCTTT}$
1591		GCACTTGTTCTCCATCTAAGCCGG
1592		CGGTTTGGGCGAGGCGATTTACTT
1593 1594		ACGTCCGGTAGGCTGAACAGCCCA GTAGGCCCATGGCTGAACCGAAAC
1595		GGCACTCCCCTAGAAATGTTGGCC
1596		GGTGAGGACAATCCCAACGAAGAA
1597		${\tt GTCAGATCCGTACCCCAATGTGCA}$
1598		CGTGCAGTTTGCCGTCTAACTGCC
1599		AAGAGCCATTCATAGCCTGACGCG
1600 1601		ATGGCTCCGAGGTTTGCATTCAGC GAAAACAATGAATCCGCCAGAGCG
1602		TACGTCCGGAGGGTTGATTGAAAA
1603		CTGTCGTGCTTCAGACTCCACCAC
1604	AAACAGGTCCGGATGATGTCTGGA	${\tt TCCAGACATCATCCGGACCTGTTT}$
1605		CTAACGGTGGCGTACACGCGGTAC
1606		TTCCTTCCGCAAATGTAGGTTGGA
1607 1608		CAACTCACGGGACGACGGTACGTC ATCAGCGTCGGTTGTAGGATTGCC
1609		CTCGATGTAGACCCTGCAGCCGCC
1610		GCCCGCGCAGCTGCAGCGTAGTAT

TABLE 2-continued

	TABLE 2-conti	inued
Seq. ID No.	Decoder Sequence (5'-3')	Probe Sequence (5'-3')
1611	GGATCGCAATCCCTCCGATGACGA	${\tt TCGTCATCGGAGGGATTGCGATCC}$
1612		AGATTCGGCTCCCGTGCAAGGCCA
1613		ATATTCGTCGTTTCGTCGGCACCT
1614 1615	GCTGTTTCACCGTCGTCGTTGTTG CGCTCCCAATGTTACAACCCAGAC	GTCTGGGTTGTPACATTGGGACCG
1616		TTGGTCAAAAGTGGCTGGAATTGC
1617	ACGGGCGAAAGCTCGGTACGGATA	
1618	${\tt CGACCCGACTTTTGCTTTCGAGTG}$	CACTCGAAAGCAAAAGTCGGGTCG
1619		CGACCATGACGCAAACACTGAATT
1620		AGCCGACCCAGAACCTCATACAGG
1621 1622		ACGGCGTTTGCACCAAGTATGCCA GCCCGCATGTTTCTGTACTGGCGA
1623		CTCCACGATGAGAGCAACAGCGGG
1624	GCCACAATCTGACCCTGGGAATCA	
1625	GCTCAGTCTCGGAAGTTTCGGCTA	TAGCCGAAACTTCCGAGACTGAGC
1626	${\tt CTTCACGGGCCAACGACGGTCGAG}$	${\tt CTCGACCGTCGTTGGCCCGTGAAG}$
1627		TCCTCAAGACGGACGGAACTGTCG
1628		GGGACGTTTCGACTGCGTCTCCGT
1629 1630		GTGATCCCCTTAATCGGATGCATG CAGAAAGCTAGGGACTCCCGCAAT
1631	GTGTGGAAGATGCAATTGGAACGG	
1632		CGCCCTGTCACCTACCGTTGTAT
1633	GCCGTGGGAGTAAGGGTACAAAGG	
1634	GCACGTAGGTGGGCTACTACTCGG	
1635	${\tt ACTGTGATCTCTTGGGCAAAGGGC}$	GCCCTTTGCCCAAGAGATCACAGT
1636		GGGATGCGAGATTGTTCAGGCATG
1637	GAGCCTGGCTCCACAGCTGTGCTC	
1638 1639		GATCGCCAACGATGGTATCGAAAG
1640		CATATTCAATGCCTCACCTCCGGG TCCAGCCGCTTTTAGCTGAATGAG
1641	GAAATGCCCTGGGGACTTTTTGCC	
1642		TGCTGCGTCTGTTGTGAAGGCAAA
1643	AAATCCCAAGACGTCGGGGCGTAT	ATACGCCCCGACGTCTTGGGATTT
1644	${\tt CAACGGGCGGTAGCTAAACCGTAA}$	TTACGGTTTAGCTACCGCCCGTTG
1645	GGCCAACGACAATGCGAAACCTTC	
1646	GACATCACGCAAAATCTCAGCGCA	
1647		AACATACGGTTGTGGACGGAACGT
1648 1649	GCTCATAGGTCTTCCGTAGCCCGT GAAACGAGTCTCTCGCGCCCCTAGA	
1650		CCGATGTAACTTGCTTCTGTCCCG
1651		CACCCTCCTGGTATCGAGCGGTCA
1652	CTGGCAATAAAGACCTTCCGACCA	TGGTCGGAAGGTCTTTATTGCCAG
1653		TAATCACCAACATGACGTCGCGCA
1654		AGCGGGTGTGTTCCCACAACCAAC
1655		ACTTCCTGTGTTTCCGAACCCACA
1656 1657	GGAAAAAACGGCAATTAGCCGAGT	CCCAATAGAGGGCACTCCGCACCA
1658		AGTCTGGGCTGCAGCCTGTTGGTT
1659		CCTGGCGTGCAGATGGATCTGTTT
1660	GGAATACCGCGGCGATTATGGCTT	AAGCCATAATCGCCGCGGTATTCC
1661	${\tt TACTGTTCGCGGCAAACCGTCACT}$	${\tt AGTGACGGTTTGCCGCGAACAGTA}$
1662	GATCTCTCGTGGAGCACGTTTTCC	
1663		TTGGAGGTCAAGGTTTGCTATGCC
1664		GATATTGGCTCGCGAATCCCAGAT
1665 1666		CGGGCGTAAATGATATCCTGATCG ACGCTGAGACCGTTTCGGTACCGT
1667		TCGGTAAGAACGCAGGTATGGGAG
1668		TGTGCGACAATTAGGTTCTCGTGC
1669		CATGCGCTGTCTTGATCGTGTGGC
1670	${\tt CCCGTTAACTCACGAGCGGTCAAT}$	${\tt ATTGACCGCTCGTGAGTTAACGGG}$
1671		CACCGACAGGCAATGACCTTCTCT
1672		CCTGCTCTACTTTAAGAGGGCCCG
1673		CATTACTCCCTCGGACGCGATGT
1674 1675		GATCCGCTGGCTCGATTAGGCATT AAGCGCCGGTTTAAAAAGATCGAG
1676		GTGAGACCCTGCCTTCCAGGAACG
1677		TGGATCGCCGATAGTAAGCACAGG
1678		AACCAGGCCAATAGGGCGACTAAC
1679		${\tt TGGCATTTACAGTCATCTCACCGG}$
1680		${\tt CGAAGCGCGATGTTTTAAACCACG}$
1681		GTGGACCCCATCTTCTGCGTCTTA
1682		GGGTCGAACAAGAAGCTGTGGTG
1683 1684		GCAAAAGTGGTGGTACGGACCCGA AAATCTTCGGTACTCGGGGCTTGG
1004	COLLIGECCEGAGIACCGAAGAIII	ALLICE TOGETH CICEGGGC TIGG

	TABLE 2-conti	inued
Seq. ID	No.Decoder Sequence (5'-3')	Probe Sequence (5'-3')
1685	TCCGTGATATGGTCGTGGCGCGGT	ACCGCGCCACGACCATATCACGGA
1686		ATGCGAGGTGCCATGACACAGACA
1687		ATCAGACGTGCACAGTGCAGTCCT CAGCGGCGCTGTACATGAGGATGG
1688 1689		CTGTGTCGAGGAAGGCGCGGGTAC
1690		AAGCCTTAGTCGACCAGGACCCGT
1691		CCGGTTGTACACGCCTTCGATACG
1692	TGCCCGCCCTTTATGCAACGCTCA	${\tt TGAGCGTTGCATAAAGGGCGGGCA}$
1693		TGGCAGCCGCCGTCTCGTAAGTTT
1694		ACACCCGTTCCGTTTGTCAGACTT
1695 1696		GCCGCATACTTTGGTCTGCGCTTA TTTGCGGAGGATCTGAAAAACTGC
1697		CTGAGATCGCGTAAATGCTTCCGA
1698		GGCGTTCGTTCAACCGTTTCTGTG
1699	GCATGCTCAGATGGTCGTGCTCAC	${\tt GTGAGCACGACCATCTGAGCATGC}$
1700		${\tt ATCATGCCGGAAGCGAGAATCCTT}$
1701		TTTTCATACCAGCGCTACCCCACC
1702		CCGTTGGTTCGGTCCCGTAATAAT
1703 1704		ACGTGAACATCATGACACTCGCGC GCGGACGACCAAGTCACGAATGTC
1704		CTTGATCGGTGCCTGCACTAATGA
1706		GACTCCGATGACTCCGCACAACTC
1707		ATAGCCCGCCAAATCTGTAAAGGC
1708	ATGGCGTTTGCGAAGTCGATACAG	CTGTATCGACTTCGCAAACGCCAT
1709	TGCATCGGCCTCAATCAGAGAACT	${\tt AGTTCTCTGATTGAGGCCGATGCA}$
1710		CATTTGCCAGATTGCCATGATTGT
1711		TGCTGATCTGCACTCTTCCACGTC
1712		GACTTACTGTCCGTCCCCTGCCCT
1713 1714		GCCCGTACTAGATTCGCCCTATGC AGTTGCTAATGAGGATGCGCCGGA
1715		GTCCAATATTAGTGGAAGCGGCCA
1716		TCATTGACAAGAGCCGTCCGCCGG
1717	CGAGCAACCCAAAAGGAAGCAGTA	TACTGCTTCCTTTTGGGTTGCTCG
1718	GCGTATGATTCGGCAATCCGCCAG	${\tt CTGGCGGATTGCCGAATCATACGC}$
1719		GCGAACCAGCGTTGTAGCGGTACT
1720		TTCTCAGGTGGACCTGCCC
1721		AGCACGGTTCGGTCACAGAAGTGG
1722 1723		AATCAACTGCTGCCTGGTACCAGG TGGCGTCTCTCGACGGTACCCTAA
1723		ACTACCTCACGCGCACAAGCAACC
1725		CTTCGAGTTTCATCGGTCGAAGCA
1726	TGCCACCCATACTATGCCCAGTGG	CCACTGGGCATAGTATGGGTGGCA
1727		AACGTCTTCACGCGTTGCCGCACA
1728		CTGATCCGAGGCCAGCTTCTCTCA
1729		GGGCACGTACTCGAATTCGCAATA
1730 1731		TCGATCACTGGGGAACCCCTCTCG AGAATTAGAACGACACCGCAGGCA
1731		TTGGGATGACCCACAATGACGCAC
1733		CAACGTTGGTATGCTGGGAGCCCT
1734	AACTAGCCGCACCTTTGTGCAGAG	${\tt CTCTGCACAAAGGTGCGGCTAGTT}$
1735		${\tt GTTCCCATTGAAGGGCTGGGCTAA}$
1736		AGACTACCCGTACAACCGAGGCCG
1737		ATATGCGGGTCCGCGCCTCAAAGA
1738 1739		GCTGCGACACAAGGGCGAACCATC GACCCGCGGCCTGTATTGAATCTC
1740		AAAAACGGAACCTTCCTTCGCCCT
1741		GAACCAGTAGTGGCAGGGGTCGAG
1742		CAGTAATGCGTAGACCGCGGAACA
1743		${\tt TTAGCGGGTGTAGGACGTCGTCTC}$
1744		AATCACGTGTCGCTGTCGCAATCT
1745		TACCGAGAAATGCCCAACGGTATC
1746		TCCGTCGCTGAATGCCTCCCAATC
1747 1748		GAACCTACGCCCTCGTTTCCTCCT GCTAGGCGTCAGACGTTGTTTGGC
1748		CGCGTGCATCCTTTCCGCATTAAA
1750		CCATCCCATTTTAACGCCCGATAA
1751		TGCTAGCGATGAACGAATCCAAGG
1752	AAGTGAACGTGCAGTGGTCTTCGA	${\tt TCGAAGACCACTGCACGTTCACTT}$
1753		${\tt AGGCGTTTGAACGAGGGGTAAGGA}$
1754		ACAGGCCATGCATGGTTCAGGAAT
1755		TAGTTCGTGATCGAGCGTCTCGCT
1756		TTCTAAACAGCGAGCCAGACCAGC
1757 1758		AGACCTATCTTTATGCCGCGCACG AGACTGTCCGATGTGAGTGCCAGA
1/30	101000ACTCACATCGGACAGTCT	

Seq.	ID	No.	Decoder	Sequence	(5'-3')	Probe	Sequence	(5'-3')
	759							TCCAATGGT GACCCTGGA
	760 761							BACGGCATAT
	762			TCAACACT				BACGCCAGCA
1	763		CAGGGCGG	TGCGGTGA	ACTAGCCA	TGGCT	AGTTCACCGC	CACCGCCCTG
	764			GCCGTACAT				CAGTCCATG
	765			PACGCTGGC				TATGGCCGG
	766 767			ACCTGTACTC CACCAGTCGA				GTGTCCGCT GTGTGGCTCC
	768			GAAATTGA <i>I</i>				CCGGTGGCG
1	769		TGAAAGGG	ATGTTGCTT	CTTGACG	CGTCA	AGAAGCAAC <i>A</i>	ATCCGTTTCA
	770			GTGAAGAG				ACCGCTTCAA
	771			AGCTGCATTO				CTTGGTTCG
	772 773			CGCTTGCAAT ATAGTTGCCT				CGCAGACTC
	774			TCCATATTC				BAACGCCTGC
1	775			CTAATACCTO				AGTTGGCGC
	776			CAGTGCAACG				CTGAACGCCA
	777			FACGGGTATO				TCAGTTTTG
	778			CTGGAACCC AAGCGCAATT				AGCGACACCT CTTTTGGAAG
	780			CTCGCAAT				AGAAGCCCGA
	781			AATGCGCTG				TCTTTTGGC
1	782		TGGTGCCC	CGCACCGAGA	AGACTGTA	TACAG	ICTCTCGGT0	GCGGGCACCA
	783			TAGTGGGG				TACGGCCTCG
	784 785			CGCATAGAGO CCGGCCTTCT				GCGCAGATCG CGATTGCACA
	786			GGACCGCTA				CAGGTGATC
	787			TTAAGGACO				ACTCCCCAT
1	788		CATTGTGG	GACAGCCAAT	GGTGGCT	AGCCA	CCATTGGCTG	STCCACAATG
	789			CATGCCACGG				ATGGTGATGG
	790			GTCGTTGGT				ACACGGGTGC
	791 792			FTTCCGCGA <i>I</i> FCCTTTCGC <i>I</i>				AACCCACTCC GAAATCCCC
	793							TGATCAATG
1	794		AGCAGCGC	CTGCGCTTGT	TTCGGAT	ATCCG	AAACAAGCGC	CAGCGCTGCT
	795			CGCGGTTGCT				CGTTACTCG
	796			SAACATAGGT				TTCCAGGCCA
	797 798			CAAGCGTTT <i>I</i> CACAGTGGGC				TGGTGTGCG TGAAGGTGA
	799			CCTGAGCCC				GGATATTTG
1	800		GGGAGCTG	GTGAGCAGA	ATGTAACG	CGTTA	CATCTGCTCA	ACCAGCTCCC
	801			CTTTTGCGTT				AGCAATCCT
	802			GGCGCTACG				CCAAACGAT
	803			TCCCAAATG AAGCTCATGG				ACAAATCGG TTGACCCTT
	805			CGTTCAAGG				CGACGTCAGA
1	806		CGCACCAC	CTCCGAGGTA	ATTTGTCT	AGACA	AATACCTCGG	BAGTGGTGCG
	807			GAAAAAGGAG				TCACCCCTT
	808			CAAATGGCC				GCGTGGTTT
	809 810			SATGACGCCT AGAGCGGACO				TCCCTTCTG CTCGTCATG
_	811			GTTTGTTTC				CATGTCCAG
	812		AAGACCGA	ACTCTCGTCG	STTTGCAC	GTGCA	AACGACGAG <i>A</i>	AGTCGGTCTT
	813							STAATCGCGC
	814							CCGGTCAGTG
	815 816							ACTTGCACT CGCACCAACC
	817							CGGGACGACC
1	818		GACTAGTA	ACGATCACGO	GGCGGGT	ACCCG	CCCCGTGATC	CGTACTAGTC
	819							TCAGGTCGG
	820							CAGTGAGCA
	821 822							CCGGTGCCA
	823							ACCGTGCCTC
	824							CATCTGCAT
	825							GCTATCGCA
	826							ACACGCCAT
	827 828							AGCTGCATTG CACTGATCCT
	829							CAAGATGTG
	830							GATAATGCG
1	831		ACATCCGC	CAGACTCCCT	TATAGCCC	GGGCT	ATAGGGAGTO	CTGCGGATGT
1	832		GTGAACCC	CGAACGAGG	GAGTCTC	GAGAC'	rccctcgt1	CGGGTTCAC

TABLE 2-continued

a -		3.7	D 1	G	/F1 31:	D	G	/F! ^!	
Seq.	ID	No.	υecoder	Sequence	(53.)	Probe	sequence	(53	)
1	.833		GCGTAGGG	SAATTTGCCT	CACGACT	AGTCGT	[GAGGCAAA]	TCCCT	ACGC
	.834			STCGCTCGGT			CAACCGAGCG		
	.835			STCTAGGCGG			AACCGCCTAG		
	.836 .837			FATAACGAAT FCGTGTGCGA			CATTCGTT <i>E</i>		
	.838			CATGAGGAGG			AGCCTCCTC#		
	.839			ACGCCAGTAC			CGTACTGGC		
1	840		GCTATCAT	TTTGGTGTAA	GCCCGCC	GGCGGC	CTTACACC#	AATGAT	ſAGC
	841			CAGGGCGGT			CACCGCCCI		
	.842			TAATCCCCAA			CTTTGGGGAT		
	.843 .844			GGCAGGTTA AGAGGCAGGC			GATAACCTGC GGCCTGCCT		
	.845			CCCGTCGTA			AGTACGACGG		
1	846		CCTATACO	CGTCGTGGTT	CCACGTT	AACGTO	GAACCACG <i>A</i>	CGGTAT	ſAGG
	847			GCGCTAATA			AGTATTAGCO		
	.848			CAGTGAAAT			GATTTCACT		
	.849 .850			CGAATACTGC AGGTTCAGGT			CAGCAGTATT IGACCTGAAC		
	.851			CGAAGACAC			AAGTGTCTTC		
	852			CCAGGGCGAT			CAATCGCCCT		
	.853			ACGCTGGGCT			TAGCCCAGC		
	.854			CGACTAGAAG			GCTTCTAGT		
	.855 .856			CGGCTCACC			CGGGTGAGCC CTCCTAAGCG		
	.857			GCGTGACTT			TAAGTCACG		
1	.858			CTGCGTCTGA		CCACTO	CTTCAGACGC	AGTGG	CAGT
1	.859		GCGCCAG	CAAATTTCGT	GTGGTGT		ACACGAAATI		
	.860			TCGAGCCGA			ATTCGGCTCG		
	.861 .862			CGGGCGCTAT CGGCTCTGAA			AAATAGCGCC		
	.863			CAGGCAGAT			CGTTCAGAGO TTATCTGCCT		
	.864			CCGACAGGG			TCCCTGTCG		
1	.865		GGGGAATA	ACCCGGCGTT	TGTAATA	TATTAC	CAAACGCCGG	GTATT	CCC
	.866			TGAGGTTAT			ACATAACCTO		
	.867 .868			GTTCAGTCG			AGCGACTGA		
	. 869			GTGCCGGTG GAATGATGG			AGCACCGGC <i>I</i> GCCATCATT		
	.870			ACCGTCCAGC			CGCTGGACG		
1	871		AGGGAATA	ATAACAACAC	CGCGCAC	GTGCGC	CGGTGTTGTT	TTATA'	CCT
	872			GAAACCAGC			PAGCTGGTTT		
	.873			ACTTAGATAG			GCTATCTA <i>I</i> GACGCAAAGG		
	.874 .875			CTCCTTTGCG IGCATACCCA			TTGGGTAT		
	876			TTCCCTAGE			TTCTAGGG#		
1	877		CGAAGTAC	CGCAATAGTO	CCACCCT		GCACTATTO		
	.878			CGGATCACC			TAGGTGATCO		
	.879 .880			ACCGTTTCA TTTCATAGTO			CCTGAAACGO AGGACTATG <i>A</i>		
	.881			TCATAACGA			GTCGTTATC		
	882			CTGCATCGTT			CGAACGATGC		
	.883			AGTTTCGGAG			CGCTCCGAAZ		
	.884			CGTTCGATGA			CTCATCGAZ		
	.885 .886			CAATGACCO			AGCGGTCATT		
	.886 .887			TCTACCAAG TCGCGTATA					
	.888			CTAGTGGGG					
	.889			CATCCGACC					
	.890			CGAGAGGGTG					
	.891 .892			TTCTGGACCA CATAAAGAAT					
	.893			ATAAATCCG					
	894			CACGCTCTT					
	.895			AGCTGTCACC					
	.896			CCGGTAACAA					
	.897 .898			CGCCTTACA CTCCTGTGCT					
	. 899 . 899			CGATGGTCGG					
	900		TCAGTTCC	SATGGCTATT	GCGCCTC	GAGGCC	GCAATAGCC <i>A</i>	TCGAA	CTGA
	901			AACGGACGCA					
	902			GTTGCGGCT					
	.903 .904			AGACCGCCGT ACCGAATTTC					
	.904			CAAGATACGA					
	906			CAGCATCCAC					

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Seq. ID	No.	Decoder	Sequence	(5'-3')	Probe	Sequence	(5'-3	')
1007		an amagaa		тасаат	ътаса	33 M3 CCM 3 MC	magaga	
1907 1908			CAAATACGTA IGAAGCACGA					
1908			CGGAAGATC					
1910			GCAAACGAA					
1911			CTCACACGTG					
1912			CTCCAAGTAC					
1913			ATTACGGCGG					
1914		ATCGACGO	CAACCGGATA	AGTCTCTG	CAGAGA	ACTATCCGGT	TGCGT	CGAT
1915			AAACCGGCAT					
1916			AATACGGGTC					
1917			TTGCCATGCT					
1918 1919			CTACTGCGCA					
1919			GCCCGTGCTA GGTGGATTGT					
1921			CCTCAATTO					
1922			CCTGCCAGA			ATCTGGCAG		
1923			TCGGCAAT					
1924		CTCAGAGO	CACAATCTGC	CCTGCCT	AGGCAG	GGCAGATTO	TGCTC	IGAG
1925		GCTAGGA	AAGTCGGCAT	TCATGGG	CCCATO	GAATGCCGAC	TTTCC	IAGC
1926			CAAAATTCCG			GCGGAATTI		
1927			GCTAAGGGAC					
1928			rgggatgagt					
1929 1930			rcgtgattgo cttccgggac			CACCAATCAC FGGTCCCGG <i>A</i>		
1930			ITTCCGGGAC [GACCAAGCT					
1931			ACTGCAATTO					
1933			GAGCCGGCG					
1934			ATGCGGGGCC					
1935		TGAGGCTT	TAGCCTACG	CGCAGGT	ACCTG	CGCGTAGGCT	'AAAGC	CTCA
1936		CAGCGTTA	ATGAGCGCGG	SAGTTTAT	ATAAA	CTCCGCGCTC	'ATAAC	GCTG
1937			rgaccacgg <i>a</i>					
1938			CTCCTACGCC					
1939			GGCATGATG					
1940 1941			CGCCAAAGAC GGATGGGGTC					
1941			CAAAACGTTT					
1943			rgggccgate					
1944			CGTATCCGCC					
1945		GAAGGCGA	AACCACTGAA	AACTACGC	GCGTA	TTTCAGTG0	TTCGC	CTTC
1946			rgcaacggg1					
1947			TAGGTTTTG					
1948			ATGAAGCGGC					
1949 1950			CGCGTTGGTA AGAAACAGCA					
1950			IGGAGTGAAA					
1952			AGAATGCCCC					
1953			TTCGGGACC					
1954		GAGAAGCO	CGGTTCTCAG	GAGCACAT	ATGTG	CTCTGAGAAC	CGGCT'	ICTC
1955		TTGCGTTC	GCAAGATATO	TGGCCCG	CGGGC	CAGATATCTT	GCAAC	GCAA
1956			ATGTTCAGGC					
1957			AGGTGACATA					
1958			ATACGGGTTC					
1959			GCGCTTCTTC					
1960 1961			STAAGCGTAC SACAATGTGG					
1962			TCTGCTAGG					
1963			STCTGACATA					
1964		CGCCTCA	ACCCAATCT	GAGAACGT	ACGTT	CTCAGATTG	GTTGA	GGCG
1965		TTACGCTT	PACTGCGAGO	TGGGTCC	GGACC	CAGCTCGCAG	TAAGC	GTAA
1966			GGGCAATAC					
1967			CTTTGGATGC					
1968			CATCACGTAA					
1969 1970			GATGTGGTT GCAACTGAG					
1970			CACTTGTTAC					
1972			CTTCAAGCCT					
1973			GAGGTCATGA					
1974			CTTGAAGTC					
1975			GCATGATGAT					
1976			TTCTCGCTGC					
1977			CAACCACATT					
1978			AACAGCGGTC					
1979 1980			FAGCGGGGAT FAAAACCTGT					
1300		CCIIAACC	nnncc1G1	JUJJAU	303610	LITERADAC	.103111	DUA.

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TABLE 2-continued

Seq. ID	No. Decoder	Sequence	(5'-3')	Probe	Sequence	(5'-3')
1981					CTTGCTTAT	
1982					TTGTCGCCCA	
1983					SATCATGCGAG	
1984					TAGACTCCT	
1985					BACGCACGATA	
1986					PACTCGGAGC	
1987					ACAGATAGGT	
1988					CATTTGGTTT	
1989					CAGCTCCCAG	
1990					SAGGACTATGO	
1991 1992					ATGACTTACC( CGCATCAAT(	
1992					PATTCCGGAA	
1994					AGCATTTCAT(	
1995					CACGCCAGTA	
1996					ATCTCACGAT	
1997					CGAGATGCG	
1998					CTGGATTAC	
1999					CAATGTAGGT	
2000					AGCACAGTCA	
2001	CTATGGT.	ATCGAGACAT	CGGCGGA	TCCGCC	CGATGTCTCGA	ATACCATAG
2002	CCTCGTA	CTCCGTCGTA	TGCACAA	TTGTGC	CATACGACGG	AGTACGAGG
2003	TGGTGCG'	TCCGTAGTGC	CTGCACT	AGTGC	AGGCACTACG	GACGCACCA
2004	CGCGATC	CTAGTTGAAA	GCTTTGC	GCAAAC	CTTTCAACT	AGGATCGCG
2005	ACGATCC.	AGGTGTTGGG	CACTAAG	CTTAGT	GCCCAACAC	CTGGATCGT
2006	CCAATCT.	AGGATACACC	ACGCCCG	CGGGCC	TGGTGTATC	CTAGATTGG
2007	GATACGT	GGGGTATAGG	CGGGCCC	GGGCCC	CGCCTATACC	CCACGTATC
2008		CAAACCGTCG	TAGGGGA	TCCCCT	TACGACGGTT	IGTTCCATG
2009		CGCAGTATTC	GAGTCGT	ACGACT	CGAATACTG	CGCGAGTGT
2010		TCGAAGGTGA			SATCACCTTC	
2011		CCCCGTGGTA			SATACCACGG	
2012		GTAGTTCCGG			CACCGGAACT	
2013		ACCCAGGGGT			AAACCCCTGG	
2014		TGCATGGCGT			TAACGCCATG	
2015		TGGCGGACGG			CTCCGTCCGC	
2016					CGGTTGAGTT	
2017 2018		GAAACGCTGC			CGCAGCGTT	
2018		FAGGTCGCGG CCTTCTGGGC			GCCGCGACC'. AGGCCCAGAA	
2019		CCATTGGCCC			CGGGCCAAT(	
2021		GCTGAGCAAC			TGTTGCTCA	
2022		TAAGCGTCCG			GCGGACGCT	
2023		CGCAACATGT			CACATGTTG	
2024		ACAGCTAAGC			AGGCTTAGCT	
2025		GCCGGGATCC			ACGGATCCCG	
2026	TGCGGTC'	TGGAAAGGAA	.GGGAGGG	CCCTCC	CCTTCCTTTC	CAGACCGCA
2027	GCTGCCA	CCTGGACATC	GCATACA	TGTATO	GCGATGTCCA	GGTGGCAGC
2028	GCAGGCA'	TGACAGTGGC	GTAGTAC	GTACTA	ACGCCACTGT	CATGCCTGC
2029	GCGGCCC'	IGATGGTTTG	GCTGAGC	GCTCAC	CCAAACCAT	CAGGGCCGC
2030		TTAGTCCCCT	CCATCAC	GTGAT	GAGGGGACT	AAATGGGGA
2031	GCAACAC.	AAATGCGAGC	GTAGGAG	CTCCT	ACGCTCGCAT:	TTGTGTTGC
2032		GTATTCGAGC			GGCTCGAAT?	
2033					TTCCACGTGC	
2034					CAACGGAGCG'	
2035					CTTGCGCTTT	
2036					CAGAGTCTT	
2037					STTCCTACGA	
2038					CCAGATACAG	
2039 2040					STCATGGGCC( ACCCCTACAG(	
2040					CTTTTAGCCC	
2041					ACGCGCCCTA	
2042					GCGCGCTAT	
2043					GCGCGCTATO GCGGGCTGCCO	
2045					ACGCAGCAAC	
2046					SATTCGTTAG	
2047					ACCTAAGGGC	
2048					CAACCCTTT	
2049					GTAATATTG	
2050					TTCTGTAAAG	
2051					TATTGCGGT	
2052	ATGAGGT	CGTGCTGCGT	TCACGAG	CTCGTC	GAACGCAGCA	CGACCTCAT
2053	CGAGACT.	AGTGCCGATG	CAGGGTA	TACCCT	GCATCGGCA	CTAGTCTCG
2054	GCCTCAT	CATAGACGCT	GGATGCA	TGCATO	CCAGCGTCTA	TGATGAGGC

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		TABLE 2-CONC	
Seq. II	No.	Decoder Sequence (5'-3')	Probe Sequence (5'-3')
205	5	GACAGGCGTCGGTAAGCTCTCAAG	CTTGAGAGCTTACCGACGCCTGTC
205	5	GCTACGAATCTTCCCTGTCGCCAC	C GTGGCGACAGGGAAGATTCGTAGC
205	7	TTTGGCAGAACGTACCAGTGGGG	ACCCCACTGGTACGTTCTGCCAAA
205	3	GGACAATAAGCACCGGAGAATGC	GCGCATTCTCCGGTGCTTATTGTCC
205			A TTCGCGGCATCAGAAGGTTCATGA
206			C GCACGTTTTTAAGGTAATGCGGCG
206			AATCAATGAGGCGGTTGGACTCGT
206			C GGCGGAAGAGTAGCAACTCTTCGC
206			A TCACGAAAAAGATTGTTGCCGACG
206			GCGCGTCTCACGGGTGCACAGGATT
206 206			GGCTCGCGTTGATGCATATAGGTT TTTCCGGGCTGTTTTGCCAAGTTC
206			A TITCCGGGCTGTTTTGCCAAGTTC
206			TATTGTGTCCACAACCCGGTGCACT
206			A TTTCTTGGCGTGTGAAAAGCCAGG
207			CCAGGCTTCAGGCTACGCTGAGTG
207			GCACACCGCTGCGGTCGATAATTC
207			GCTCGGCCACCATGTGATGTCAC
207			A TCACTGGTGACTCGGCAAGGTGCT
207	4	TAGGTTGCAGGAATGGTGGGCAC	GGTGCCCACCATTCCTGCAACCTA
207	5	GTCCCATACGTGTGGTACGCGGA	TATCCGCGTACCACACGTATGGGAC
207	6	TCGGATACTCTCGCGTGCCACGG	CCCGTGGCACGCGAGAGTATCCGA
207	7	CAACGTTCGCCCCTAAGCCCAAA	T ATTTGGGCTTAGGGGCGAACGTTG
207	3	GTTAGGTCACCGCGGCATATCCT	A TAGGATATGCCGCGGTGACCTAAC
207			T AAACCCAAGTAGAGGCCGGTGAAC
208			GACCACATGACCTAGACGCGGATT
208			C GGGTACCACCTCCAGAGGCGTAGC
208			A TTGGACCCTTTGTAGCATTCCCTG
208			G CTGTTAACCGGGCAGCTAACCCTT
208			C GGCATAAATATCGCGCTTGCGAGG
208 208			A TTCCCTTGACCATGACCGGGAGGC C GTGCACAGGTCGCCGCTCAACAGC
208			G CGGCACATCAGAGCTAAGTCAGCG
208			A TTCCTTCGTGATGAATGCCATGAA
208			CATTCACACGCGGGCATAACACTA
209			A TGCCCACGACCGTGCCCTTACATG
209			GTGCATCACGGAGCGAGCTTCCTG
209			A TGCAGTGAGGTTGCTATCAGCAGG
209	3		G CGCCTAGACCCTGCCCCTCGTAGT
209	4	CATAATGTGGGTGCTGACGCCGA	T ATCGGCGTCAGCACCCACATTATG
209	5	TAGCGAATCCACACAGAGCCGCTC	C GAGCGGCTCTGTGTGGATTCGCTA
209	6	TCGCGAAATCCCTAAATGCTGTG	C GCACAGGATTTAGGGATTTCGCGA
209			C GAGTTGGTGGCTTGATTCGTGCCA
209			G CGTCAGATAGCAAAGACGGTCCGC
209		AGGCCCCGCCTTGTAATTGGTCA	
210		CTGGTCCCATACGCCGCTGACTAC	
210 210			C GACTCTGTAGGGCCGCAGTTAGCA CGGACGCTACCGAACATAAAACCA
210.			G CATCCCGTGGGAGAAGTTTGAGCT
210			C GATGCGGATTTCACTATCTTCGCG
210			A TGCAACCCGCGAGAGGTTTCACTC
210			A TTGACGTCACTGCAGAGCATTCGA
210	7	AGGTGGCAATGATCGACGACCCTC	CAGGGTCGTCGATCATTGCCACCT
210	3	GTCCGGAGCCGTGCAAAGCAATA	A TTATTGCTTTGCACGGCTCCGGAC
210	9	CTTTTGGGGATTAGAGGCCGACA	A TTGTCGGCCTCTAATCCCCAAAAG
211	0	GGCATAAAGGCTTCCGTTCCTGTC	C GACAGGAACGGAAGCCTTTATGCC
211			CTATCTGCCCGCTTTACGGTCCGC
211:			G CGTGGATTCGATGCACTCTTGAAA
211			C GGCAACAGCGAGAAGGGATGCCGG
211			A TGCACTCCGTTCGCGTCTCTGTGT
211			T AGTAACGAGTGGGAGAATGCCGCT
211			C GACTTGCGAGGCGCAGTACGCTCC
211 211			A TTATCTGCCGTGTCATTCGGGTTT A TGTCGTTTTATCGATCCGCTGGTT
211			A TACCGGCGTTAACGGGTGGACACC
212			A TTTAACGCAAGCCACGTCGCGCT
212			C GTCGTTGGACCTATAGCCGTGGGA
212			CACCTAACGGCATCGTTCGTTGAT
212			GCCTCGGCCATACGGCTTAGCCTC
212		ACGGTCCGAAATGGTTAGAGGCAG	C GTGCCTCTAACCATTTCGGACCGT
212	5		C GCCTACTCGAGGAATGGTTTGCGT
212			A TATGGCCCAATAGCGAGCGTGTAA
212			CCGGCGTTCTAAACCCGTGCCGAG
212	3	ATTCGGTAAGGTATCGGGCTAGC	G CGCTAGCCCGATACCTTACCGAAT

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Seq. ID No	.Decoder Sequence (5'-3')	Probe Sequence (5'-3')
2129	AGCACACCGTTATACATGACGGCG	CGCCGTCATGTATAACGGTGTGCT
2130	AGTCCCTGCCGTTCGCTCATGGAA	TTCCATGAGCGAACGGCAGGGACT
2131	GGGCTTATGACCAGTCAGGTTGGA	TCCAACCTGACTGGTCATAAGCCC
2132		AGACCAGGCACTCGTGTGGTGACC
2133		GAGGGTTTCGGGAGACACGATCAA
2134		TTAAGAAATGCCGATCGCGACAAT CAGCAGCGAGAAGTCGTTGGACCC
2135 2136		CCACTATGGCCCCCAAGGAATTTG
2137		ACCGTCTAACGGCGGATACTCTGG
2138		CCAGACACGAGATGATCTGCAGGA
2139	TGCGGGAGATTTGAACAAGCTGTA	TACAGCTTGTTCAAATCTCCCGCA
2140		GACGTTGCCTAGCTCGGCGTCTAA
2141		GTTGAATCGGAGATTCTGCCGAAA
2142		TCTGTCTTGTAGGTCTGCCCA
2143 2144		TGGCCGATGTACCGGTCTGTCGCC GGTCCCACGAAACGCAGGTCTAGA
2145		TGAACGTATGGTACCACGCTCGGC
2146		AGCCACAGAAAGCGGGTGTGATTA
2147	GGCCGGAGCCATTGGACACTTCTT	AAGAAGTGTCCAATGGCTCCGGCC
2148		CAGCGATCCATGCAGGTCTACAGG
2149		TGCTTATTTTGCGGGAACGGCGAT
2150 2151		CGTTTTCACTACCCCGTTGATCCA CAGCTCAAGAAAGCATCGTCGCTT
2151		GCAAGCGTAGAACACGTGCCCGTG
2153		TTTCTAGCTCTTGTCCCAGCCCGT
2154		GATGTGAGAGCGGAGCCAGTTACC
2155	ACTCTGGCTGTTGGCGAACGTGAC	GTCACGTTCGCCAACAGCCAGAGT
2156		GAGAGCAAGGACTGGTCCTCGGTC
2157		TGCCGTTAGGCCGCAAGAGCTACT
2158 2159		CACTGCTCTCCCCCAGGACAAGAA ATGAGCCGACAACCTCCCTGCTAA
2159		GGCGGAGCGTACAATCCACGTTCT
2161		CATTGGTGGCTCCAGGCTGTGAAG
2162		CCGCTGGTGCGTTTCATCGATCTC
2163	GGGTCCAGAGTTGGTGTGGGATAA	TTATCCCACACCAACTCTGGACCC
2164		GTGATTCCTATCTGGGGTGGACGG
2165		TCGTAGATTCACAGAAGCGAGGCA
2166 2167		CCGTTATGCGCGGACGCTGTGATC AAGGTGCGTCATGTAAGGCGTCAT
2167		TGAACTAAGGCGTTATTCCACGC
2169		CGGTCGGCCGAGAAATGGTAGACC
2170		TGAGCGTCTACGCCAGAGAGGTGT
2171	GTAGAGGTGCTCAGGACTCGTCGC	GCGACGAGTCCTGAGCACCTCTAC
2172		TTCGCGCCTTCGCCTCCTGCTTAC
2173		AGGTCGATTGAAACGGCCCTTAGA
2174 2175		TCGGGCTGACCCTGAAATCAGGTT TAATAGGTGGGCCAATCGCGTGAC
2176		ACTAGGTTACATGCGCGGCATCGT
2177		CAGGCGTTGACGAGACATCTCTCA
2178	GCATATCTCGCGGTGACAGACGAA	TTCGTCTGTCACCGCGAGATATGC
2179	GACCCAACGTCGAAATTGTGCGAT	ATCGCACAATTTCGACGTTGGGTC
2180		CCAAACTAGATGCCCCGATTTTCA
2181		TGCGTACACAAATCCTTTTCGCGG
2182		AGCGAACTGCGGATAAATGGAATG ATAGACGCTGGCTCGACAGACAGG
2183 2184		GCATAACTTGTTTAGCCGCGCTGA
2185		CTCTCTTGGGTCGTTCGTAGGCGT
2186		GATCCAGACAATGGTAGATGCGCA
2187	AAGTCCGCGCTCGCTCCTGTAATA	${\tt TATTACAGGAGCGAGCGCGGACTT}$
2188		TGGTTACTCGAGCAATGACCCAGC
2189		GTCGGTCATTGCCAGAACGCTCCA
2190		CCGAATTGGCCAAGAATTGACTTG
2191 2192		TAACCTGGGATCCTTGCATGAACG AGCATCCCCAGCTTCTATTGGCAT
2192		GAACGCCTCAAGGGAGAGTTAGG
2194		AATGTTTGGAACCTTCGCCGAGAT
2195		GAAAACCGCAGCGTAATCTGTCGC
2196		${\tt GTAACGTGTTGGCCGTCTGGGCTT}$
2197		CCACGGGATGTGATTTGAACTTGA
2198		CGCCTCACAGACAGACGACAATC
2199 2200		TGCCATGCCGGAACATAGTTCGGT AACGGCATTGCACACCCGATGACG
2200		AGTGCACAAACGTGACTCCGTCCG
2202		CGGCAAAGGCACACGACTTGTTTA

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Seq. ID	No. Decoder Sequence (5'-3')	Probe Sequence (5'-3')
2203	TAATTACTGGCCTGTGGAGCAGGC	GCCTGCTCCACAGGCCAGTAATTA
2204		TAAGAGCACCATTCGGGCCGCTCC
2205		ACGCACATCCAAGCCTTGCTTAGT
2206		GTAGCGTACTGCCGCTGAGCTGCC
2207		AAATCCGCGGATAATTCGCCTCGC
2208		TAGCACCCCAAGGTGTGTCGTATG
2209		AAAACGGGGTTTAAAGCCCAAGCA
2210		CCGATATTTGCGTTTTCCAACCGG
2211		CTTGCGGGTGCGGCTAGCTAGTTT
2212		CTGCGTGATCACTGGTGGAACAAC
2213		AACGATGATCATCTTGTCAGCGGC
2214		GGGCATCGGTTGGCTTTATGAAAG
2215		CACCCGCTTTCGAGATGCAGTCAG
2216		ACGTGGCCGATTCTCCGAAGAAAT
2217		GCGCAGTAGCTAGGGCCCGAAATG
2218	CCGATCCCGCACATCCGTATCCTG	CAGGATACGGATGTGCGGGATCGG
2219	TATCACCGGGAGCGTCTTATCGTG	CACGATAAGACGCTCCCGGTGATA
2220	TAGGGCTCGTGCACCGATTAGAGG	CCTCTAATCGGTGCACGAGCCCTA
2221	GCGTGGCACTCGCTTGTCTAGGTA	TACCTAGACAAGCGAGTGCCACGC
2222	CTCAACGAACTCAAGGGCCGCTAC	GTAGCGGCCCTTGAGTTCGTTGAG
2223	AGCCTGGTATCGACCAATCCTGCA	TGCAGGATTGGTCGATACCAGGCT
2224	TACGCGTTCTAGTTGGCCGGATCC	GGATCCGGCCAACTAGAACGCGTA
2225	TTTATGGGTTTGTGCCTGATGGGT	ACCCATCAGGCACAAACCCATAAA
2226	GGGACCCCTAGCAACGTCACCTTA	TAAGGTGACGTTGCTAGGGGTCCC
2227	CTGCCTCCCCAGGAGTCATTGGAT	ATCCAATGACTCCTGGGGAGGCAG
2228	AACCCCGCAAGACCAGTACCAATC	GATTGGTACTGGTCTTGCGGGGTT
2229	GGTCACATACGCGCTAAAAAGCGC	GCGCTTTTTAGCGCGTATGTGACC
2230	AAATGGCTCCGACCAGTTAGGGAC	GTCCCTAACTGGTCGGAGCCATTT
2231	AACGCGGCACGCTTAAAGGTGCAT	${\tt ATGCACCTTTAAGCGTGCCGCGTT}$
2232	GATCGCACGCCGATTAACCTTACA	${\tt TGTAAGGTTAATCGGCGTGCGATC}$
2233	CCTCCTGATTGGGAGTGCGGAATT	AATTCCGCACTCCCAATCAGGAGG
2234	CGGAGGGTAATAGGCTCCTCTGCG	CGCAGAGGAGCCTATTACCCTCCG
2235	ACAAGAACTGGACATTACCGCGGG	${\tt CCCGCGGTAATGTCCAGTTCTTGT}$
2236	TGTCGTCTTAAAGGCCTTTGTGCG	CGCACAAAGGCCTTTAAGACGACA
2237	GGTGACCATGTGGCGTTTTAGCTT	AAGCTAAAACGCCACATGGTCACC
2238		GTTCTGGTACCGTGCGCAACCGTG
2239		GGGCAGGGGACCAAACAATAAAGG
2240		ATTGACGGTAGAATGCAGGCGCAC
2241		CGGCGGCAAGCCATCAACGTAAAC
2242		ACATTCACGTCCTACCACCGACGG
2243		AGCACAGGGATTCTGGGGCGATCA
2244		AAAGCAACCGATTTTTGGCTGCTT
2245		AGGCCCTGCTACTAAGTCCCGTCG
2246		CTACTTGGTCGTTTCGCGAATCGG
2247		TGAGAAAGATTGGAGTTGGGGTGG
2248		GACGCCGGTAGTCGTCTACTGCAC
2249		GAATTGCTTGATACGATGGGCGAA
2250		TGACCCGACGGGTAGTCGCGATTC
2251		ATTATAACCGATGGCGAGTGCTGG
2252		CACCGACCGGAGTTCTACGGTTCG
2253 2254		CATCCTGGGGCTCTGTCATGGTGC
2254		TCACCCTTATTCTGCGGTAGCCCA TGTTTCCTTCGACACGACA
2256		GCAAACGCTCGCTATCGGTGAGGC
2257		TGTCTCGTTTTAGCCGGCGCGCAC
2258		CTGTCACAAGAAACTCGTCTGCGG
2259		GCTTCCTAGCACGCGATTGCGAAC
2259		TTCACCGGATGCATGTGTACAACA
2261		CGCGCCCTTATATCGTGTTCAGTG
2262		ATCGTCTTGCTAAGAACCATCGCG
2263		CGTCCCCATTTCTTCCTTGGTGTA
2264		GCTGCACCTAAAACGCAAGGCACG
2265		GCCGTTAATGCCCAGACAAACGAC
2266		ACGTTTGTACCGAACGAGAGCCTG
2267		TGGGTTCTGGTGAAACAGTGTCCG
2268		TACGCTTCTTCCGCATCATGGGTA
2269		CGGTTCTCATCCGCTTAAGGACAG
2270		GCACAAAACCGTTCTCATCTCCCG
2271		CGGCCTGAGTACAGTCGCGATCTA
2272		ACGACAGTCGCGCGAACTGTTTTA
2273		ATTGGGCTTATGTGGAGCTCCTCG
2274		AAGATGATTCCCCATCCCTAGCCA
2275		CAATGCATCCAGGCACCCAATCCT
2276		ACCTGCTTCAGGCCGGTAGATACA

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Seq. ID	No.	Decoder	Sequence	(5'-3')	Probe	Sequence	(5'-3'	)
2277		TCCCTAC	GCGCATGACT	CGCTTAC	GTAAG	CGAGTCATGC	GCGTAG	GGA
2278			ICACCTGTGA					
2279		TGGGGGT	AGTCCATGCA	TCAATTG	CAATT	GATGCATGGA	CTACCC	CCA
2280		CCCTGCCZ	AGGATTACTA	TTCCGGA	TCCGG	AATAGTAATO	CTGGCA	.GGG
2281			CGGGGAATTT					
2282			GCAGGAACTT					
2283 2284			CATGCATGCG					
2284			CTAGTGGACG ATCTCATCAG					
2286			CCACTGCTCC					
2287			GATGGACCTT					
2288		GGTTCCG	GAATTTGTCA	CCGCTTC	GAAGC	GTGACAAAT	TCCGGA	ACC
2289			ATAGTCTGCG					
2290			AGTGCTGCCA					
2291			GGTGTCGGA					
2292 2293			CAGACAATGO FCAAAGAGGG					
2294			CAAGACGAAG					
2295			rccgaggage					
2296			CTCAGAGTCG			TCGACTCT		
2297		ATCAACGO	GCCACCTCCT	CGCCGAG	CTCGG	CGAGGAGGT	GCCGTT	GAT
2298			GAATAATTCC					
2299			IGCGTATCGC			TTGCGATACG		
2300 2301			CTTACCATCA GATAGGCCAG					
2301			GGTCATTTT					
2302			GCGGCTTACG					
2304			ACGTAACTTC					
2305		TCGGCAG	CCAATGATCA	TACCTCT	AGAGG'	PATGATCATT	GGCTGC:	CGA
2306			GATCCGGTCC					
2307			AGACTAACAG			CCTGTTAGT		
2308 2309			GCACTCTAAG CCCACGCGGA					
2310			CTCCAGAGGA					
2311			ATCAACCCAG					
2312		ACAGCTC	GAAGGCAGCC	ACATTGG	CCAAT	TGGCTGCCT	TCGAGC	TGT
2313			GTACCGCGAC					
2314			AAAAACCAGC			AGGCTGGTTT		
2315 2316			AGCACTTTCG CTGGGTATCA			GTGATACCC		
2317			PATCGCTGCA			CGTGCAGCG		
2318		GAAGGAA	rcccggatae	TCCGTGG	CCACG	GACTATCCGG	GATTCC	TTC
2319			CTCAGCCAAA					
2320			GACGTTTCCC			CGGGAAACG		
2321 2322			GCGCACGGGA AAGCCAACTT			ATCCCGTGC		
2323			GCAAGGTAGG			GACCTACCTT		
2324			ATCTCCTCGA		ATGCA	ATTCGAGGAG	ATGGCC	ACC
2325			FAAGTTGCAC					
2326			AGCGTTTTCG			CGCGAAAACG		
2327 2328			FTGTGAGAGG CGAGCAGAC <i>A</i>			GCCTCTCAC GATGTCTGCT		
2329			TTCGGGTCG#					
2330			rgaactcgc <i>a</i>					
2331		CGATTCC	CATCATAATG	TGGGTCC	GGACC	CACATTATGA	\TGGGAA	TCG
2332			GATAATCCAG					
2333			CCCTATGATI					
2334 2335			CATGCGCTGT CGAAGATCGC					
2336			GTTTTGAGA					
2337			CGGGAAATCT					
2338		TGCTTGCT	PATCCGAAAA	AAGCAGG	CCTGC	TTTTTTCGG#	TAGCAA	GCA
2339			ATCAAATTCG					
2340			ACGAGTTACC					
2341 2342			GTCCGGAGGG CCGGAGGATG					
2342			AATGTCCACG					
2344			rgccacgcgc					
2345			GCACGGCTCT					
2346			CCCGAGCGAC					
2347 2348			AGTCTATCCG CTCCTGGGTC					
2349			AGGGAAGTAC					
2350			GCGGACAAA					

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Seq. ID	No.Dec	oder	Sequence	(5'-3')	Probe	Sequence (5'-3')
2351	AGA	TCATC	GGGACGCT	TCATGCTA	TAGCA'	TGAAGCGTCCCGATGATCT
2352	CCC	TTCTG	ACCGCTAA	GGCCATAA	TTATG	GCCTTAGCGGTCAGAAGGG
2353						AGACACCCCACGGCTCACG
2354						AGCGGAGACGACCAAGGTA
2355						ACGTAGCATTTTGCGGCGA
2356						GGCAGCCATTAGGTCACTC
2357 2358						GGGTTGGCCAAGTTCCTTT TAGGTGGAGTGCGAAAACA
2359						GCCCTTATGAAACCCATTG
2360						GGACCCTTGTGTGTTAGGC
2361						ATCCTCGGACCGCATGACG
2362						TTACTCCGTGCCCGTGTGG
2363	CAT	CAGAC	ATAGGTCG	CGTGCCGA	TCGGC	ACGCGACCTATGTCTGATG
2364						TCCTCCCTTGGTTTCATCT
2365						GCTGAGCCTATGGGTAGCC
2366						GAACACACCCTCACAAGCC
2367						TTGCATTCGCCGTAACACA
2368 2369						ACGGCGCGACCTGTTATCG CTGGAGCCTCACTTTATCA
2370						TGCAGATCCGTGCACAATT
2370						ACTGGTGACAGTACATTGC
2372						CAAGTGTTACCGATATGCC
2373						CCACGCTGGTTTGAGACCC
2374	GTC	TCCGG	GACCATTG	AGCTGGAG	CTCCA	GCTCAATGGTCCCGGAGAC
2375	GGC	CTTCG	GCATTCAG	ACGGGTTG	CAACC	CGTCTGAATGCCGAAGGCC
2376	CGT	GATAG	GCCACAGC	GCTCAATT	AATTG	AGCGCTGTGGCCTATCACG
2377						TCATCCTCGCGGGCCTGCC
2378						CTGTTATCAACCATACCCG
2379						ACGGTCCCAAGGACGTCGT
2380 2381						GGCTCAGGCTCGATATCAG AGCATACAGGCCAATGGGA
2381						ATGAAACAATCGACGACAC
2383						AATCGGCTACTGGCTTTCG
2384						CAGTGGAATAAGCCGAACC
2385						TAAAAAGTTAGCCCTCGCT
2386	CGG	CGCTG	ATGACGGG	ACTCGATT	AATCG	AGTCCCGTCATCAGCGCCG
2387	TCA	CAGTG	CTCGGCGT	AAGGACTA	TAGTC	CTTACGCCGAGCACTGTGA
2388			GAGCACAC			GGTGTGTGCTCGTAATGGG
2389						TGCGTAAAGATTAGCGGCC
2390						CTGGACACTAGGAAGCCGT
2391 2392						ATTGGGTAGGACCTGACAG TTCAGTGGGATGGGCTGTG
2392						CGTTGCGTGTATCGTTTGT
2394						GCCTGCTAGCTGGCCGCCA
2395						GCACGCATCGTTTCGAGAT
2396	ATC	TCGAG	AACAGCGT	GCGTGCGG	CCGCA	CGCACGCTGTTCTCGAGAT
2397	GAA	GAAAT	CCGCCGAC	ATCTACGG	CCGTA	GATGTCGGCGGATTTCTTC
2398						ACAGCCAAGGTTGCTCCGC
2399						AACAAGTCTTCGGAACGCG
2400						ATGGATGGGCTTCAGGTCA
2401 2402						TTATCCGGAATGAATACCA
2402			GGTCATTG CTGTGTAG			CATCAATGACCCGCAACGC GCTCTACACAGAATGCGGT
2403						AGCTGCGATTGTCTATTTG
2405						ACCTTGATTTGTCAGGACA
2406		TTGCA	CTCGCGGA	GATTTCCT	AGGAA	ATCTCCGCGAGTGCAATTT
2407	TGA	CGCCC	ATTTCTAT	ATGGTGCA	TGCAC	CATATAGAAATGGGCGTCA
2408	TGT	TCCGA	CAGGGCAC	TGCTAGAC	GTCTA	GCAGTGCCCTGTCGGAACA
2409						GGCCTTCCCAAGCCAGCGA
2410						TACGCCAACGGAGGTGCAC
2411						CCGATCGGTCCCAAATGAG
2412						TCCATTGACAGACACTGGC CACAGAACCTGCCGGGCAA
2413 2414						TGCGTCTCGGTTCGCGGGT
2414						CCTTGACCAATCGCACGGA
2416						GGTTCAACCGAGACGCCCT
2417						CTTGCTCTTTGAACGGTCA
2418	ACA	CTCAC	CTGCTGTC	CCTGCTGA	TCAGC	AGGGACAGCAGGTGAGTGT
2419						CACCCAAGGAGTTAAACGC
2420						AGAGTTACCTGCGCAGGCG
2421						GCCGCTGGGAAATTCGATT
2422						CCCAGGATCCCACCTGCTT
2423						GAAGAGCGAGTCTGGGATT AGCCGGCCCTTATAACCGT
2424	ACG	JIIAL	טטטטטמני.	CLIGCGAC	GICGC	ACCOGCCCTTATAACCGT

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Seq. ID	No. Decoder	Sequence	(5'-3')	Probe	Sequence (5'-3')
2425					GTCTAAGCCCGCTCTCGTA
2426 2427					AACCGTGGGTCAAAATCGC CCATCCAAATTATACAGCT
2427					ATCGGCTAAGACTCGCGGA
2429		GCTCCGTAAG	CCGATAG	CTATC	GGCTTACGGAGCTGATGCC
2430					GCTCGAACTGCCAATAACA
2431					CCCAAGCAAAAAGGCTCGC
2432 2433					GACGCTGACCTTTTCTTCT IGCTTCAAGGGTCGACCCG
2434					FAAGTTTGTGAAAACCGAG
2435					AGGCTCCGGATAGGACTGC
2436					ACAACAAATAGCGCACCTT
2437					IGTCGGCATGGATTCCACT
2438 2439					CGCAGGAATTACGCCTGTA CGTGCTTCTCGCACTTCGG
2440		GGTATGGCC			CCGGCCATACCAGTCCTT
2441					PATGAGGTTGGCGGTGTCC
2442					AGTCCAGGCGAACACCATT
2443					FCCCGTGTACGCTTTCCTA
2444 2445					CCTCATCATTGGGGTGAGA ACAGTGTCACACGGACACG
2445					GTATCCGCAACAGCCTGGA
2447					ICGCGACCATTTTGGCTAC
2448					CAATGGGGTCCACGGAGAT
2449					PAGCGTTGACGGCATATTC
2450 2451					TTACCAAACGCTTCCGGAA CCCTGGTATTCCTATCGAA
2451					PAATCCTCCTCAAATGGCC
2453					AAAGTCCAGGTCAGAAGGT
2454					GCTCAACTGCGGATTGGTC
2455					ACTCATGGTGAGTGGCCGA
2456 2457					FTTCGAACATGTGAGCGCT GGATCGCGCCTTTGCGTTA
2458					GTAATATTTGGCCCACCCA
2459					GGATGCCCCTTTCGAGGAC
2460					ACGCCTCCCACCAGATGGG
2461					GAGTTTGCAGACCGCGCAC
2462 2463					ACCTAGGGTTGGCAACACA CCGACGAGAACAGCATCAG
2464					CGCTCACCTTTTGCAGCTT
2465	TCTGACG	CGTGCTTGG	SAGTCTAT	ATAGA	CTCCCAAGCACGCGTCAGA
2466					CGGCGCCTCCAAGTAATTC
2467 2468					ACCTAGGTCGGGAAGAATC CAACATGGGATACGCTGCG
2469					GGCGAACAATTCCATCTC
2470					CTAGACCGATCCAGGCATC
2471					ATAGCTTAGCAGTCGCTGC
2472					GCCGATGTAAATTAGCCCT
2473 2474		ACATCCTCACO AGCCGTAATTA			FTCGTGAGGATGTGCACTT FTTAATTACGGCTGCCTGA
2475					AGTGCGATTTCCCCAGTGG
2476					CGTAGGTGGCTTTGGACAA
2477		GAATAGATTGO			ACCCAATCTATTCCGCCCA
2478					CTAGAAGAGGCGAATTCTA
2479 2480					GCATCTGCAGGAAGTAATG FACCCCAGCTAGCATTTCC
2481					PAGATTCGCAAGTGGCGGC
2482					GCGAGCTGTCCGCTATTGT
2483					CCGCACCGAGAGCCTAACT
2484 2485					FAACCGCTTCTCAGGCCCA FAGGCGTCGCTCAGAGCGT
2486					CTGGGACACGATCACCAGG
2487					CTCAAGCGAATGGACACGC
2488	ATCCTGA	ACGGCGATGA	ACCACCAC	GTGGT	GTCATCGCCGTTCAGGAT
2489					TGATCGGTGAGAAACGTAA
2490 2491					ITTAGCCACTCAAGACGGC ITCGAGCCGCATCGTAGAT
2491					TTGGGGACGAGTCTTGGTT
2493					IGCCTCCACCACCGCAGTT
2494					GTAGGTGGAGAAGATCGCA
2495					TTCACGGTTCTAAGCGCCT
2496 2497					CGTTTCCCAAAATTTTCCA GGAGAAGGTGCGGCGCTGG
2498					AAGATTCGCCAGCCGTCTA

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May 22, 2003

2499 TACCATACAAGGACCGCA TGGGCTCGTTCTCTTGTATGGTA 2500 GTAGCCGGAGGATTTTTCACCC GGGGTGAAAATTGGTCTGGGTA 2501 GCCAAACTCCCCTGCCCTTTACCCT AGGCTAAAGGCAAGGGGATTTGC 2502 ATCCGCTGATAACCGCCAGGGTAA TATCCTGGGGTTATCAGGGGAT 2503 AGTCTCAGTTCGGCGAACGGTAT TATCGTGGGGTTATCAGGGGAT 2504 ACCTCCAGTCCCCCATATGCTAT AATCGATTCGGGGTTATCAGGGGAT 2505 AACCTCCAGTCCCCCATATGCTAT AATCGATGAGGGCAGTCAGGGGAT 2506 AACCTCACATCAGCCCCAGATGTAT ATTCGAGGGCAGTCAGGGGAT 2507 AACTCCAAACTGAATTGGGCCACATTATA TATCATCAGGGCAGTCATGAGACT 2508 ACTTTATTGGCCGCAATTGGATTATCGGGCATTACCGGGATACTGAGGAC 2509 TGTTTTCAGGCGGCATCCTTATA ATTCATCAGGGCAGTCCCTCCTTA 2509 TGTTTTCAGAGCAGCACCT 2511 ACGCTCAGAACCCCTGCCAT 2512 CGATCGGTTGTTGCCACA TGTGGCCATTTCCCGCAAATTACACCCTGCTA 2512 CGATCGGTTGTTGCTCTCCCAA 2513 ACTGCCATATCTCCCACA TGTGGCATTACCCCTGCAACCCT 2514 CTCGCTATCTACGCGTCTCCGAAA 2515 TGCCAGTATTATCCCTCAACCCT 2516 TGCCAGTATTATCCACACACCACCCTGCCCAAA 2517 TTACAGGATTCCAAACCCACCAAA TTTCGGAGACCGCTTACGTCACCAA 2518 TGCCAGTATTATCCAAAACCCACCACCAA 2519 TTACAGGATTACCAAACCCACCCACCAAA 2510 TTACAGACTCAAACCACCCCCCCCCAAA 2511 TTACAGACCTCAGAACCACCCCCCCCCAAACTACCCCGCTTACGCCCAAACCACCCAC			
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2518 CGGTACCAACGGCGGGGCATATGA TCATATGCCCGCGCTTGGTACGA 2520 ATTTCAGACCTCGGGACAACCTGG 2521 GAAGTGGGGTAACTTAGGGAGC 2521 GAAGTGGGGTATTAGGGAGCC 2522 TTGGCCAGGTATTAGGGAGCC 2523 ATCGGCCGGTATTAGCTGCCCT 2524 CGCAGGTATGAGCGAGCC 2525 ATCGGCCAGTATTAGCTGCCCTC 2524 CGCAGGTAAGCTGCCATT 2525 TTGGGAACTGTCAGCAT 2526 CATCTCGGCAAACTGTGCCAT 2527 ACGCGTAAATCACGGCCCTC 2526 CATCTCGGCAAACTGTGTCATAAAACACTTGCCCAAACACTGCCAAACACTGCCAAACACACTGCCAAACACACAC			
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2520 ATTTCAGACCTCGGGACAACCTG 2521 GAAGTSCGCTAACTTAGGGACC 2522 TTGGCAGGTCATCACTCTGCCAT 2523 ATCGGCGGTCATCACTTCGCAT 2524 GCAGGTAAGCCGAGCCATC 2525 TTGGAAACGCGAGCATGTT 2525 TTGGAAACGTGCTAAGCTACCTCC 2526 CATCTCGGCAACTGGTGCTAAACACTTCCTCACCTCC 2527 ACGCGTAAATCACGGCCCTC 2528 CCTAGGTGAAATCATCGCCCAC 2529 TTCGAAACAACACGTGTGCT 2529 TTCGAGCAACTTGTCCAA 2530 ACGATATTCGCCCAC 2529 TTCGAGCACACTGGTCGTCGACACCGATGTTACCTCCG 2529 TTCGAGCCAAATAAACGGTTGGC 2531 GCACAAATTCTCCCGGTCGAGA TCTCCAACCACACTTACCTCCG 2529 TTCGAGCCAGAATAAAACGGTTGGC 2530 ACGAAACTTTCTCCCGAGCAACT 2531 GCACAAACTTTCTCCCGAGCAACT 2532 ATTGCCGCGTCTGTATCAAAAAA 2533 ACGAGAATGGTCTCCCAA 2534 TATAATCATTTCGCCCAC 2534 TATAATCATTTCGCCCAC 2535 AATTTCCCCGATTTAAAAAAA 2536 ACGAAAACTTCTTCCCCAACCACTTCTCC 2537 CGGGAAACACTTCTCACCAACACACACACACACACACCACATTTCTC 2538 CGAGAAACTTCTTCCCCGAGCAACT 2539 ACGCGGTTCCTTATCAAAAAA 2530 ACGAGAATGAATGAACCAACCTCACTCACCACACCCCCAATTCTCTC 2531 TATAATCATTTGCGACTCGCCCCA 2532 ATTGCCCGGTTCGTATCAAAAAA 2533 AAATTTCCCCCGATTTGAAGAAAC 2534 TATAATCATTTGCGCACCCCCA 2534 TATAATCATTTGCGCACGTATT 2535 AAATTTCCCCCGATTTGAAGAAGC 2537 CGTGAGCCGTTCCTACCAACCG 2538 GCAGAATCGAATTGGCTCGCCCCA 2539 CTCTCGGGTTTCCTAACCAACCG 2530 CCTCTGCGTTTCCAACCGACGTCC 2531 TTCCCCACTTCTCCCCACTCCAC 2532 CCCCCCAATTCGATTCTCCC 2534 GCAGAATCGATTCTCCACCCACATTCCACTACCACCCCAATTCGATTCTCC 2534 CCCACCTCTTCCACCCACTCCACCCCAATTCGATTCTCC 2538 GCAGAATCGATTCTCCACCCCC 2538 GCAGAATCGATTCTCCACCCCC 2540 GACCACTTTCGCCTCCCCC 2551 TCCGCGACTTACCACTCC 2551 CCCACCTTTCCACCCACCCCCCCCCCCCCCCCCCCCCC			
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TTGGGAACGTGCTAGGCGCCCTC GAGGCCGCTAGCACGTTCCCAA 2526 CATCTCGGCAACATCGTCCTCTATA TATACAGCACCAGTTGCCGAGATG 2527 ACGGTAAATCAACGACGTGTCG CGACCAGTTGTCTGATTTACCGCC 2528 CGTAGGTGTAAATCAGGACGTGGTCG CGACCAGTCGTTGATTTACCGC 2529 TTGCAGCCAGAATAAAACGGTTGG CCAACCGTTGTTATTCTGGCTCGAA 2530 AGACATATTCGGCCTCGGTCCGAA TCTGACCGAGAGCCGAATATTCTCTG 2531 CGACAAAGTTTCTCGCGAGCAACT AGTTGCTCGAGAACACTTTGTCG 2532 ATTGCCCGGTCTCGTATCAAAAGA TCTTTAACGACACAGCGGCAAT 2533 CGGAGAATGGATTCTTG CGAAGAACCTGCATCATCTCCG 2534 TATAATCATTTGCGACTCGCCCCA TGGGCGAGATCCATTCTCCG 2535 AATTTTCCCCGATTTGAAAAGA TCTTTTCATAACGACACGGGCAAT 2536 CCGCATACTTCGTCGGCCAGTTTA AATACTGCCCGACGAACTTATAC 2537 CGTGAGCCGTTCTCATCAAACG CCGCTTCTTCAAAATCGAGCAACTATTCAC 2538 GCACAATTGGAATTGGGGTGGTTT AATACTGCCCGACGAACTATTCGC 2539 CTCTCGGTTTCTCATCCAAGCG CCGCTTGGATGAAACGGACTCAGC 2539 CTCTCGGTTTCTCATCCAAGCG CGGCTTGGATGAAACGGACTCAC 2530 CTCTCGGTTTCTCAACCGAGCTC CGACCTCGGTTGAGAAACCGACCACCCAATTCGAATTCTGC 2531 CTCTCGGTTTCTCAACCGAGCTC CGACCTAGTCAACTGGTC 2532 CTCTCGGTTTCTCAACCGAGCTC CGACCTCGGTTGAAAACGGACCACCCCAATTCGATTCTGC 2534 CCCAAGTCTAGCAGATCCTG CGACCTAGACTATGCACTAACTGGTC 2540 GACCAGTTAGTGCAGCAATCCTG CGACCTAGCTTAGCACTAACTGGTC 2541 TTCTCGCACAACTAGTCAGCCGAT ATCGGCTGACTAGCCGAAGACTTGGC 2542 CCCAGGGACTTGCTCATCCACCAGCTCACCCAAGACTTTCGC 2544 CCCAGGGACTTACTCCATC CAGGATCACCCAAGCCTATCCATC 2544 CCCTGGGGACTTTCTCCACCG CAGGATCACCCAAGACTTGCC 2545 GCGGCTCTGCCTAACATTTCCAC CGACTAGACCTAGCCCACTTTCGC 2546 CCCCCTCAACGTAGACTAAAA TTTTTCAATCGACCAAGCCACTTTCGC 2547 TGCACCTGTCTGAAATTACCACA CAGCACGCCCAAGCCCACTTTTCGC 2548 CATAAAGCAAGACTACATTGCCGTA ACCACACCCCTACCTTTAGGC 2550 GGGTCATCCTTGCACTGAAATA ATCAGACCAGCCGACAATTTCCACCG 2551 CCCGATAATCCTTTTGTCCACCG CGCTGAAAATACGGCCTACCTTTTAGC 2552 CCGATAATCCTTTTGTCCAGCCG CAGCACAATTTCACACCAGCAGC 2554 GAGCACCAATCGTCTTGAAATTC CACCAGCCAAAACACTACTTCGGACCACACCAC			
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TATAATCATTTGCGACTCGCCCA TGGGGCGAGTCGCAAATGATTATA 2535 AATTTTCCCGATTTGAAGAAGCG CGCTTCTCAAATCGGGAGAATTGCG 2537 CGTGAGCGTTCTCATCCAAGCG CGCTGAGTAGAAAACCGAGAGTATT AATACTCGCCGACGAAGTATGCG 2538 GCAGAATCGAATTGGGGTGGTTT AAACCCACCCCAATTCGATTCTGC 2539 CTCTCGGTTTCTCAACCGAGCTC CGACCACTTGGATCAGAAAACCGAGAG 2540 GACCAGTTAGTCCAACGAGCTCT CCAAGCTTGGTGAGCGATTTCTCCA 2541 TTCTCGCACAGCTAGTCAGCCGAT 2542 CCAAGTCTTGCGTGAGCGATCCT 2543 GCGAAAGTGGCTCGATATTCTCCA 2544 CCTCGGGACTGTCCGACTAACACTGCCAT 2545 AGGCGAGTTTCCGACCATTCCATC 2546 GCGCTCTGCCTACCATACCATGG 2547 TGCACCTGTCTGAGATTTCCCA 2548 CATAAAGCACGGCACTTTCACA 2549 CCCTCAACGTAGGCGATTATTCACA 2549 CCCTCAACGTAGGCGATTATTCACA 2549 CCCTCAACGTAGGCGACTTTCA 2549 CCCTCAACGTAGGCGACTTTCA 2550 GGGTCATCGTCGAGTATTCCGC 2551 CCCGGATAATCCTTTGCGTGACCAACACCGCCCACCTCGCCT 2551 CCCGGATAACCTTTGCTGAAAAA TTTTTCAGTCGGACAGCCGCCC 2551 CCCGGATAACCTTTGATAACAATCACATCGCCTCACCTGCCCT 2548 CATAAAGCAACGGACCACTTTCA 2559 GGGTCATCGTGCGACTTACAT 2550 GGGTCATCGTGCGACTTTCA 2551 CCCGGATAACCTCTTCCAACCTACCATGCC 2551 CCCGGATAACCCTTTGCTCAACCAT 2552 TCCGAATAACCTTTGCTCAACCAT 2553 CCTGCTGGTTCGGTCGTAAACAAT TTCGCCTGACCTACACTGGC 2554 GAGGCACCAATTCGTCCAACGTAC 2555 TACGAAAATGGTTACCATTCC 2555 TACGAAAATGGTTCACATTGGC 2556 GAATCACCCTCAACGTCACATTGCC 2557 CCGAATCAGCGACTCACATGGGT ACCCCGGCCCAACCATTTCCGTC 2558 CCTGCTGGTTCGGTCGTAAACTG 2559 TTTTGGGGATCACCATCGAA 2560 AGTGACACCGCTTACCTCCATCCA 2561 CCATGAGTTTTCTGGACTCCAA 2562 GCCAATTCTGGTCCTACTCCATCCA 2563 TCCTGTGCTTTTTCTGGACCAC 2564 GCCCACATTCTGGTCCTACTCCATCATTCA CGATTCAGACCAGCAGGAC 2566 GCCCAATTCTGGTACCTCCGTCTT TACCAGCAAATACGGCTGATTCGG 2567 CCTGAGTTTTCTGGACTCCATTCA CGATCAGCGTTACCACACGGCC CGATCAGCTTTCCGGCATT TTCCAGCAAATACGGCTGATTCGGA 2566 GCCCACATTCTGGACTCCATTCACTCA TCCAGCAGAAACACCACTCATGG 2567 CCTGAGCCCGTTAACCACCGC CCCAACACTTCCCGTCTT TACCAGCAAATACGGCTTACCACCACGGCC CCCAACACTTCATCGGCC CCCAACACTTCCTCGTCTT TACCAGCAAATACGGCTTACCACACGCC CCCAACACTTCACTCCATCACTCA CCCACACTCACCACGCCC CCCAACACCATTCCGCCAACACCACCACCACCACCACCACCACCACCACCAC			
2535 AATTTTCCCGATTTGAAGAAGCG 2536 TCGCATACTTCGTCGGGCAGATATT AATACTCGCCGACGAAGTATTCACAGCGG 2537 CGTGAGCCGTTCTCATCCAAGCGG 2538 GCACAATTGGATTGGGGTGGGTTT AAACCCACCCCAATTCGATTCTGC 2539 CTCTCGGTTTCTCAACCGAGCTC 2540 GACCAGTTAGTCAACCGAGCTC 2541 TTCTCGCACAGCTAGTCAGCCGAACCACTTGAACCGAGAG 2541 TTCTCGCACAGCTAGTCAGCCGAT 2542 CCAAGTCTTGCGTGAGCGACTCAGCAACCACTAGCTAACTGGTC 2543 GCGAAAGTGGTCCGACTGAAAAA 2544 CCTCGGGACTGTCCGACTGAAAAA 2545 AGGCGAGTTGCGACTAGACACATTCCCACCAAGACCTTTGC 2546 GCGCTCTGCCTACCAAGAATTTCCCA 2547 TGCACCTGTTGTAGATTTCCCA 2548 CATAAAGCACGAGCGCACTTGAT 2549 CCCTCAACGTAGGATTATCACA TGTGAATATCGTAGGCAGCACC 2547 TGCACCTGTCTGTAGATTTCCCA 2548 CATAAAGCACGACGACGACTTGAT 2549 CCCTCAACGTAGGATTATTCACA TGTGAATATCCTTAGGCAGCAGCCGC 2550 GGTCATCGTGCGAGCAGCCTTCAT 2551 CCCGGATAATCCTTTTGTCCAGCCG 2552 TCCGGATAACCTCTTTGTCCAGCAGAACCCCTACGTTGAGGA 2553 CCTGCTGGCTGAGTTATTCCAGCC 2554 GAGGCACCAATCCGTTATTCCCAGCATAACCACCAGAGAGCCCC 2555 CCCGGATAATCCTTTTGTCCAGCCG 2555 CCTGCTGGTCGTAGAATAG 2556 AATTGCCGGAACACTTGAT 2556 AATTGCCGGAACACCTTGAT 2556 CCTGCTGTTCGTAAACAGT 2557 CCGAATCAGCGAACACCATTGCGAACACCCCTACGTTTATCGG 2558 CCTGCTGGTTTCGTAAAATG 2559 TTTTGGGAACACCACTGGAT 2556 AATTGCCGGAACCATTGCTA 2557 CCGAATCAGCCGTATTTTCTCAAAATG 2560 AGGCACCAATCGGTCTAAACTGGAT 2561 CCATGAGTGTTCTGACTCCAAGGACCACACCATTCGGC 2551 CCGATTACTCTGTACTCCAGCGAACCACTTCGGCAATTCGGC 2552 TCCGAATCAGCCGAACCATTGCTCAAAATG 2553 CCTGCTGGTTTTCTGACTCCATCGAATACCGACCGAACCATTTTCGTA 2556 AATTGCCGGAACCAATCGGTCTCAAAATG 2557 CCGAATCAGCCGTATTTCGGACCACGAGGACCACCAATCTCGTACTTCGGACCAAAACACCTAATACGGCCGAATTCGGCAATCACATCGGACACACCACGGCCCAACCATTTTCGTAACCACCTCAAGGACACACCAAGGACCAACACATTTTCGTAACACCACCAGGGCCCACCAATCCGGACCAACACATTTTCGTAACACCACCAGGGCCCCCAACCAA			
TCGCATACTTCGTCGGCGAGTATT  2537 CGTGAGCCGTTTCTCATCCAAGCG  2538 CCAGAATTCGATTCGATCGAGCG  2539 CTCTCGGTTTCTCAACCGAGCTG  2540 GACCACTTAGTCCAATGGT  2541 TTCTCGCACAGCTAGTTGGCG  2541 TTCTCGCACAGCTAGTCAGCCGAT  2542 CCAAGTCTTGGTGAGCGATCTG  2543 GCGAAAGTGGCTTGACCGAT  2544 CCTCGGGACTGTTTCTCCA  2544 CCTCGGGACTGTTTCTCCA  2545 AGGCGAGTGTCCGACTGATTCTCCA  2546 GCGCAACGTTGCGGCTACCATG  2547 TGCACCTTACCTAGACAAAAA  2548 CAAAAACCACCCCAATGCACACCCGAGACTTGC  2546 GCGGTCTTCCGACGATAACCA  2547 TGCACCTTGCTAGACAAAAA  2548 CAAAAACACCCCACAGACCTCGC  2548 CAAAACACTTCGCATAACCA  2554 CCCCCAACCTTTCGATTTCCCA  2554 CCCCCAACCTTTCACCCATG  2554 CCCCCAACCTTTCACCATG  2554 CCCCCAACCTTTCACCATG  2555 GGGTCATCGTCAACCATGATATTCACA  2554 CCCCTCAACGATATTCACCA  2555 GGGTCATCGTCGACTTTCC  2556 GGGTCATCGTCTACCATTCACCC  2551 CCCGAATAATCCTTTTGCCGTA  2552 TCCGATAAGCGAACTCACATGGTA  2553 CCTGCTGGTTTGGTCGTAACAATG  2554 GAGGCACCAATCGGTCTAACCATGGTA  2555 TCCGAATAACCTTTTGCCGCA  2555 TCCGAATAGCGAACTCACATGGGAT  2556 AATTGCCGGAACTCACATGGGAT  2557 CCGGATCAGCTCACATGGAATC  2556 AATTGCCGGAACCACTGAATAC  2557 CCGAATCAGCTTAACCAATGGTA  2560 AGGCACCAATCGGTCTGAAAATG  2561 CCATGAGTTTCGGCCGGGTCT  2562 CCCCCTTATCTTGTCACCCA  2563 TCCTGTGTTTTTGGGCAAATCG  2564 GCCCCACATTCTGCTCACCAAGCACACCACTTTTCGTA  2566 CCCCCACATTCTGCTACCACTGGCC  2567 GCCACATTCTGCTACCACCGCC  2566 GCCACATTCTGCTACCACCGCC  2567 GCCACATTCTGCTCCACCC  2566 GCCACATTCTGCTACCACCGCC  2567 GCTGATCGGCTTAACCATCCATC  2566 GCCACATTCTGCTACCACCGCC  2567 GCTGATCGGCTTAACCATCCAC  2566 GCCACATTCTGCTACCACCGCC  2567 GCTGATCGGCTTTAACCATCCAC  2566 GCCCCACATTCTCCCGCCACCGCCCACCACCACCACCACCACCACCACCACC			
2537 CGTGAGCCGTTCTCATCCAAGCGG 2538 GCAGAATCGAATTGGGGTGGGTTT 2539 CTCTCGGTTTCTCAACCGAGCTCG 2540 GACCAGTTAGTGCAATTGGGTTGGCG 2541 TTCTCGCACAGCTAGTCAGCCGAT 2542 CCAAGTCTTGCGTGAGCGATCCGCCCCCAATTCGACTAGCTGGC 2543 GCGAAGTGGCTGGTTTTTCTCCA 2544 CCTCGGGACTGTCATCCATCCATCGCTCAGCCAGACTTTGC 2545 AGGCGAGTGTACGGCTCATCCATC 2546 GCGCAACCATTGCAGCCACT 2547 TGCACCTGTCATCCATC 2548 CATAAAGCACGACTAGTTCACCA 2549 CCTCAACGTAGATATTCACA 2549 CCCTCAACGTAGATTTTCCGCT 2550 GGGTCATCGTGAGATAA 2551 CCCGGATAATCCTTTTTCCACCCCCCCCCCAAGCCTTACCCCCCCC			
CTCTCGGTTTCTCAACCGAGCTCG GACCAGTTAGTGCAATGGTTGGGG GACCAGTTAGTGCAATGGTTGGGG CGCCAACCATTGCACTAACTGGTC CGCCAACCATTGCACTAGCTGGAC CGCCAACCATTGCACTGAGCAGAC CGCCAACCATTGCACTGAGCAGAC CGCCAACCATTGCACTGACAGACAGAC CGCCAACCATTGCACTGAGCAGAC CGCCAACCATTGCACTGAGCAGAC CCAAGTCTTGCGTGACGAGAC CCAAGTCTTCGCGTGACTACCATGC CAGGATCGCTCACGCAAGACTTGC CCCGGAAAGTGGCCTCACCATG CAGGATCGTCCGACTGAAAAA CGGCAGATGTACGGCTCATCCATG CAGGATCGTCCGCATACCATG CAGGATCGTCCGCATACCATG CAGGACAGTCTCGCCT CAGGATCATCCATG CAGGACAATTCTCACA CAGGATCATCGCCTACACTTCCAC CAGGATCAGCCGCACTTCCATG CAGGACACCGCACCTTCCCCTACGCTTCCGCCT CAGCCTCTCTCTCTAGATATTCACAC CAGGATCATCGCCTACATTCACAC CAGGATCATCCGCCTACACTTCCCCC CAGGATCACCCGCACCCCTACCTTTCC CCCCCAACCGACCGCACTTCTCC CCCGCATAATCCTTTGTCCCACCC CCGCCTCACCTTTTCTCCCACCCC CCGCCTGACCACTTTTCTCCCACCCC CCGCCTGACCACTTTTTCTCCACCCC CCGCCTGACCACCATTTTCCCGCC CCGCCTCACCTTTTCCTCCACCCC CCGCCTGACCACCACTTTCCCTCCCCCCCACCCCCCCACCCTTCCGTTCACCCCCCCC			
2540 GACCAGTTAGTGCAATGGTTGGCG 2541 TTCTCGCACAGCTAGTCAGCCGAT 2542 CCAAGTCTTGCGTGAGCGATCTG 2543 GCGAAAGTGGCTGAGCGATCTG 2544 CCTCGGGACTGCTGATTTCTCCA 2544 CCTCGGGACTGCCGACTAGAAAAA 2555 AGGCGATGTCCGACTGAAAAAA 2545 AGGCGATGTCCGACTAGATTTCACCA 2546 GCGGCTCTGCCTACGATTTCGCG 2547 TGCACCTGTGTAGATTTCGCG 2548 CATAAAGCACGGACGCACTTGAT 25549 CCCTCAACGTAGGTTTCGGCATTTCG 25549 CCCTCAACGTAGGTGATTTCGCGT 25550 GGGTCATCGTGAGATTTCACCA 25550 GGGTCATCGTCAGTAGCTTC 25551 CCCGGATAACCTTTTTTCTCCAGCC 25552 TCCGATAACCTTTTTTCTCCAGCC 25553 CCTGCTGGTCGTAAGCGAA 25554 GAGGCACCAATTGATCACAATGGGT 2555 TACGAAAAATGGTCGCAGATTACCGGT 2555 AATTGCCGGACGCCACTTGAT 2556 AATTGCCGGAACCACACAGGAACCACAGCAGG 2557 CCGGATAACCTTTGTCCAGCCG 2558 CCCGCTTATCTGAAAAAG 2559 TTTTGGGGAGCAGTCAGAATCG 2559 TTTTGGGGAACACGACGAACCACATTTCCGTA 2560 AGTGACAGCGTTATTGGGCAG 2561 CCATGAGTTTTCGTGAAAATG 2562 GCCACATTCTGTACCACTGGTT 2563 TCCTGGTTTTCGGACAAATCG 2564 GAGGCACCAATGGGTCT 2565 TTTTGGGGACAGCAGCAGCACAAAAGAATTCGACAATT 2566 CCGCCTTATCTGTACCACTCCAAAAAAAAAAAAAAAAAA	2538	GCAGAATCGAATTGGGGTGGGTTT	${\tt AAACCCACCCCAATTCGATTCTGC}$
TTCTCGCACAGCTAGTCAGCCGAT  2542 CCAAGTCTTGCGTGAGCGATCCTG CCAAGTCTTTCGCTGAGCGATCCTG CCAGAGTCTTCGCTGAGCGATCCTG CAGAGTCTTCGCTGAGCGATCCTC CAGAGTCTTCGCTGAGCGATCCTC CAGAGTCTTCGCATCCATC CAGAGAAATACGAGCCCACAGACTTTCGC CATCGGACTGTCCGACTGAAAAA TTTTTCAGTCGGACAGACCCCC CATCGGCACTGTCACCATC CATCGATAATCCTACCATC CATCGATAATCCTACCATC CATCGATAATCCATCCATC CATCGAAAATACGACAGCACCCC CATCAACCTTACAGATATTCACA TTGCACCTTACAGTCATTCGCT CATCAAACCACACCGACCCCACACCCC CATCAAACCACACCGCACCTTCAAT CAACACCGCAAATCTACACACCCCC CCCCAAACCTTACCATCACCCCC CCCCCAACCTTAGACCCCCCCCCC			
CCAAGTCTTGCGTGAGCGATCCTG CAGGATCCTCACGCAAGACTTGG CGAAAGTGGCTCGTATTTCTCCA CCTCGGGACTGTCCGACTGAAAAA TTTTTCACTCGGACGAGCCACTTTCGC CATGGAGAAATACGAGCCACTTTCGC CATGGAGAATTCCGACTGAAAAA TTTTTCACTCGGACAGACCCCT CATGGATCATCCATG CATGGATCATCCATG CATGGATCATCCATG CATGGATCATCCATG CATGGATCATCCATG CATGAAAATACCTTCGCCT CATGGATCATCCATG CATGAACACTCGCCTACATTTCACCA CATGGATCATCCATCATT CACCCTGTCTGTAGATTTCACCA CATGAACTCCGCTCATCACATTTCACA CATGAACTCCCCCTACATTTATG CCCCCAAAACCACGCACGCACTTCATC CCCCCAAAACCACTCAGCATATTCCCACCG CCCCCAAAACCCTACGTTCACACCCC CCCCCAAAACCCACCGACCCACTTCCACTTCACGTCACG			
GCGAAAGTGGCTCGTATTTCTCCA  2544 CCTCGGGACTGTCCGACTGAAAAAA  2545 AGGCGACTGTCCGACTGAAAAAA  2546 GCGGATGTCCGACTGACAAT  2546 GCGGATGTCCACGCTTCCATC  2547 TGCACCTGCCTACGATATTCACA  2548 CATAAAGCACGGACGCGACTTGAT  2549 CCCTCAACGTAGGCCGACTGAT  2551 CCCGCATAGTCCAGCGATATTCCACA  2552 GGGTCATCGTCAGACTATTCCACA  2553 CCTCGACGACGCGACTTGAT  2553 CCTGCTGGTTATGCCGTA  2554 CCTGAAAATCCTTTGTCAGCGCT  2555 TCCGATAAGCGAACTCACATGGGT  2555 TCCGATAAGCGAACTCACATGGGT  2555 TACGAAAATGGTTGCGGTA  2555 AATTGCCGGAAACTCACATGGGT  2556 AATTGCCGGAACCATTGATATTCCGGA  2557 CCGAATCAGCCGTCTGAAAATG  2558 CCCGCTTATTTGCTGGAAAATG  2559 TTTTGGGGACACCATTGATATTCCCGCAAACCACTTTCTGGA  2556 AATTGCCGGAACCATTTTGCTGAAAATG  2557 CCGAATCAGCCGTTATTAGCGCACA  2558 CCCGCTTATCTTGTCAGACAATG  2558 CCCGCTTATCTTTTTGCTGAAAATG  2560 AGTGACAGCGGTCACCACGGTCCA  2561 CCATGAGGGTTCCATATTAGCGCA  2561 CCATGAGGGTTCACCACGGTCCA  2562 GCCACATTCTGCTACCTCCGTGTT  2563 TCCTGGGTTTCGGCACATCGAA  2564 GACGCACATTCTGCTACCTCCGTGTT  2565 GTAGGCCCGTTATCACCTCCGTGTT  2566 GCCACATTCTGCTACCTCCGTGTT  2566 GCGCCCGAAACACCATTTCAGGC  2567 GCTGATCAGCCTTTAACCATCCAA  2566 GGCCCCACATTCTGCTACCTCCGTGTT  2566 GCGCCCAATTCTGCTACCTCCGTGTT  2566 GCGCCCGGAAACACCATTTCACGGCC  2567 GCTGATCGGCTTTACCCGCCTATA  2568 TACAAAATCGTTGGACACCATCTCA  2569 TTGGCGGAAATGGACTTTACCG  2567 GCTGATCGGCTTTTCACCGCCTATA  2568 TATCAAAATCGTTGGACACCATCTCA  AGGACCCGTCGTTAACCATCTCA  2569 TTGGCGGGAAATGGACTTTACCG  2567 GCTGATCGGCTTTACCCGCTATA  2568 TATCAAATCGTTGGCACGCGACTA  2569 TAGGCCCGTCTTTACCCGCTATA  2569 TAGGCCCGTCTTTACCCGCTATA  2569 TAGGCCAGAATTCACCTTCACCTCCTATA  AGAAACCGAACACCATTTCAACCACCGGCCCACACCACA			
AGGCGAGTGTACGGCTCATCCATG  2546 GCGGCTCTGCCTACGATATTCACA  2547 TGCACCTGTCTGTAGATTTGCGGT  2548 CATAAAGCACGGACGCGACTTGAT  2549 CCCTCAACGTAGGGCGTACACTTCGT  2550 GGGTCATCGTGCGTAGTTTAGCGGT  2551 CCCGGATAATCCTTTGTCCAGCCG  2552 TCCGATAAGCGAACTCATGGT  2553 CCTGCTGGTTGTAGATTTGCCGGT  2554 GAGGCACATCTGTAGATTTGCCGTA  ATCAGGTCACGTCGTGTTTAGGGG  2555 TCCGGATAATCCTTTTGTCCAGCCG  2555 CCTGCTGGTTCGTCAAAATG  2555 GAGGCACCAATCGGTCTAAGCGAA  2555 TACGAAAATGGTTGCGCGGGTCTT  2555 TACGAAAATGGTTGGCCGGGTCT  2555 CCGGATTAGCTGAAATG  2555 CCGGATCGGACCAAACGGATTCGCT  2555 TACGAAAATGGTTGGCCGGGTCT  2556 AATTGCCGGAAGCAGACCACAGGTC  2557 CCGAATCAGCGATCACATGGCA  2558 CCCGCTTATCTGTACCACCG  2559 TTTTGGGGATCACATCGGA  2560 AGGGACCAATCCGTTCACACTCCC  2561 CCATGAGTGTTTCGGGACAACCGC  2562 GCCACATTCTGCTACCACCGTCC  2563 TCCTGTGCTTTGGGACAACCGA  2564 GACCGCATATCACCTCCTGTT TACGACAGATGTCCCAAAA  2566 GGCCCACATTCTGCTACCTCCGTCT  2566 GACCGCATATACACCTCATCGC  2567 GCTGATCGGCTTACCATCTCA  2568 TATCAAATCGTTGGCACGGTCC  2567 GCTGATCGGCTTTCACCTCCGTCT  2568 TATCAAATCGTTGCACCTCCTC  2567 GCTGATCGGCTTACCATCTCA  2568 TATCAAATCGTTGCACCTCTCACCCCCCCCCCCCAACCCCCCCC			
2546 GCGGCTCTGCCTACGATATTCACA 2547 TGCACCTGTCTGTAGATTTGCGGT 2548 CATAAAGCACGGACGCACTTGAT 2549 CCCTCAACGTAGGGCGTGACTTTC 2550 GGGTCATCGTGAGGACGCACTTTC 2551 CCCGGATAATCCTTTGTCCAGCCG 2551 CCCGGATAATCCTTTGTCCAGCCG 2552 TCCGATAAGCGACACTCGAT 2553 CCTGCTGGTTCGGTCGTAAAGCGA 2554 GAGGCACAATCTACGACAGGACACAGGACAGCAGCAGCAGCAGCAGCACACAGCAG	2544	CCTCGGGACTGTCCGACTGAAAAA	TTTTTCAGTCGGACAGTCCCGAGG
2547 TGCACCTGTCTGTAGATTTGCGGT ACCGCAAATCTACAGACAGGTGCA 2548 CATAAAGCACGACGCACTTGAT ATCAAGTCACGTCGTGCTTTATG 2549 CCCTCAAACGTAGGGCGTGACTTTC GAAAGTCACGCCCTACGTTGAGGG 2550 GGGTCATCGTGCAGTTATGCCGTA TACGGCATAACTGCACGCCCTACGTTGAGGC 2551 CCCGGATAATCCTTTGTCCAGCCG CGCCTGGACAAAGCACAGCCC 2552 TCCGATAAGCGAACTCACATGGGT ACCCATGTTAGGACGAACCAGCAGCAGACCAACCAGCAGAACCAATCGGTCTAAAAATG CATTTTCAGAACCAACCATTTTCGTA 2555 TACGAAAATGGTTGCGCCGGGTCT AGACCAGTTGAGCCCTC 2556 AATTGCCGGAACCAGTCAGAAATG CATTTTCAGAACCAATTGCTCCTC 2557 CCGAATCAGCCGTTATTGCTGGAA TCCAGACCATTTTCGTA 2558 CCCGCTTATCTGATCACCACCACCATTTTCGGA 2559 TTTTGGGGATCCCTAATAGGACCAAATAGCACAGATCAGCAGA 2550 AGTGACAGCGCTCACCACGGTCCA 2561 CCATGAGTGTTTCGGGACATCTTA TACGACCGATGACACATTTCGGCACACCATTTTCGGACCGATTTTCGGGACCATCTTCACACAGGACCATCACACAGGACACACCATTTTCGGACCACACACCATTTTCGGACCACACACCATTTTCGGACCACACACA			
2548 CATAAAGCACGGACGGACTTGAT ATCAAGTCGCGTCCTTATTG 2549 CCCTCAACGTAGGGCGTGACTTCTC 2550 GGGTCATCGTGCAGTTATGCCGTA 2551 CCCGGATAATCCTTTGTCCAGCCG 2552 TCCGATAAGCGAACTCACATGGGT 2553 CCTGCTGGTTCGGTCGTAAGCGAA 2554 GAGGCACCAATCGGTCGAAAATG 2555 TACCAAAATGGTTCGAAAATG 2555 AATTGCCGGAACCAGTGGAACCACCATTTCGTA 2556 AATTGCCGGAACCAGTTGAAAATG 2557 CCGAATCAGCGTATTTGCTGAAAATG 2558 CCCGCTTATCTGCTAGAAATG 2558 CCCGCTTATCTGCTAGAAAATG 2559 TTTTGGGGATCCCTATTAGGCGCA 2560 AGTGACAGCGGTCACAACCAGTTCCGCAAAA 2560 AGTGACAGCGCTCACCACGTCC 2561 CCATGAGTGTTCGGCACCACCATTTCGGC 2562 GCCACATTCTGCTACCTCCGTCT 2563 TCCTGGCTTACCTCCGTGTT 2564 GACCGCCATATCACCTCCGTGTT 2565 TCCTGAGTCGTTACCTCCGTGTT 2566 GCCACATTCTGCTACCTCCGTGTT 2567 GCCGCTAATCACCTGATGGCC 2568 TACCAGAACACCTCTACACACAGCACCATTTCGCGCCAAACCACCATTTTCGCGACCCC 2567 GCTGATCGCTTAACCACCACGGCCCC 2567 GCTGATCGCTTTACCCCCAAAACACCCAAAGCACCAGGTCCC 2568 TATCAAATCGTTGGCACCCCCCCCCCCCCCCCCCCACCAAACCACCACCACC			
2549 CCCTCAACGTAGGCCGTGACTTTC 2550 GGGTCATCGTGCGGTTATGCCCGTA 2551 CCCGGATAATCCTTTGTCCAGCCG 2552 TCCGATAAGCGATCACACTGGGTA 2553 CCTGCTGGTCGGTCGTAAGCGAA 2554 GAGGCACCAATCGGTCTGAAAATG 2555 TACGAAAATGGTCGGAAAATG 2555 TACGAAAATGGTTGGCCGGGTCT 2556 AATTGCCGGAAGCAGTCGAAATG 2557 CCGAATCAGCTATTGCTCGAAATG 2558 CCCGCTTATCTGTAAGCGAA 2559 TTTTGGGAGCAGTATTGCTGAAATG 2559 TTTTGGGACAGCGATTAGGCGAA 2560 AGTGACAGCGCTCACTATTAGGCCC 2561 CCATGATTTTCGGGACATCGCA 2562 GCCACATTCTGCTACCACCGGTCAAAAATG 2563 TCCTGGCTTACCACCGGTCTA 2564 GACCGCATATACACCTCCTGTTT 2565 GTAGGCCCTGAAAAATGGACGTCCC 2566 GCCACATTCTGCTACCTCCGTGTT 2566 GCCGCTAATACACCTGATGGCC 2567 GCTGATCGGCAACCACTTTACGGTC 2568 TACCAAAATGGACTTTACCACCTCCTACACAAAACCACAGGACACCACTTTCACCACAACACTCACACGGTCCC 2567 GCTGATCGGCAAACACCTGATCACCACGGTCACACACGGTCCC 2567 GCTGATCGGCTTTCACCACCTCCTACACACACGGCCCTACACACAC			
2550 GGGTCATCGTGCAGTTATGCCGTA TACGGCATAACTGCACGATGACCC 2551 CCCGGATAATCCTTTGTCCAGCG CGGCTGACAAAGGATTATCCGGG 2552 TCCGATAAGCGAACTCACATGGGT ACCCATGTGAGTTCGCTTATCCGGA 2553 CCTGCTGGTCTGAGAAATG TTTGCGTCAGCCAACCACCAGCAGCACCACCAGCACCACCAGCACCAC			
2551 CCCGGATAATCCTTTGTCCAGCCG 2552 TCCGATAATCCTTTGTCCAGCCG 2552 TCCGATAAGCGAACTCACATGGGT 2553 CCTGCTGGTTCGGTCGTAAGCGAA 2554 GAGGCACCAATCGGTTTATCGGAAAATG 2555 TACGAAAATGGTTTGGAAAATG 2555 TACGAAAATGGTTTGCAGCCGGGTCT 2556 AATTGCCGGAAGCAGCAGCAACCACTTTTCGTA 2557 CCGAATCAGCCGTATTTGCTGGAA 2558 CCCGCTTATCTGATCGCA 2559 TTTTGGGGATCCCTATTAGGCGCA 2550 AGTGACAGCGCTCACCACGGTCCA 2561 CCATGAGTGTTTCGGGACCATTTTCGTAC 2562 GCCACATTCTGCTACCTCCGTGTT 2563 TCCTTGCTTTCGGACCATTCACCACGGCCCACACCAGGACCACTCAGGACCACTCAGGACCACTCACCACGACCACGCCCCCCACAA 2564 GACCGCTAATCTGCACCTCCGTGTT 2565 GTAGGCCCGTCGTTAACCATCCCACAGGACCACCATTTTCGCGACCCCCACACCACGCCCCCCCC			
2553 CCTGCTGGTCGGTCGTAAGCGAA TTCGCTTACGACCGAACCAGCAGG 2554 GAGGCACCAATCGGTCTGAAAATG 2555 TACGAAAATGGTTGCGCGGGTCT 2556 AATTGCCGGAACCAGTTGGTGCCTC 2557 CCGAATCAGCCGTTATTTCCTGAA 2558 CCCGCTTATCTGTACTCGATCGCA 2558 CCCGCTTATCTGTACTCGATCGCA 2560 AGTGACAGCGCTCACCATTTTGCTGAA 2560 AGTGACAGCGCTCACCACGGTCCC 2561 CCATGAGTGTTTCGGACACCTT 2562 GCCACATTCTGCTACCTCCGTCT 2563 TCCTGTGCTTTCGGACACCTT 2564 GACCGCATATAGCGCCC 2565 GTAGGCCCGTCGTTAGCGCC 2566 GCCCACATTCTGCTACCTCCGTGT 2566 GCCCCACATTCTGCTACCTCCGTGT 2566 GCCCGCTGTTACCTCCGTCT 2566 GTAGGCCCGTCGTTAACCACTCCACACAGCACCACGGCCCTACCCGGCCC 2567 GCTGATCGGCTCACCACGGCCCC 2568 TATCAAATCGTTGGCACGCCCTACACACCGGCCCTACCCCCACGCCCCCCCC			
2554 GAGGCACCAATCGGTCTGAAAATG CATTTTCAGACCGATTGGTGCCTC 2555 TACGAAAATGGTTGCGCCGGGTTT AGACCCGGCGCAACCATTTTCGTA 2556 AATTGCCGGAAGCAGTCAGAATCG CGATTCTGCTCCTCGCAAT 2557 CCGAATCAGCCGTATTTGCTGGAATT TTCCAGCAAAATACGCTGCAATT 2558 CCCGCTTATCTGTACTCGATCGCA TGCGCAATACAGGTACCCCAAAA 2560 AGTGACAGGCCTCACCACGGTCCC GGGCACCATTATGGCGGC 2561 CCATGAGTGTTTTCGGGACATCGTA TACGATGTCCCCAAAA 2562 GCCACATTCTGCTACCTCCGTGTT AACACGGAGGTAGCAGAATGTGGC 2563 TCCTGTGCTTTGTACCATCCGTGTT AACACGGAGGTAGCAGAATGTGGC 2564 GACCGCATATACACCTCATGGCC GGCCCATCAGGTGTTAATACGCGTC 2565 GTAGGCCCGTGTTAACCATCTCA TGAGATGGTTAACACACCTACTCC CGCCAAACACCGCACTACCCTACC	2552	TCCGATAAGCGAACTCACATGGGT	ACCCATGTGAGTTCGCTTATCGGA
2555 TACGAAAATGGTTGCGCCGGGTCT AGACCCGGCGCAACCATTTTCGTA 2556 AATTGCCGGAAGCAGTCAGAATCG 2557 CCGAATCAGCCGTATTTGCTGAA TCCAGCAAATACGGCTGATTCGG 2558 CCCGCTTATCTGTACTCGAC TGCGATCAGAATACGGCTGATTCGG 2559 TTTTGGGGATCCCTATTAGGCGCA TGCGATCAGATAAGCGGG 2550 AGTGACAGCGCTCACCACGGTCCC GGGACCGTGGTGACCCCAAAA 2561 CCATGAGTGTTTCGGGACATCGTA TACGATGTCCGAAACACTCATGG 2562 GCCAATTCTGCTACCTCCGTCTT TACGAGGAGGTAGCAGAATGACGC 2563 TCCTGTGCTTTGTGACGTGCTAG GCCCAACAAGACACTCATGG 2564 GACCGCATATACACCTCATGGGCC GGCCCATCAGGTCTAACAGGA GACCGCATATACACCTCATTCAC TGAGATGTTTAACGAGTCG 2565 GTAGGCCCGTCGTTAACCATCTCA TGAGATGTTTAACGACGCCTAC 2566 CGGCTCGCGAAATGGAGTTTAACCATCTCA TATAGCGGTGAAAAGCCCATCAGC 2567 GCTGATCGGCTTTTCACCGCTATA TATAGCGGTGCAACAGCACCGACCAC 2569 TTGGCGAGGATCCCCTAGGGCTAC TAGTACCCTAGGACTTCACACACACACACCACTCACACACA	2553	CCTGCTGGTTCGGTCGTAAGCGAA	${\tt TTCGCTTACGACCGAACCAGCAGG}$
2556 AATTGCCGGAAGCAGTCAGAATCG 2557 CCGAATCAGCCGTATTTGCTGGAA 2558 CCCGCTTATCTGTACTGCATCGCA TTCCAGCAAATACGGCTGATTCGG 2559 TTTTGGGGATCCCTATTAGGCGCA TGCGACCAGTACAGCAGCAGAACACCCCAAAA 2560 AGTGACAGCGCTCACCACGGTCCC GGGACCAGTGCACCACCACCGCTCCC CACAACACCACCGTTCTCACTCCGTGTTACCTCCGTGTTACCTCCGTGTTACCTCCGTGTTACCTCCGTGTTACCTCCGTGTTACCTCCGTGTTACCTCCGTGTTACCTCCGTGTTACCTCCGTGTTACCTCCGTGTTACCTCCGTGTTACCACACAAGCACAAGGA 2564 GACCGCATATACACCTGATGGGCC GGCCCATCAGGTGTATATGCGGTC 2565 GTAGGCCCGTCGTTAACCATCTCA TGAGATGGTTAACCAGGACCCTCCCGCCACACCCCGCTCGTTAACCACCGCGTCACTACCCGCGTCACCCCGCGCACCCCCGCGTCGTTACCCGCCACCACCCCCACCACCCCCACCCCCCCC			
2557 CCGAATCAGCCGTATTTGCTGGAA TTCCAGCAAATACGGCTGATTCGG 2558 CCCGCTTATCTGATCGCA TGCGATCAGATAACGGGGT 2559 TTTTGGGGATCCCTATTAGGGCAA TGCGACCAGAAAAGACACACCAAAA 2560 AGTGACAGCGCTCACCACGGTCCC 2561 CCATGAGTGTTTCGGGACATCGTA TACGATGTCCCGAAAACACTCATGG 2562 GCCACATTCTGCTACCTCCGTGTT TACGATGTCCCAAAAAGCACAGGA 2564 GACCGCATATACACCTGATGGGC CCTAGCACGTCACAAAAGCACAGGA 2565 GTAGGCCCGTCGTTAACCATCTCA TGGAGATGGTTAACGACGGCCTAC 2566 CGGCTCGCGAAATGGACTTTAGCG CGCCATCAGTGTAAACCAGGCCCTACACAAAGCACAGACCGCACTAAACCACCGACCATAAACCACCGACCATAACCACCGCCCAAAAAGCACAGACTCACAAAAGCACAGACCACACACA			
2558 CCCGCTTATCTGTACTCGATCGCA 2559 TTTTGGGGATCCCTATTAGGCGCA 2560 AGTGACAGCGCTCACCACGGTCCC 2561 CCATGAGTGTTTCGGGACATCGTA 2562 GCCACATTCTGCTACCTCCGTGTT TACGATGTCCCAAAACCTCATGGC 2563 TCCTGTGCTTACCACCTGCTGTT AACACGGAGGTACACAAGCACAGGA 2564 GACCGCATATACACCTGATGGCC CCTAGCACGTCACAAAGCACAGGA 2565 GTAGGCCCGTGTAACCATCTCA TGAGATGTTAATGCGGTC 2566 CGGCTCGCGAAATGACCATCTCA TGAGATGGTTAACGACGGCCTAC 2567 GCTGATCGGCTTACCATCTCA TGAGATGGTTAACGACGGCCTAC 2568 TATCAAATCGTTGGCACGCACTA TACTCCCATAGCTTACAGCTTACAGCTTACAGCTTACAGCTTACACACCGCATCAC 2569 TTGCCGGAGATGTGGGCTATA TACTCCCTAGCGACCTC 2561 AGTCCCTAGGCCGTTCTA TACTCCCCAACACCCTCCCCAA 2570 AAGTCCTGAGGCCGTTCGGTTTCACCGCAACACCCCTCCGCCAA 2571 ACTCCGGACATCTCGGCCAGAGTA ACCACCGACTTCGCCAA			
2559 TTTTGGGGATCCCTATTAGGCGCA TGCGCCTAATAGGGATCCCCAAAA 2560 AGTGACAGCGCTCACCAGGTCCC GGGACCGTGGTGAGCGCTGTCACT 2561 CCATGAGTGTTTCGGGACATCCTT TACGATGTCCCGAAACACTCATGG 2562 GCCACATTCTGCTACCTCCGTGTT ACCACGAGGTGAGCAGAATAGGAC 2564 GACCGCATATACACCTCATGGGCC GGCCCATCAGGTCTATATCGCGTC 2565 GTAGGCCCGTCGTTAACCATCTCA TGAGATGGTTAACGACGGGCCTAC 2566 CGGCTCGCGAAATGGAGTTTAGCG CGCTAAACTCCATTTCGCGAGCCG 2567 GCTGATCGGCTTTCACCGCTATA TACGCGTGAAAAGCCGATCAGC 2568 TATCAAATCGTTGGCACGCGACTA TAGTCGCGTGCCAACGATTTGATA 2569 TTGGCGAGGATCCCCTAGGCGTACT AGTACGCCTAGGGATCCTCGCCAA 2570 AAGTCCTGAGGCCGTTCGGTTTCT AGAAACCGAACGGCCTCAGGACTT 2571 ACTCCGGACATCTCGGCCAGAGAT ATCTCTGGCCGAGATGTCCTGGACTT			
2560 AGTGACAGCGCTCACCACGGTCCC GGGACCGTGGTGAGCGCTGTCACT 2561 CCATGAGTGTTTCGGGACATCGTA TACGATGTCCCGAAACACTCATGG 2562 GCCACATTCTGCTACCTCCGTGTT TACGAGGGTGACACACAGAGTGTGGC 2563 TCCTGTGCTTTGTGACGTGCTAGG CCTTAGCACGTCACAAAGCACAGGA 2564 GACCGCATATACACCTCATGGGCC 2565 GTAGGCCCGTCGTTAACCATCTCA TGAGATGTTAACGACGGCCTAC 2566 CGGCTCGCGAAATGGAGTTTAGCG CGCTAAACTCCATTTCGCGAGCCG 2567 GCTGATCGGCTTTCACCGCTATA TATGCGGTGAAAAGCCCACGCCTAC 2568 TATCAAATCGTTGGCACGCGACTA TAGTCCGTGCCAACGATTTCATA 2569 TTGGCGAGGATCCCTAGGCGTACT AGTACGCCTAGGGATCCTCGCCAA 2570 AAGTCCTGAGGCCGTTCGGTTTCT AGAAACCGAACGCCTCACGACTA 2571 ACTCCGGACATCTCGGCCAGAGAT ATCTCTGGCCGAGATT			
2562 GCCACATTCTGCTACCTCCGTGTT AACACGGAGGTAGCAGAATGTGGC 2563 TCCTGTGCTTTGTGACGTGCTAGG CCTAGCACGTCACAAAGCACAGGA 2564 GACCGCATATACACCTGATGGGC GGCCCATCAGGTGTATATATGCGTC 2565 GTAGGCCCGTCGTTAACCATCTCA TGAGATGGTTAACGACGGGCCTAC 2566 CGGCTCGCGAAATGGAGTTTAGCG CGCTAAACTCCATTTCGCGAGCCG 2567 GCTGATCGGCTTTCACCGCTATA TATTGCGGTGAAAAGCCGATCAGC 2568 TATCAAATCGTTGGCACGGACTA TAGTGCCTGCCAACGATTTGATA 2569 TTGGCGAGGATCCCTAGGCGTACT AGTACCCTAGGGATCTCTCCCCAA 2570 AAGTCCTGAGGCCGTTCGTAGACGACGACTTCGCCAA 2571 ACTCCGGACATCTCGGCCAGAGAT ATCTCTGGCCGAGATGTCCGGAGT			
2563 TCCTGTGCTTTGTGACGTGCTAGG CCTAGCACGTCACAAAGCACAGGA 2564 GACCGCATATACACCTGATGGGCC GGCCCATCAGGTGTATATGCGGTC 2565 GTAGGCCCGTCGTTAACCATCTCA TGAGATGGTTAACGACGGGCCTAC 2566 CGGCTCGCGAAATGGAGTTTAGCC CGCTAAACTCCATTTCGCGAGCCG 2568 TATCAAATCGTTTGCACGCGTACT TATAGCGGTGACAAAGCCGATCAGC 2569 TTGGCCAGGATCCCTAGGCGTACT AGGCGTTCGCCAA 2570 AAGTCCTGAGGCCGTTCGGTTTCT AGAAACCGAACGGCCTCAGGACTT 2571 ACTCCGGACATCTCGGCCAGAGAT ATCTCTGGCCGAGATGTCCGGAGT	2561	CCATGAGTGTTTCGGGACATCGTA	${\tt TACGATGTCCCGAAACACTCATGG}$
2564 GACCGCATATACACCTGATGGGCC GGCCCATCAGGTGTATATGCGGTC 2565 GTAGGCCCGTCGTTAACCATCTCA TGAGATGGTTAACGACGGGCCTAC 2566 CGGCTCGCGAAAATGGAGTTTACGC CGCTAAACTCCATTTCGCCAGCCG 2568 TATCAAATCGTTGGCACGCGACTA TAGTCGCTGCCAACGATTTGATCAGC 2569 TTGGCCAGGATCCCTAGGCGTACT AGTACGCCTAGGAGTCCTCGCCAA 2570 AAGTCCTGAGGCCGTTCGGTTTCT AGAAACCGAACGGCCTCAGGACTT 2571 ACTCCGGACATCTCGGCCAGAGAT ATCTCTGGCCGAGATGTCCGGAGT			
2565 GTAGGCCCGTCGTTAACCATCTCA TGAGATGGTTAACGACGGGCCTAC 2566 CGGCTCGCGAAATGGAGTTTAGCG CGCTAAACTCCATTTCGCGAGCCG 2567 GCTGATCGGCTTTCACCGCTATA TATAGCGGTGAAAAGCCGATCAGC 2568 TATCAAATCGTTGGCACGCGACTA TAGTCGCGTGCCAACGATTTGATA 2569 TTGGCCAGGATCCCCTAGGCGTACT AGTACGCCTAGGGATCCTCGCCAA 2570 AAGTCCTGAGGCCGTTCGGTTTCT AGAAACCGAACGGCCTCAGGACTT 2571 ACTCCGGACATCTCGGCCAGAGAT ATCTCTGGCCGAGATGTCCGGAGT			
2566 CGGCTCGCGAAATGGAGTTTAGCG CGCTAAACTCCATTTCGCGAGCCG 2567 GCTGATCGGCTTTCACCGCTATA TATTAGCGGTGAAAAGCCGATCAGC 2568 TATCAAAATCGTTGGCACGCGACTA TAGTCGCGTGCCAACGATTTAGTA 2569 TTGGCGAGGATCCCTAGGCGTACT AGTACGCCTAGGGATCCTCGCCAA 2570 AAGTCCTGAGGCCGTTTCT AGAAACCGAACGGCCTCAGGACTT 2571 ACTCCGGACATCTCGGCCAGAGAT ATCTCTGGCCGAGATGTCCGGAGT			
2567 GCTGATCGGCTTTTCACCGCTATA TATAGCGGTGAAAAGCCGATCAGC 2568 TATCAAATCGTTGGCACGCGACTA TACTCGCCAACGATTTGATA 2569 TTGGCGAGGATCCCTAGGCGTACT AGTAGCCTAGGGATCCTCGCCAA 2570 AAGTCCTGAGGCCGTTCGGTTTCT AGAAACCGAACGGCCTCAGGACTT 2571 ACTCCGGACATCTCGGCCAGAGAT ATCTCTGGCCGAGATGTCCGGAGT			
2568 TATCAAATCGTTGGCACGCGACTA TAGTCGCGTGCCAACGATTTGATA 2569 TTGGCGAGGATCCCTAGGCGTACT AGTACGCCTAGGGATCCTCGCCAA 2570 AAGTCCTGAGGCCGTTCGGTTTCT AGAAACCGAACGGCCTCAGGACTT 2571 ACTCCGGACATCTCGGCCAGAGAT ATCTCTGGCCGAGATGTCCGGAGT			
2570 AAGTCCTGAGGCCGTTCGGTTTCT AGAAACCGAACGGCCTCAGGACTT 2571 ACTCCGGACATCTCGGCCAGAGAT ATCTCTGGCCGAGATGTCCGGAGT			
2571 ACTCCGGACATCTCGGCCAGAGAT ATCTCTGGCCGAGATGTCCGGAGT	2569		
2572 CCAAGGGGAACACAGGATCGTAGA TCTACGATCCTGTGTTCCCCCTTGG			
	2312	CCAAGGGAACACAGGATCGTAGA	TOTACGATCCTGTGTTCCCCCTTGG

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								_
Seq. ID	No.	Decoder	Sequence	(5'-3')	Probe	Sequence	(5'-3')	
2572		атаааат			amman.			_
2573 2574			AAATCCGCCT FCTCGTCCAT					
2574			CCAGTGCCA					
2576			TTTTCCAGGG					
2577			IGCTGGAGCG					
2578			CTATGACGAT					
2579			GCTTTTAAGA					
2580			PACCGTTCTA					
2581			GCTGGGTTC#					
2582			CACACAGGCA					
2583			GTCCCCATT					
2584		ATACTCG	rcgacgaga <i>a</i>	GCGGAAA	TTTCC	CTTCTCGTC	GACGAGTA:	т
2585		GCAGAATO	STGTTGTCTT	CGCAGCC	GGCTG	CGAAGACAAC	CACATTCTG	С
2586		CACCATGO	CCTTCATCTT	GGCCTAG	CTAGG	CCAAGATGA	AGGCATGGT	G
2587		ACTCTTC	AACGCCAGGT	TAAGCCA	TGGCT	PAACCTGGC	TTGAAGAG	т
2588		GCGACCT	GCGGCGTGTG	TATTCTC	GAGAA'	FACACACGCC	GCAGGTCG	C
2589		TCGGTGT	ATGCACCCTT	TCTCCAT	ATGGA	GAAAGGGTGC	CATACACCG	Α
2590			AATCTTGCGG					
2591			IGCTCCCGGC					
2592			ACACCACGTO					
2593			ITGTCAGACG					
2594			IGCTCGCTGT					
2595			CGCGGGAAAG					
2596			CGGGCGTCTA					
2597			CACCCATGCT					
2598 2599			GGCCTGTCAA AGCCTTTGCT					
2600			ATAGCCTTTGCT ATAGCGTTAC					
2601			CGCGCGAACG					
2602			AAGCAGTCCA					
2603			CATCCAATGO					
2604			TTGGTAATTT					
2605			GGTAGTTTGA					
2606		CAAGCACA	AAGCCCATGA	AATTTCA	TGAAA	TTTCATGGGC	TTGTGCTT	G
2607		CGGTACAC	GCGGATAGCC	AAGGATA	TATCC	TGGCTATCO	GCTGTACC	G
2608		CCATGCT	CTTCGCTGCA	GCATACT	AGTAT	GCTGCAGCG <i>I</i>	AGAGCATG	G
2609		CGCGGCA	AAGATTAATT	CCCGGCG	CGCCG	GAATTAATO	TTTGCCGC	G
2610			CGTCCGGGTT					
2611			GGAGGATGTG					
2612			GGGGTGGCT					
2613			ATGATCACGA					
2614			GCGAAGCCTT					
2615 2616			CATCTACGGC AGCTCTCGC <i>A</i>					
2617			ACGCCACATO					
2618			CTGCCTCGAT					
2619			AATTTCGGAA					
2620			GATCAGATAC					
2621			CTAGCGCCAG					
2622		TGTGGAC	CTAGAAAATT	GCCAGCC	GGCTG	CAATTTTCT	'AGGTCCAC	Α
2623		GAATAATO	CATCGCGGTC	CTCATGG	CCATG	AGGACCGCG <i>I</i>	TGATTATT	С
2624		GGGATTG	GCTCTTGGTT	GGAAGAA	TTCTT	CCAACCAAGA	GCCAATCC	С
2625		ATTGTGC	TTCCTCGAAC	TGGGAAA	TTTCC	CAGTTCGAG	AAGCACAA	Т
2626			CCCCGTAAGT					
2627			CGACGGTGCA					
2628			FCACAGTGCA					
2629			AGGCGCGAAG					
2630			CGTCGCGATC					
2631			CGCGAAGTGT FGCCCGATC <i>A</i>					
2632 2633			TTCTCAACGO					
2634			CGTATCCCGC					
2635			CAACTTAAAG					
2636			GCAGTCGATC					
2637			IGGTCGACAG					
2638			ACGCCCTCAG					
2639			GCCGAGGTCC					
2640			GTGACGAAGG					
2641			GCGGTGCTTG					
2642		GGAGATTO	GACTTCGCGT	TTCACCA	TGGTG	AAACGCGAAG	TCAATCTC	С
2643			AGAAGGTTCG					
2644			GCATTCTCGG					
2645			GAACCAATCO					
2646		TGCTCTTC	GTGGTCACTC	GAGAGGA	TCCTC	rcgagtgaco	:ACAAGAGC	A

	TABLE 2-conti	nued
Seq. ID No.	Decoder Sequence (5'-3')	Probe Sequence (5'-3')
2647	${\tt TTGGGAGCACGGTTACCGCCTGTG}$	CACAGGCGGTAACCGTGCTCCCAA
2648		${\tt CGAAACTACCGTTAGCTCGCGTTG}$
2649		AGGTGAAGGTGAGCGCTCAGCGTT
2650		TTGAAGCCTCCAGATCTACGACGG
2651		GGTTACAGTGTGCCCATGCCATCC
2652 2653		GGCGTGAAGGATATCTACGAGCGA GTGTTTTGGACGCGGTATTGCTCC
2654		TGGGCAGCGCCTAAGTCTGAACAA
2655		AGGACAGTGGAAAGAGTACCGCCG
2656		CTCTGGCACGTGGGCAATCGTCTT
2657	AGGTGAGCGCAGGCATATTGCAGT	ACTGCAATATGCCTGCGCTCACCT
2658		ACGGCTTTGCTGTACAGGCCCGAG
2659		GATCATAGGCAGCACTAGCGCGCA
2660	CCATCCTTTGCCTTGAGGGTTGGC	
2661 2662		CCCTGTCCGTCTTACGCTGTTGTT AATATTGTGAGCCTCGACCGCCTC
2663	CGAGGTTAGACGCCTATGACCCAC	
2664		TTGCTGCGCCCGGTATAGCAAGTT
2665	${\tt CGCGGTGAATCGCATACACAGCGC}$	GCGCTGTGTATGCGATTCACCGCG
2666		AGAGCCATATGGCTTGATTCGGTG
2667		GGCAGCGCCTAGGATAGCTGTTAA
2668		ATGCGGGGTACACTTCGCGCTTCT
2669 2670	TGCATGGTATTTGCGTGCGATAGG	CCTATCGCACGCAAATACCATGCA TTTCCATCTCACATAGGTCCGGCC
2671		GCTTGGGATCAGGACTCAGGTTGA
2672		ACACGCCTCCCTGAACGGTAAGCA
2673		AGGTGGCTCATCGCGTAACTCTCC
2674	${\tt CGGTATGCGGTGTACAGCTTTCGT}$	ACGAAAGCTGTACACCGCATACCG
2675	GTAAGCCGGGTCTCGTGTCGCCGT	ACGGCGACACGAGACCCGGCTTAC
2676		TAGGTCGGGGCGTTCGCACTACGC
2677 2678		CGAATTTGACGTAAGCCGCGAGGA CCTCCTCTCCCGCTTTGAACGTCG
2679		ATCTCAACATGTCGGGGTGCCTCG
2680		CTTGTCCGACGCGCACGAAATAG
2681		CAGTTGACACGTCACTGAGCAGCC
2682	${\tt ATCACTCGTGCGTACCCGACCGTC}$	${\tt GACGGTCGGGTACGCACGAGTGAT}$
2683		TTCGCCACGGTATAGGACATCTCG
2684		TTTCATTTATGGGGCTCGGTGTGA
2685 2686		CGCTTTTGCTCGAGACACGTAGCT CGCCGCTGAAAAAACTCGCCCTGA
2687		CGGGGCAAAAATAGACAGAACGAA
2688		GTAGGCTGGATCCTGGGCATACCA
2689	TCTCAGTCGTTAGGCCAATGGCGG	CCGCCATTGGCCTAACGACTGAGA
2690		GCCGATCGCTCCACGGTGATCTTT
2691		GCATCACGAGTGCAAGTCCTGCTA
2692 2693		CAGCCTTGAACGGTACCGTGGGCA CATTACTTAGGGCGACGCACCTCA
2694		GGGTTGCGGGTTGTAACCCTTGCT
2695		TTGTGGCGAATACTGGCTGTTGTG
2696	GGCAACACCATACTCGACGAGCTC	GAGCTCGTCGAGTATGGTGTTGCC
2697		${\tt AGGGGCTAAATTGTCAATCCAGCC}$
2698		CTGACGCGTGTAGCATTTCTCACG
2699		AAGGAACAAAATGGGGCAGATGCG
2700 2701		CACCGTTCTGCCGACTAGGCCGAC AGCACATTTTTGGAAGGTGAGGGA
2702		CGGTCTGTTCTCATGTTCTTGCCC
2703		TCTACGCAAGTCGTACCAGGACGA
2704	TGGCGGTTGCATGTGATGATCAAG	CTTGATCATCACATGCAACCGCCA
2705		CGGACGGTTTTTACTCACGCGAGG
2706		CTGGCCGCATTCTGTGGCGGAAGT
2707 2708		AACGGGGCTACCCAAGCTCTACAC ATGTGTGTTAACTCGGATGCTGCG
2709		ACCAGCGGATCATCCCAGGCTCAT
2710		AAGCATGTCGGCACTTATGCCAGG
2711		CGTCCGTCGTAGTTTTTCATGCGC
2712		${\tt AGACGCTCCCATCGACCCATCTTT}$
2713		GATAAATCCGCTCGTGCCCAGGAT
2714		TCGCGTAACTATCAAATGCGGTGA
2715 2716		ATAACACCAGAGTCCGCTCCACCA TGGGGCCATTGTTTTTTCATTGTG
2717		GTTGGTACCACAAGCGCGGCAAGG
2718		TCTTTCGTGTGGCAAAGGTCTCGG
2719	ACCGCGGTGTACACCTGAGCAGGC	GCCTGCTCAGGTGTACACCGCGGT
2720	GTCGTACGCTTACCGCAGCGGAGA	TCTCCGCTGCGGTAAGCGTACGAC

				IADDE	2-001101	IIIueu	
Seq.	ID	No.	Decoder	Sequence	(5'-3')	Probe	Sequence (5'-3')
2	2721		TCGTAATT	TGACCGAC	ACACGCAG	CTGCG	IGTGTCGGTCAAATTACGA
	2722						CTCAGGGTATCCGTCTAGG
2	2723		AAGCGACA	AGCAGAGGT	TCAGTCGC	GCGAC!	IGAACCTCTGCTGTCGCTT
2	2724		GCGTGGA	CGATATCAC	CTGGGCGT	ACGCC	CAGGTGATATCGTCCACGC
2	2725		GTCGGAGA	AGCCAGTGG	TACGGCTT	AAGCC	GTACCACTGGCTCTCCGAC
2	2726		TATCCGCA	ACGGTATAG	CAGTTGCA	TGCAA	CTGCTATACCGTGCGGATA
2	2727		CATCAGTO	CGGGCTACC	TTCAGCCT	AGGCT	GAAGGTAGCCCGACTGATG
2	2728		CGGATTA	ATGCCTTTC	CTCGGAAT	ATTCC	GAGGAAAGGCATTAATCCG
2	2729		TTCGTCGT	GCCAAGCT	AATGCAAG	CTTGC	ATTAGCTTGGCACGACGAA
2	2730		GGCCGAGA	ACCACCAGT	AACAGGTT	AACCT	GTTACTGGTGGTCTCGGCC
2	2731		CGCGCGG	AAGCATTGA	AGTTACTA	TAGTA	ACTTGAATGCTTCCGCGCG
2	2732		TCGGCTTA	ACCGCTTCG	TCTGACTT	AAGTC	AGACGAAGCGGTAAGCCGA
2	2733		GACTGACO	STCAAGGCA	AGCAACAC	GTGTT	GCTTGCCTTGACGTCAGTC
2	2734		AGAGGAAG	GAGGGGCT	GTGACAGA	TCTGT	CACAGCCCCTCCTTCCTCT
2	2735		TTCCAATO	GCGAGAGAT	GGCAGGCT	AGCCT	GCCATCTCTCGCATTGGAA
2	2736		AAATGGGG	TGCTTCGA	ATATGTCG	CGACA!	PATTCGAAGCACCCCATTT
2	2737		GCTGTCGC	SATTATTGC	ACGCCTGT	ACAGG	CGTGCAATAATCCGACAGC
2	2738		CCGACTTT	GTTTATGT	TGCTGGCG	CGCCA	GCAACATAAACAAAGTCGG
2	2739		GCTGCGAT	TATAACCCG	TCCCAGAA	TTCTG	GGACGGGTTATATCGCAGC
2	2740		TGAGCTG	GCGTCAAC	TCCGAAGA	TCTTC	GGAGTTGACGCCCAGCTCA
2	2741		CCCAAGC	ATCCTAAAT	CTCCCTCG	CGAGG	GAGATTTAGGATGCTTGGG
2	2742		CGACAGC	ATCCACAT	GCATTCTT	AAGAA!	TGCATGTGGATTGCTGTCG
2	2743		TGAATGGT	CGGGAAAC	CAATGCAT	ATGCA	TTGGTTTCCCGACCATTCA
2	2744		CTTTGCAT	CGAGATGG	GGGGTAGC	GCTAC	CCCGCATCTCGATGCAAAG
2	2745		TCCATTTC	CCTCCGCAA	CTCTCAGG	CCTGA	GAGTTGCGGAGGAAATGGA
2	2746		CCACTACO	CCATCCTG	ACAACGAG	CTCGT	IGTCAGGATGGCGTAGTGG
2	2747		TAGTAAGG	CCAATGTA	CGCCGTCC	GGACG	GCGTACATTGGCCTTACTA
	2748						CAGGCCCCATATGCATGAC
2	2749		ACCGGTAC	BACGTTAGC	GGGTTCAA	TTGAA	CCCGCTAACGTCTACCGGT
2	2750		TTGGTTC	AAACGGCCA	CACGTCTC	GAGAC	GTGTGGCCGTTTGAACCAA
2	2751		GACACAA	ACTGCAAGG	GAGGCATG	CATGC	CTCCCTTGCAGTTTGTGTC
2	2752		CTCGAGC	CTGTCATC	ATATCGGC	GCCGA	TATGATGACAGCGCTCGAG
2	2753		GCGGCTA	AGGCACAAG	TAGACGTG	CACGT	CTACTTGTGCCTTAGCCGC
2	2754		ACAGCCTA	AATGGCGC	AAGACCGA	TCGGT	CTTGCGCCNTTTAGGCTGT
2	2755		CCGATGAT	GTAAGCCG	TCGGCCCT	AGGGC	CGACGGCTTACATCATCGG
2	2756		AGGAGCAZ	AACAAACGC	CAGTGACA	TGTCA	CTGGCGTTTGTTTGCTCCT
2	2757		ACGAATTO	GGTAGCCG	GACTGAGA	TCTCA	GTCCGGCTACCCAATTCGT
2	2758		CTGTTCC	AGTTCGGCA	AGTGCGGC	GCCGC	ACTTGCCGAACTGGAACAG
2	2759		AGACAAGT	CAGGAACG	CGTTTCCG	CGGAA	ACGCGTTCCTGACTTGTCT
	2760						GCGTATCTGGCCGTCGTCT
2	2761		AGGAAGCO	CTTCTTCC	GGTTCTTC	GAAGA	ACCGGAAGAAGCGCTTCCT
2	2762		GATGGAC	CAAACACA	AGGCGATC	GATCG	CCTTGTGTTTGCGTCCATC
	2763						ATGCGGAGACTGCTATGCG
	2764						CTGTTGCACACCGGAACCA
	2765						TTCTGGAGGTGGCATACGG
	2766			AACCCCTCG			ICCCGAGGGGTTCCTTTAC
	2767			SCTCGTTAA			ATTTTAACGAGCATCAGGC
	2768						TCTCATGGTCCAAGTGCGA
	2769						CTCTTGCCCAGCCTGAGAA
	2770						CCCAGCATCCCCAGGTCCG
	2771						GCCAACCCTATCGGCTCGA
	2772						CGTGTGTGGGACACACGTA
	2773						GCGAAACGCGAATTTCACA
	2774						ITTTTTTGGAGCATTGCAA
	2775						AGCCACAGCCATGATGAGA
	2776						CCAAACCAAGCGGTGTAAT
	2777						ACTCTGTGCATTGCACGGC
	2778						ICCGACACGGTCTGATCTC
	2779						GTCGCATCAAGATAGGTGG
	2780						AGACATAAACGGCGATCGG
	2781						GTGCCTTACCGTGATTTTC
	2782						ICGTTGGGAAGCGAGAATC
	2783						GAGACTGCCACATTTCACA
	2784						GATGAGGCACGCAGGATCG
	2785						ACCCTCGCCCACTTGAGGG
	2786						ACACACGAGGCGGAGGCGA
	2787						CCAATGAGCTGAAAGCGAA
	2788						ICCGCTTGTTCAGATTACA
	2789						GCGCTCAAGAAAGATTCCA
	2790						GCGGTTAAAGATGAAAGCC
	2791						PTAGGAATGGCTCGGATCA
	2792						TAGGACATCACGCCTACCA
	2793						GGCCTTCTTACCGATGCCT
2	2794		CGCCGCGI	AGACGATCC	TTATT	AA'I'AA'	PAAGGATCGTCTCGCGGCG

Seq. ID	No.Decoder Sequence (5	'-3') Probe	Sequence (5'-3')
2795	ACATGGACGAAATTACGCCC	CGTCA TGACGO	GCGTAATTTCGTCCATGT
2796	ACAGAAAGGTGGGGAGCCTA		
2797	AGGCTTGCGAACATGGGTAG	GTGAC GTCAC	PACCCATGTTCGCAAGCCT
2798	GCGTGGGCCTTGCTCCTGT	TTAAC GTTAA	ACAGGAGCAAGGCCCACGC
2799	GAATACAGAGCGTCCGATG		
2800	GCGACTCTGTAGGGAGCGC		
2801	GGTGCACTCATATGCGTCGC		
2802 2803	CTGTCCCACGGGGAAACCTT TGGCTTACTGTCGCAATCTA		
2804	GCACTCAGTTTCCGGTATC		
2805	GTGAGGTTCACGTAAGGCAG		
2806	GTAACGCCTTTGTCCCCAG	CGTAT ATACGO	CTGGGGACAAAGGCGTTAC
2807	GCATTGATATGGTCGGTCTC	CGCCT AGGCG	AGACCGACCATATCAATGC
2808	GTGGGTTTAAGTGACAACG		
2809	CAAAACCCTGCCGAAGATG		
2810 2811	TCCGAGGAGACTGAACCTGG		
2812	CGGGGAAGAACGGATTCGCT TGGTTAGCTTATGTCGGAGG		GCGAATCCGTTCTTCCCCG
2813	ACGCGTCGATGAACTAAGG		CCTTAGTTCATCGACGCGT
2814	TTCTCCTGACGAGTACGCA		
2815	TCCGCGGTTGCCGGTTTGT:	ragga TCCTA	ACAAACCGGCAACCGCGGA
2816	TGGCGCATCTTTCAGGGGA	GATG CATCA	FCCCCTGAAAGATGCGCCA
2817	TCTTTGGTCCTTGGTGTTT		
2818	GAGAACTCCCGCTACAAAG		
2819 2820	TTAACGTGGGAACCGTTGG: GGGACACCATCCTTGGGTT:		
2821	CAACAAACCGCCTTGGGAAC		
2822	TTGAAGGCCACCGATACTGA		
2823	TCGTAATAGAACTGCGCCC	AATGC GCATT	GGCGCAGTTCTATTACGA
2824	GGCACGTTGCCCAAGTTGG	ATCCA TGGAT	CCAACTTGGGCAACGTGCC
2825	ACATAGCTTGGCCGGACAC		
2826	CTTGCCGCCTTGCGAGTGG		
2827 2828	AATGGCTCGCCAGATACCGC CAAAAGGCGTGTCCGAACT		
2829	CGTCCACTTAGGTGGAGATA		
2830	GAGCCTCTTCGTCCTGAAGA		
2831	AACATCAAGCGGCAATCTC		
2832	CGTCCTGACATTATTAGCGC		
2833 2834	TGTGCAGACCCTAACGACCT TTAGGTCGGCCTAGACCCTC		
2835	TCACATCGCTTAACTGAGC		
2836	AGACCTTCCCACGCGAGATO	GCTAC GTAGC	ATCTCGCGTGGGAAGGTCT
2837	TTCTTGCCAAAATGTGTCC		
2838	CAGTTTTCATTGCAGCGAA		
2839 2840	GTGCCGATCCCGAGACAAG: CATCCGGCCTCAGTGATTC:		SAATCACTGAGGCCGGATG
2841	TGCTGGAAGCCACAAACGT		ACGTTTGTGGCTTCCAGCA
2842	GAACGGCCAGGGGACAACT	ATCGT ACGATA	AGTTGTCCCCTGGCCGTTC
2843	TCATCTAGGTCGAAGCGCAA		
2844	TTTGGTTACCAGCACCCATC		
2845 2846	GACAACAGTCTGTCCGCCAC GCCAACAGGAGATGCTTGCA		
2847	CTAAGGACGCATTGACCCC		
2848	GGTCGCGTAGTGAGTCAGAC		
2849	TTACCTCATGAACCCTTCG	CGGCG CGCCG	CGAAGGGTTCATGAGGTAA
2850	TATACAGCATCGTCGCCGGG		
2851	GCTTAGTGGCGTCTTCGTC		
2852	TGCACTCCGCAACCTTGTG		
2853 2854	AACCCGTCATGCCGACTCCA AGCACTAGTGGCGTGCGACT		
2855	TAAAAAGTGCCGCTAACCA		
2856	CGCGGAATATTTGTCGTCC		
2857	TTCTGCTATGCGTATGGGG		
2858	CGAACTACTGCGTCAGCCTC		
2859 2860	AGATGACGAATTAGCGGGG: AATAACAGTGGCAATGAGC		
2861	ATATGTTGATTCCCGTGCT(		
2862	AGAGTGGGCACCACCAGGC		
2863	AGGCCTGGGTTTCTGCGTC	TTAGT ACTAA	GACGCAGAAACCCAGGCCT
2864	CGGACGTGACAAACGGACA		
2865	CAAGTGTTTCGGCCCAACTC		
2866 2867	GAACCCTTATCGGGATAGGG CAGGACGATACCAAGCAGA		
2868	GCGTCTTGTGATTCTGCCC		

	TABLE 2-conti	inued
Seq. ID	No. Decoder Sequence (5'-3')	Probe Sequence (5'-3')
2869	AAACAACCATCAATGTCGGGTCCA	${\tt TGGACCCGACATTGATGGTTGTTT}$
2870		GAGAGCCGCCAACTGGTCTTTACA
2871	GCGTTTTGACTCGGTGGTCAGTCC	
2872 2873		GCGTGTCAGCGGGAACCTAGGTAA
2874		
2875		
2876	CAACGATGGAATTGTCTCCTTGGG	${\tt CCCAAGGAGACAATTCCATCGTTG}$
2877		
2878		
2879 2880		
2881		GGGCCTCCTCTTAACCCTGCATTT
2882		ACAGCGGGAGAATCAGTCCTTGCA
2883	GTTTTCGGAACGCCGCAGAGTTCA	TGAACTCTGCGGCGTTCCGAAAAC
2884	CCCTCGATGGTTCATTGGGAAGAC	$\tt GTCTTCCCAATGAACCATCGAGGG$
2885		
2886		
2887 2888		TGAGGATAAAGGCACACAGGTGGA TGCGCTACAGCGGTTCACGGAGGA
2889		GCGGGGAAACCGTAAAAATCTCAA
2890		
2891	CCCGAACTTTGAGATCCGAGAACA	TGTTCTCGGATCTCAAAGTTCGGG
2892	TCACGCAGCTAGAGTCGCGTTACC	$\tt GGTAACGCGACTCTAGCTGCGTGA$
2893		
2894		ATTCGGCATCGGAGCTCTAAGCGT
2895		
2896 2897		TACGATGCACAGTTCTACCAGCCG
2898		TCCGCGTGGGAAGTACATTTCGAA
2899		
2900	CGTTTGGTTGCTTCAAGAACCGGT	ACCGGTTCTTGAAGCAACCAAACG
2901	CATACTTGGTTGTTGTGCCCACGC	${\tt GCGTGGGCACAACAACCAAGTATG}$
2902		
2903		
2904		
2905 2906		ACTCGATGCGCGGCATTTATATTG
2907		TTCTCGGGGACTGCTGATGAAGAA
2908		
2909	CCGACTTTCGTCCACGATTCCTCT	AGAGGAATCGTGGACGAAAGTCGG
2910		
2911		
2912		
2913 2914		
2915		TCTAATCACACCAAACTTCGCCGG
2916		GACTCAGCACAATCTGGCGGTGCA
2917	ACATGTGAAGTGAGTGCCGTCCAA	TTGGACGGCACTCACTTCACATGT
2918		AGCGTGGCTAATCCCCTCCAGAGG
2919		CCGTTGCCAGTGACATGGCTATTG
2920		CGAAAGAACGTTGGAACCATGGGT
2921 2922		TTTGGAGGATGCCAAGACCAGATT TTGCTTCAGCATGCACCGGTATAC
2923		CGGGTCGACTCGAACCAGAACACT
2924		GTCCTCGTGTGTGTCGAATACCCG
2925	AGTGCAACAGAGCGCTTGGTCACG	CGTGACCAAGCGCTCTGTTGCACT
2926		${\tt CACCGGCACCAAACTATAGGTGCA}$
2927		CTCGAGTGTCCTGGTACGTGAGCA
2928		CGCCTGTCGTTCGAGGTGTGGACT
2929		TAGCGCTCTTTGACCAGGTCGGCG TCGGAAAACGACAGGCCCTTAGGC
2930 2931		GAGACCGGAACATAAGCACGCACA
2932		GATTTTTGTTACGGCCAACGGTTG
2933		CGAGATGGTACGCCTTGATTCTCG
2934		${\tt CCATTCCCTGGAGGCTGCCTACGC}$
2935		ATTGGTCTTGGCGAAAACACCATC
2936		GTGGGCAATTCTGTCCCTAGCTTG
2937		GCCACGAACGGTTTCGCCTATTTA
2938 2939		ACATGAACACATTGCGGGTCTTGA TTGTGCAAAGAGTCTACCAGCCGC
2940		CCGTTTGGTTCAGGTTTACGCCTG
2941		TGATGAACCTCAGCACAGATCGGC
2942		${\tt CGCGTGATATTGCGACGCGATATC}$

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TABLE 2-continued

Co	TD	Ne	Dogodo	Coguese	/E! 2!\	Duchs	Cominer	/E! ^	2 ' \
Seq.	ID	NO.	vecoder	Sequence	(5:-3:)	rrobe	sequence	(53	, )
	2943			CGATTAAGCC					
	2944			CAGATTTGTG			CACACAAATC		
	2945			CCCGTATTC			TGAATACCG ACCAATGGC		
	2946 2947			IGGCCATTGG CAATCAGGGT			CACCCTGAT		
	2948			AGGGAGTCTT			CACCCIGAT		
	2949			GTAAGGAAA			TTTTCCTT		
	2950			CAGGCACCTC			CGGAGGTGCC		
	2951			GGCCACGTG			TCACGTGGC		
	2952 2953			CGAGAGCGC CGCCGAAATG			AGGCGCTCTC CCATTTCGG		
	2954			CCGCTATAG					
	2955			CACGCATGA			TTCATGCGT		
2	2956		CTTACGCC	TCCAATGAC	TGCCACC	GGTGGC	CAGTCATTGG	ACGC	TAAG
	2957			TAGAACTCGA			SATCGAGTTC		
	2958 2959			SAAACTAGTG			CCACTAGTT		
	2960			CAACCGACAC GCGCTACCCA			AGTGTCGGT GTGGGTAGC		
	2961			CCCGACAAT			TATTGTCGG		
	2962		CCAATATT	TACGGCCTG	ATCAGCG	CGCTGF	TCAGGCCGT	'AAAT <i>I</i>	ATTGG
	2963			CCCTTACTO			CCAGTAAGG		
	2964			GGCAGGCTT			CAAGCCTGC		
	2965 2966			BAGGCTGCAA FTCGCCACCA			CTTGCAGCC		
	2967			ACCGATGCAC			TGTGCATCG		
	2968			CAATCGCCT			GAGGCGATT		
2	2969		AGGTTGGT	TAGGAAATC	GAGCGCT	AGCGCT	CCGATTTCC	TACC	AACCT
	2970			CACTGTGGTC			TGACCACAG		
	2971			TACGACACGG			ACCGTGTCG		
	2972 2973			CCGCAATGT CTCGACCGCT			CACATTGCG GAGCGGTCG		
	2974			CTGCTGGCAT			TATGCCAGO		
2	2975		TCTTGGGG	CTCGGTAGTT	CAGCACT	AGTGCT	GAACTACCG	AGCCC	CAAGA
	2976			CGAGCCCAT			TATGGGCTC		
	2977			GCATCAACG			CCGTTGATG		
	2978 2979			CCGATGTGT CGCTGCTAAC			GAACACATCO AGGTTAGCAG		
	2980			CTCTCCACC			TGGTGGAG <i>P</i>		
	2981			CACCGGCTT			GAAGCCGGT		
	2982			ACCCGCTCTG			CACAGAGCGG		
	2983			CTGTTTCATC			CGATGAAAC		
	2984 2985			TGTTTGGGG TTCACGTGA			ACCCCCAAAC CTCACGTG <i>A</i>		
	2986			AGTCGATTGC			GGCAATCG <i>A</i>		
	2987			CGGAGACCGC			TGCGGTCTC		
	2988			ACCGGTGCAC			AGGTGCACCG		
	2989			GCATGCAAG			ACTTGCATO		
	2990 2991			PAGCTCGAGC CTGCCCGAGC			AGCTCGAGC TGCTCGGGC		
	2992			ATCTCTTGT			GACAAGAGA		
	2993			CACGCCGAA			ATTCGGCGT		
	2994			SACGTTTACA			ATGTAAACG		
	2995			ACCTGAGGCC			GCGGCCTCAG		
	2996 2997			TTCAATGGAG ATTCGCCGCC					
	2998			CCATGGAAT					
	2999			CACGAAGGC					
;	3000		CACCCTAT	GCGTCTCC#	ATTCCTG	CAGGA	TTGGAGAC	CATA	GGTG
	3001			CATCGCTGAG					
	3002			CACGCTCACT AACCTCCTCT					
	3003 3004			AACTTGGCCG					
	3005			CAACAGGCA					
;	3006		CTTGTCAC	CGAATATTC	CCAAGCG	CGCTTC	GCGAATATI	CGTG	CAAT
	3007			GAAACACGG					
	3008			ATGGGCGCCC CCAAGCGCCT					
	3009 3010			CAAGCGCC1 AGGCACCGCT					
	3011			ATTGCCAGT					
	3012		AGTCGACO	CCCAAGGCAA	CTGGGTC	GACCC	AGTTGCCTTG	GGGTC	CGACT
	3013			TAGCTCGAC					
	3014			ACTTGACGGT					
	3015 3016			GTTTGAACG AATCGGGTCT					
•					SOUTH	11000			

	TABLE 2-conti	inued
Seq. ID	No.Decoder Sequence (5'-3')	Probe Sequence (5'-3')
3017	GATTTTGGCGTCTCATTGCGTGAT	ATCACGCAATGAGACGCCAAAATC
3018		TAATTGCGTTTCCTCCCTATGGCA
3019		GGACACCACTAACATGGGCACCTC
3020 3021		TGGTGGTCGTATGACCGCTAAAGC CGTTAATCGGATTGTTGGTAGCGG
3021		CTTTCTCGATGTGGCCAGATCCTC
3023		CGGCAAAACGTGGTACCAAACGAG
3024	AATACACGCGGCGTAAACAGACGA	TCGTCTGTTTACGCCGCGTGTATT
3025		GCCACTGTCATTTGGCCCATGACA
3026		TCGTACACGGGTCGGAAGTGCTGT
3027 3028		GGCAAAGCTGTGCTCTTTACGGAG GAGGACCGATCCCTACCTGTTCGT
3028		CGATGGCGCGGTAAGGTGGATCCA
3030		CTTGCCGCGCCGCTATTTGATACT
3031	GAATTACATTGTGGATGGAGGCGG	CCGCCTCCATCCACAATGTAATTC
3032	CTCCTCGGGGAGTCGAGGAGTACG	CGTACTCCTCGACTCCCCGAGGAG
3033		ATTGGTGGGAGTTGGCTCGACACT
3034		GCTGTGGCCAAACGGATGTCATTT
3035 3036		CCAGTTCGATGGCGATATGATTCG TGCGCACCAAGCGAGTGCATTATA
3030		CGCCATAATTACCATCTGCTTGGC
3038		AGTTCTACGTGCTCTTCCCGCGTG
3039		CGCTGTTCTCCAAATTCTCGGGTA
3040	TGACGGCAAACTGTGGCATCTATC	GATAGATGCCACAGTTTGCCGTCA
3041	CACAGTGTTCCAGCCCTTGACGAT	ATCGTCAAGGGCTGGAACACTGTG
3042		CCAACTTTCATGTGTGGGCGGGTA
3043		CGTCGCCGAATCTTAAATATGCCA
3044		CCCGCTACCCGTTCTTTTTCAGT CAATGACCACCTATTGCGGTCAGA
3045 3046		ACGAGAGAGGCCCGCCAAAAAGT
3040		CGGATCGCGCAATGATCTGGGCAG
3048		GCCGGTTAAAGCATTTAACCTCCG
3049	AGGCGTCTCCAAACGTCCTTCTGT	ACAGAAGGACGTTTGGAGACGCCT
3050	AGATGCTATCCTGAGTGGGCCTGC	GCAGGCCCACTCAGGATAGCATCT
3051		CATCCCACGGTCTCTTCACCCTGT
3052		CGTCGTGTCGTCCGTTAGACAGTC
3053		ACCGGTTGTCGGGTCCTAACAGCT
3054 3055		AGAGGAAATGCCCACACTACGCAA TACATCAAGGAAAGAAGCGCGCAT
3056		CTGAATAGACGCGGACGCCCTTAA
3057		GGGCCGCGGTACAAGTTTAAAGGT
3058	AGGGATGCAGAGGCACCACATGTT	AACATGTGGTGCCTCTGCATCCCT
3059		TGCGGATGCTCATACGTCGAACCG
3060		AACCTCCATGTGACTATCGCCCTG
3061		ACATATGAAACGGGGCAGTCAAGC
3062 3063		TCGGGTAATTGCACAACCCCTTCG AATTTTGTCATTGCGGTGCGTTTT
3064		CGGTTGAGGGTCTTGTCCAGGAAT
3065		CCTCACCGCTAGCAGGCAGGTAGG
3066		TCCAATTCCTCCCCATTTACGAGC
3067	ACATGAAAACAGGCTCAATTGGGG	CCCCAATTGAGCCTGTTTTCATGT
3068		GAGACCTCAATCCATGTGCGGAAC
3069		TTCTTCTTCGTGGTATTGGGTGCC
3070 3071		AAAGATGGAGTTCGAAATGCCCCT CACCGACGTTCCTTTGTGATGATG
3071		GCTGCTGCTGACGGTGGGTCTTTA
3073		CTATGTGGTGCATTACGCCTGGGG
3074		TTCAACCACTAGCGTTCGACCTGC
3075	GGAACTTAGGAGTTCACGTCGCCA	TGGCGACGTGAACTCCTAAGTTCC
3076		GCCACCTCAGCTAGCCGTATCTGC
3077		GAACGCCGAGGCTCTAGGCCTGTG
3078		TAATGAACCTCATGCGCGCAAAAC
3079 3080		TAGTACTGCTGGCATCAGGCGCAA GCGGCAGTGGGAAAGCCTGATATC
3080		TTCATAGATCTCCGTCTCCGCGCA
3082		GTCCACTCTCAGCCAACACCAATG
3083		TATTAATGGTGCCCAAGTGCCGAC
3084		CTCCGTGGTGAGACACCGATCGAT
3085		${\tt CTATCGACACGGTGGAAGGCTACG}$
3086		CCCCTTTTCCTCAGACGGAGAGCG
3087		GCAATATATCCTTGGCTGGGGCGA
3088		GACGGCAGAGTTCCTTGCAAGAGA
3089 3090		TAACACCCTCCGTCTGTCCAGGAC GATTACGAGCCCGCTTAATTTGGC
3070	JCC/INITI/INGCGGGCTCGTAATC	III INCONSCICULIANTI I IGGC

	TABLE 2-conti	inued
Seq. ID No.	Decoder Sequence (5'-3')	Probe Sequence (5'-3')
3091	CCATTTGTTGACCGATGGGAGGGG	${\tt CCCCTCCCATCGGTCAACAAATGG}$
3092		TCCTGGATCGTGCTCTTTTGACCA
3093		GTGGACAGGGGCGTCTTAGTAGCG
3094 3095		CAGTGAATCCAAGCGGGAGGTATG TTGTAGATGACATTCCTTCCGCGG
3096		CGTCCTGTGAATGAATGTCCCGTG
3097		TTTTGTGCGGAGTGGGTGACTCCT
3098	TCATGACAGCGCACCCCATACCAT	${\tt ATGGTATGGGGTGCGCTGTCATGA}$
3099		CAGCACGATCGATAGTCCCCTACC
3100		CCGCTACGTGCGGTAGTGAGACAT
3101 3102		GCAGCGAACGAGTCGCTCCTCCGT GTCCGTCCACCGGCGACAGACTTC
3102		CGCTCGTCCGAATACACGTTACGG
3104		ACGATTGGTTAAGTCGCTTCCACG
3105		CTAGTGTGAGGCATAGCCCATGCC
3106		ACGAACGATGCTGAAATACGACCC
3107	AATGGTCGCGCAAACCGTAAGAAT	ATTCTTACGGTTTGCGCGACCATT
3108 3109		AAACGTTGGACGTACCGAATCCAG TTCTTGGCTACGGGTGTTTTTGCG
3110	TATGGATACGCTTTTGGACTGGGC	GCCCAGTCCAAAAGCGTATCCATA
3111		ACCAGCGTGAAGCGCGTTTGAAGC
3112	TACAGCCCGCTCTACCTCGCCACC	
3113	${\tt TCAACCGATGTCAAAATGCACGTT}$	${\tt AACGTGCATTTTGACATCGGTTGA}$
3114		TACCGCCCTACTTCGGAGAGAGCT
3115		GGAGCCAAGTCTCCATGTGTGCGT
3116 3117		TAGCGCCCCACTAGCTTTCAAGAA CACAGAATAGCCCAGCCGTGATTG
3118		ACTCTTTCACCGACGGTCGCCAC
3119		ACTTAACTGGTTCGGCATTCGACG
3120	TGCGTATTTGCATGCTCACAGCTG	${\tt CAGCTGTGAGCATGCAAATACGCA}$
3121		GCAGCCGTGCACAAACCAACTGCG
3122		CGATGCCAGTTTTCACGGAAAAAC
3123 3124		TCAAATCGTGGTGGAGGAACCTGT CGCAAGGACCTAAAAGCGCGCTAG
3124		CACCGGTTGATCCCTTTGATTTTG
3126		TGCCTGACTCACTGGGGTTACGTT
3127	TCAACCGGTGCACTTTAGAACGCC	GGCGTTCTAAAGTGCACCGGTTGA
3128		AGTATTCGCCTGCAACTTTGCGAT
3129		GTTGTGCAGCACCCAGGGACATAT
3130 3131		CCACCGCAGCACTACAAAGTGCCA CGAGCTTAGAAGGACGTCGTGCGT
3132		CGAAATCCCTATAGTGCACGTGGG
3133		GCAAGGATGACTGACCAAGCGCGG
3134	${\tt AGCGGCTCAGGGAATAACAACAGG}$	${\tt CCTGTTGTTATTCCCTGAGCCGCT}$
3135		ACTGGTTGCCTCCGATCGCGTTGT
3136		TGGGTTTCTACGGAGGCAATTGCT
3137 3138		CGATAGCAGGCGATGCCACGACTC TCGCAAGCGCAGTATTTGCATAGA
3139		CGGCCACACCGTAACTTAAGCTGA
3140		TTCTGATCCCTGTTCGACCTTGGA
3141	GTTAGGCTGGCGTCAATAGCGCTT	AAGCGCTATTGACGCCAGCCTAAC
3142		CGATGCCCTCTTCCTTATGACACC
3143		AGAAATATTGATCTAGCCCGCCGG
3144		TCGGGGCGTAAAACTTGACGTTAG CCGCAAATCGGAAAACTGTGCTGC
3145 3146		CAGTCATCCCTCCCCTTGCGTGCG
3147		CTTGTGACGTCCTTTTCGGCCCCG
3148		CTACCGGTTAGCCGTGTTGGAGAA
3149	TTACAGCCTGGCCCGAGGTAGTTG	CAACTACCTCGGGCCAGGCTGTAA
3150		TTCGATAACTCATGCTGCCCGAAA
3151		ACTTCGAAGCAGGGCGTCCAGTAG
3152 3153		TTGGTCTTTTCACGTCGGACGACC
3153		CCTGCGGAGAAAGAGCTCGAAAAC CTGTGACACTGGGTACCTTCACGC
3155		GTGTTGCGTCGAAGCGTTCAGAAA
3156		ACGGGCTAGGCGTGCTTATTAGCA
3157		$\tt CGCCGGAGCCACCACAATTAATTT$
3158		TGTCAGTGAGCCCGAGGATTGTAA
3159		GTTGCCCACGCCTTGTCCTTCAGC
3160 3161		ACCATTGCGAGGGTCTCCTATCCC TTCATGCGCAAGGACGTACTGCAA
3162		GTTCGCACCCAATCCAGTGATCAA
3163		ATCATCTCTCGCAACGTCTGCAGA
3164		ATCCGCTTCGATCCCTGCTAGACT

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TABLE 2-continued

Seq. ID	No. Decoder Sequence (5'-3') Probe Sequence (5'-3')
3165	GGGGTCCCGCAACAACTAATGAAG CTTCATTAGTTGTTGCGGGACCCC
3166	CAACCTCTTATGTGGTGTGCGCGA TCGCGCACACCACATAAGAGGTTG
3167	CTCGCTGGGTTGCTGGAGTAGCAC GTGCTACTCCAGCAACCCAGCGAG
3168	CGTTGTATTGTGCAACGCGAAGTT AACTTCGCGTTGCACAATACAACG
3169	GGGCTCAAAGTGCCTGAGTCGAAA TTTCGACTCAGGCACTTTGAGCCC
3170	CTGCTGTGCCCTCTCAGTGAGAGC GCTCTCACTGAGAGGGCACAGCAG
3171	CGGACGTACTGTTCGGAGTCCTCA TGAGGACTCCGAACAGTACGTCCG
3172	GTATACCACCATACCGGGACCGCA TGCGGTCCCGGTATGGTGGTATAC

[0208]

# TABLE 3

Seq.	ID	No.	Decoder	Sequence	(5'-3')	Probe	Sequence	(5'-3')
	17		TTCGCCG	rcgtgtagg(	CTTTTCAA	TTGAA	AGCCTACAC	CGACGGCGAA
	18		GTTCCCAC	GTGAAGCTGC	GATCTGG	CCAGAT	CGCAGCTT	CACTGGGAAC
	19		TACTTGGG	CATGGAATCO	CCTTACGC	GCGTA	AGGGATTCC	ATGCCAAGTA
	20		ACTAGCA	FATTTCAGGG	CACCGGC	GCCGGT	rgccctgaa <i>i</i>	ATATGCTAGT
	21		GAACGGT	CAATGAACCC	CGCTGTGA	TCACAC	GCGGGTTCAT	TTGACCGTTC
	22		GCGGCCT	rggttcaat <i>i</i>	ATGAATCG	CGATTO	CATATTGAAC	CCAAGGCCGC
	23		GATCGTT	AGAGGGACCI	TGCCCGA	TCGGGG	CAAGGTCCCT	CTAACGATC
	24		TGGACCT	AGTCCGGCAG	TGACGAA	TTCGT	CACTGCCGG	ACTAGGTCCA
	25		ATAAACTA	ACCCAGGACG	GGCGGAA	TTCCG	CCCGTCCTGC	GTAGTTTAT
	26		CATCGGT	rcgcgccaat	CCAGATA	TATCT	GATTGGCGC	CGAACCGATG
	27		GTCGGGC	ATAGAGCCGA	ACCACCCT	AGGGT	GTCGGCTCT	PATGCCCGAC
	28		CTTGGGT	CATGATTCAC	CCGTGCTA	TAGCAC	CGGTGAATC	ATGACCCAAG
	29		TGCCTAAG	CGTGCTAATC	CAGCAGCG	CGCTGC	CTGATTAGC	ACGTTAGGCA
	30		CGCATGT	rggagcatat	GCCCTGA	TCAGG	CATATGCT	CCAACATGCG
	31		AGCCACTO	GCATCAGTGC	CTGTTCAA	TTGAA	CAGCACTGAT	GCAGTGGCT
	32		GGTTGTT	TTGAGGCGTC	CCACACT	AGTGT	GGACGCCTC	CAAAACAACC
	33		TCGACCA	AGAGCAAGGG	GCGGACCA	TGGTC	CGCCCTTGCT	CTTGGTCGA
	34		GACATCG	CTATTGCGC	ATGGATCA	TGATCO	CATGCGCAAT	PAGCGATGTC
	35		GAAATAC	GAAGTCTGCG	GGAGTCG	CGACTO	CCCGCAGACT	TCGTATTTC
	36		TGTCATGA	ATGATTGAT	CGCGCGA	TCGCGC	CGATCAATC	ATTCATGACA
	37		ATATCGG	GATTCGTTCC	CCGGTGAA	TTCACO	CGGGAACGA	ATCCCGATAT
	38		GCGAGCG	PACCGAAGGG	GCCTAGAA	TTCTAC	GCCCTTCG	STACGCTCGC
	39		TTACCGG	CAGCGGACTI	CCGAATT	AATTC	GAAGTCCGC	CTGCCGGTAA
	40		GTAATCG	AGAGCTGCGC	CGCCGTCT	AGACGO	GCGCGCAGCT	CTCGATTAC
	41		CCTGTTAG	GCGTAGGCG	AGTCGATC	GATCG	ACTCGCCTAC	GCTAACAGG
	42		TAGCGGAG	CCGGCAGAAT	GAGTTCC	GGAACT	CATTCTGCC	GGTCCGCTA
	43		GGTACATO	GCACTACGC	GCACTCGG	CCGAGT	GCGCGTAGT	GCATGTACC
	44		AATTCATO	CTCGGACTCC	CCGCGGTA	TACCGO	CGGGAGTCC	SAGATGAATT

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TABLE 3-continued

Seq.	ID No	.Decoder Sequence (5'-3')	Probe Sequence (5'-3')
	45	GCCAAATCTGGATTGGCAGGAATG	CATTCCTGCCAATCCAGATTTGGC
	46	TGCATTTTCGGTTGAGGCACATCC	GGATGTGCCTCAACCGAAAATGCA
	47	CCGCTCAATTCACCATGCTTCGCT	AGCGAAGCATGGTGAATTGAGCGG
	48	CTCGGAAAGGTGCAACTTTGGTGT	ACACCAAAGTTGCACCTTTCCGAG
	49	AATTCGACCAGCAGAACGTCCCAT	ATGGGACGTTCTGCTGGTCGAATT
	50	GCCAGAGTCTCAACCTCACGGGAT	ATCCCGTGAGGTTGAGACTCTGGC
	51	CCAACAACTGGAACGGGAACCCGC	GCGGGTTCCCGTTCCAGTTGTTGG
	52	GAGAACTGATCGCTGAGGGGCATG	CATGCCCCTCAGCGATCAGTTCTC
	53	GGCACACTAGACTTGTGGCACCGA	TCGGTGCCACAAGTCTAGTGTGCC
	54	TCACATCCAAATATGGTCCGCGAA	TTCGCGGACCATATTTGGATGTGA
	55	GTCTGCCGGTGTGACCGCTTCATT	AATGAAGCGGTCACACCGGCAGAC
	56	CATCGCAGAGCATAAACACCCTCA	TGAGGGTGTTTATGCTCTGCGATG
	57	GTTGGTATCTATGGCAGAGGCGGA	TCCGCCTCTGCCATAGATACCAAC
	58	ACGAGGTGCCGCTGAGGTTCCATT	AATGGAACCTCAGCGGCACCTCGT
	59	GGAATGAGTGGACCCAGGCACATT	AATGTGCCTGGGTCCACTCATTCC
	60	TGTCAATATGCGTCCGTGTCGTCT	AGACGACACGGACGCATATTGACA
	61	TGATGAGCCTCAGGGTACGAGGCA	TGCCTCGTACCCTGAGGCTCATCA
	62	CACCGCGGTGTTCCTACAGAATGA	TCATTCTGTAGGAACACCGCGGTG
	63	TTGTTGCCAATGGTGTCCGCTCGG	CCGAGCGGACACCATTGGCAACAA
	64	TTAACCTGCGTCTGCCCCTTTCCT	AGGAAAGGGGCAGACGCAGGTTAA
	65	AGGCGCGTTCCTGCCTTAGTGACG	CGTCACTAAGGCAGGAACGCGCCT
	66	TAGGGCGATGGCACGAAGCTTCAA	TTGAAGCTTCGTGCCATCGCCCTA
	67		CATCGCCGACTTTGGCTCTATGCA
	68		TCCGTGTGGCCACCTGCCTCTCAA
	69		GCTCGTTTTTTCTCACAATGCGGA
	70		GCACCTATAGCTACGGAAACCGCC
	71		GCCCGTGGCTACGAAATTTTCACC
	72		GTGATTGTCTTCATCCTCCGTCGG
	73		TTTTGGCGAATTGGGCCAAACTGG
	74 75		CTGTGCGCACGGCCTAATAGATCC TGAAAGTCCAAACGGTGACATCCG
	76		TTAGGGACGAGCAGGATTTGCGAT
	77		GAACCTCGATTATTGCATGCCCTG
	78		CTTGGGCCCATATATCAACGCATG
	79		GTGGTTGGTCACAAGCTGCAGCTG
	80		GGTCGCCGGTCGGCAGACATACAA
	81		CCATACCTATCAACGGGCGCCATC
	. –		

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TABLE 3-continued

Seq.	ID	No.	Decoder	Sequence	(5'-3')	Probe	Sequence	(5'-3')
	82		ATGAGAA	rcgccggc <b>a</b>	ATCTGCTA	TAGCA	GATTGCCGG	CGATTCTCAT
	83		ATTTGCAG	CTGACCGCAG	GCTCGTG	CACGA	GCCTGCGGT	CAGTGCAAAT
	84		CAGGGAGA	AACGGTTAAG	STTCCCGT	ACGGG	AACTTAACCO	TTCTCCCTG
	85		AGGCCGGG	CGATCGAGGA	AGTTTGGT	ACCAA	ACTCCTCGAT	CGCCGGCCT
	86		ACACGGT	GTCTCTGAT	AGCGACC	GGTCG	CTATCAGAGA	ACCACCGTGT
	87		GTGCAAC	GCCGAGGACT	TCCATCA	TGATG	GAAGTCCTCC	GCGTTGCAC
	88		TCGGTGC	CTGATAGCCA	ATTCCGAT	ATCGG	AATGGCTAT	CAGGCACCGA
	89		TGAAATAG	CCACACAGCC	CAATTGGC	GCCAA!	TTGGCTGTGT	GGTATTTCA
	90		GCATCGT	GTACATGACT	GCCGCGA	TCGCG	GCAGTCATG	PACACGATGC
	91		CAGTGTT	CTAACGGCGC	CGCGTGAA	TTCAC	GCGCGCCGTT	PAGAACACTG
	92		CGCTTGC	AACGTTGCAC	CTACTCT	AGAGT	AGGTGCAACO	STTGCAAGCG
	93		CGAAAAA	CTAGTGGGCT	CGCCGCG	CGCGG	CGAGCCCACT	AGTTTTTCG
	94		CTTTCAG	GGAACTGCC	GGAGTCG	CGACT	CCGGCAGTT	CCCTGAAAG
	95		TTGTGGC	CTTCTTGTAA	AAGGCACG	CGTGC	CTTTACAAGA	AAGGCCACAA
	96		TCCACGAZ	ACGGCGACCC	GTTGTCT	AGACA	ACGGGTCGC	CGTTCGTGGA
	97		CGACCTTC	GCACGAAACC	TAACGAG	CTCGT'	PAGGTTTCGT	GCAAGGTCG
	98		GTGCAGC	TTCACGAGCC	CAGCCTGA	TCAGG	CTGGCTCGT	BAAGCTGCAC
	99		CGCTTTC	GTGCGAATAG	SACGATGA	TCATC	GTCTATTCGO	CACGAAAGCG
1	100		TGCGCTT	ACAGGCTCCT	AGTGGTC	GACCA	CTAGGAGCC	TGTAAGCGCA
1	01		CACGCGC	FTAGTCGCGA	ATCGCATA	TATGC	GATCGCGACT	PAAGCGCGTG
	102							CTCCCTCCG
	103							GCCGGATGC
	104							CGATTGGCCT
	105							CATTGGAAGG
	106							ATCAAGTGTT
	107							CTTGATTCCA
	108							TACGGGAGC
	109							ATTCACCACT
	110							CGCTTCAACA
1	111							GGAGCGCTG
	2							CGCTTCGAA
1	3							CCACGCGTT
	114							TTGCCGTAG
	115							ATCGCCCTAC
	117							BAGGTCGATT
	117							ATGCTGACTC
1	. 10		ONG I CNG	2214446466	CAGALIC	JAMIC.		113C1GHC1C

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TABLE 3-continued

	TABLE 3-CONT	Lnued
Seq. ID	No.Decoder Sequence (5'-3')	Probe Sequence (5'-3')
119	AGATAAAGACGCTGGCAACACGGG	CCCGTGTTGCCAGCGTCTTTATCT
120	GGTACCTCAACGCGAACCACTTGT	ACAAGTGGTTCGCGTTGAGGTACC
121	AAGCGATGGCTACCCAAGAGCGAT	ATCGCTCTTGGGTAGCCATCGCTT
122	AGAGCTTATGCAGAACCAGGCGCC	GGCGCCTGGTTCTGCATAAGCTCT
123	ATCGGTCTCACGCAGGGTTGGATA	TATCCAACCCTGCGTGAGACCGAT
124	TAGGTTGCCCGCCAGAAGAAACAT	ATGTTTCTTCTGGCGGGCAACCTA
125	CGGTGCTGTTGCAAAAGCCTGTAG	CTACAGGCTTTTGCAACAGCACCG
126	TGATGAAAGTTTGCGGCAGGACAC	GTGTCCTGCCGCAAACTTTCATCA
127	GTTGAGTGCAGGATGCAGCGATAG	CTATCGCTGCATCCTGCACTCAAC
128	AACATTGCGCGGTCCACCAGGGTT	AACCCTGGTGGACCGCGCAATGTT
129	GGGCAGTTAGAGAGGGCCAGAAGT	ACTTCTGGCCCTCTCTAACTGCCC
130	TCGAGCTGGTCCCCGTGAACGTGT	ACACGTTCACGGGGACCAGCTCGA
131	GTCTTGGGGGCCGCTTAGTGAAAA	TTTTCACTAAGCGGCCCCCAAGAC
132	ACTGTTGGCTTGCTCTCATGTCCA	TGGACATGAGAGCAAGCCAACAGT
133	AGGACCATTCGGAAGGCGAAGATA	TATCTTCGCCTTCCGAATGGTCCT
134	CTTGGGAGGCATCCGCTATAAGGA	TCCTTATAGCGGATGCCTCCCAAG
135	AATAAACGGAACGCACCGCTACAG	CTGTAGCGGTGCGTTCCGTTTATT
136	TTGTACGTGCGGTCCCCATAAGCA	TGCTTATGGGGACCGCACGTACAA
137	CGCACCAAACTGAGTTTCCCAGAC	GTCTGGGAAACTCAGTTTGGTGCG
138	ACCTGATCGTTCCCCTATTGGGAA	TTCCCAATAGGGGAACGATCAGGT
139	GGAACAGAGGCGAGGGGACTGAGC	GCTCAGTCCCCTCGCCTCTGTTCC
140	CCCTGCCTTGGCGTGTCGGCTTAT	ATAAGCCGACACGCCAAGGCAGGG
141	ACTCTGACACGCCAACTCCGGAAG	CTTCCGGAGTTGGCGTGTCAGAGT
142	CTGACGGTTTTCATTCGGCGTGCC	GGCACGCCGAATGAAAACCGTCAG
143	TGCGGTGGTTCATTGGAGCTGGCC	GGCCAGCTCCAATGAACCACCGCA
144	GCATGGCCAACTAGTGACTCGCAA	TTGCGAGTCACTAGTTGGCCATGC
145	AGGCCGTAAAGCGAATCTCACCTG	CAGGTGAGATTCGCTTTACGGCCT
146	CGAATATTATGCCGAGAATCCGCG	CGCGGATTCTCGGCATAATATTCG
147	ACAGACGAGCTCCCAACCACATGA	TCATGTGGTTGGGAGCTCGTCTGT
148	GGACGGTTTGTGCTGGATTGTCTG	CAGACAATCCAGCACAAACCGTCC
149	AAAGGCTATTGAGTTGGTTGGGCG	CGCCCAACCAACTCAATAGCCTTT
150	GATGGCCTATTCGGAGATCGGGCC	GGCCCGATCTCCGAATAGGCCATC
151	GATCCAGTAGGCAGCTTCATCCCA	TGGGATGAAGCTGCCTACTGGATC
152	AATAACTCGCGCGGGTATGCTTCT	AGAAGCATACCCGCGCGAGTTATT
153	GGAGGAGGTTTGTCTCGGAAAGCA	TGCTTTCCGAGACAAACCTCCTCC
154	CTTTGGTATGGCACATGCTGCCCG	CGGGCAGCATGTGCCATACCAAAG
155	AGAAAGGCTCGAGCAACGGGAACT	AGTTCCCGTTGCTCGAGCCTTTCT

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TABLE 3-continued

	TABLE 3-COITE	111404
Seq. ID	No. Decoder Sequence (5'-3')	Probe Sequence (5'-3')
156	AATCTACCGCACTGGTCCGCAAGT	ACTTGCGGACCAGTGCGGTAGATT
157	CGTGGCGGCCACAGTTTTTGGAGG	CCTCCAAAAACTGTGGCCGCCACG
158	TTGCAGTTCAATCCATACGCACGT	ACGTGCGTATGGATTGAACTGCAA
159	GGCCCAAAGCCCCAGACCATTTTA	TAAAATGGTCTGGGGCTTTGGGCC
160	CGCCTGTCTTTGTCTCCGGACAAT	ATTGTCCGGAGACAAAGACAGGCG
161	TGAGGCAACAGGGGCCAAAAACTA	TAGTTTTTGGCCCCTGTTGCCTCA
162	AGCGGAAGTAGTCCTCGGCTCGTC	GACGAGCCGAGGACTACTTCCGCT
163	GGCCCCAAGGCTTAGAGATAGTGG	CCACTATCTCTAAGCCTTGGGGCC
164	GCACGTGAAGTTTAACCGCGATTC	GAATCGCGGTTAAACTTCACGTGC
165	AGCGGCAGAAACGTTCCTTGACGG	CCGTCAAGGAACGTTTCTGCCGCT
166	TCGTCGAGCAGACGAGATTGCACG	CGTGCAATCTCGTCTGCTCGACGA
167	TCTTTGCCGCGTAACTGACTGCTT	AAGCAGTCAGTTACGCGGCAAAGA
168	TTTATGTGCCAAGGGGTTAACCGA	TCGGTTAACCCCTTGGCACATAAA
169	TGTTACTGTGGTTCACGGCAGTCC	GGACTGCCGTGAACCACAGTAACA
170	CGCGCCTCGCTAGACCTTTTATTG	CAATAAAAGGTCTAGCGAGGCGCG
171	ACAAATGCGTGAGAGCTCCCAACT	AGTTGGGAGCTCTCACGCATTTGT
172	CGCGCAGATTATAGACCCGAATGT	ACATTCGGGTCTATAATCTGCGCG
173	CAAATAACGCCGCTGAATCGGCGT	ACGCCGATTCAGCGGCGTTATTTG
174	CCTTCGTGCATCGGTGATGATGTT	AACATCATCACCGATGCACGAAGG
175	TGAACACGAGCAACACTCCAACGC	GCGTTGGAGTGTTGCTCGTGTTCA
176	CAGCAGATCCTTCGTAGCGGTCGT	ACGACCGCTACGAAGGATCTGCTG
177	GGAACCTGGTGAGTTGTGCCTCAT	ATGAGGCACAACTCACCAGGTTCC
178	TCATAAGCGACAATCGCGGGCTTA	TAAGCCCGCGATTGTCGCTTATGA
179	CCCAACGTCACTGAAGCTCACAGT	ACTGTGAGCTTCAGTGACGTTGGG
180	TGTCAGAGCCCGCGACTCAGACGG	CCGTCTGAGTCGCGGGCTCTGACA
181	TACACGAAGCCTCTCCGTGGTCCA	TGGACCACGGAGAGGCTTCGTGTA
182	CTCAGAAGTCCTCGGCGAACTGGG	CCCAGTTCGCCGAGGACTTCTGAG
183	ATCCTTTTATCTACTCCGCGGCGA	TCGCCGCGGAGTAGATAAAAGGAT
184	AGGCGTGCAGCAACAGGATAAACC	GGTTTATCCTGTTGCTGCACGCCT
185	ACTCTCGAGGGAGTCTCTGGCACA	TGTGCCAGAGACTCCCTCGAGAGT
186	TTGCCAGGTCCATCGAGACCTGTT	AACAGGTCTCGATGGACCTGGCAA
187	TCCACTATAACTGCGGGTCCGTGT	ACACGGACCCGCAGTTATAGTGGA
188	GCCCAGTCGGCTCTAACAAGTTCG	CGAACTTGTTAGAGCCGACTGGGC
189	CGGAACGGATAATCGGCGTCAGGT	ACCTGACGCCGATTATCCGTTCCG
190	TAAAATAAGCGCCTGGCGGAGGA	TCCTCCCGCCAGGCGCTTATTTTA
191	GCGCACTCGTGAAACCTTTCTCGC	GCGAGAAAGGTTTCACGAGTGCGC
192	AGTTTGCCAGGTACTGGCAAGTGC	GCACTTGCCAGTACCTGGCAAACT

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TABLE 3-continued

Seq. ID	No.Decoder Sequence (5'-3')	Probe Sequence (5'-3')
193	ACAACGAGGGATGTCCAGCGGCAT	ATGCCGCTGGACATCCCTCGTTGT
194	TTCGCAGCACCCGCTAGGTACAGT	ACTGTACCTAGCGGGTGCTGCGAA
195	TAACCCGATTTTTGCGACTCTGCC	GGCAGAGTCGCAAAAATCGGGTTA
196	CGTCGCATTGCAAGCGTAGGCTTG	CAAGCCTACGCTTGCAATGCGACG
197	GAGCTGACGTCACCATCAGAGGAA	TTCCTCTGATGGTGACGTCAGCTC
198	GGAGGCTGGGGGTCGCGCTTAAGT	ACTTAAGCGCGACCCCCAGCCTCC
199	TTGTGGGAACCGCACTAGCTGGCT	AGCCAGCTAGTGCGGTTCCCACAA
200	CCCTCGCACTGTGTTCACCCTCTT	AAGAGGGTGAACACAGTGCGAGGG
201	TCATTGACTCGAATCCGCACAACG	CGTTGTGCGGATTCGAGTCAATGA
202	ACAGGGGTTGGCCTTCGTACGTAC	GTACGTACGAAGGCCAACCCCTGT
203	AGGCCGTGCAACATCACACAGGAT	ATCCTGTGTGATGTTGCACGGCCT
204	GGGCCGTGGTCACGTAATATTGGC	GCCAATATTACGTGACCACGGCCC
205	GCGCGGACATGAAACGACAAGGCC	GGCCTTGTCGTTTCATGTCCGCGC
206	CTTATTGGGTGCCGGTGTCGGATT	AATCCGACACCGGCACCCAATAAG
207	GGGGCGGTTACCAAAAAATCCGAT	ATCGGATTTTTTGGTAACCGCCCC
4	CCGTCGCATACCGGCTACGATCAA	TTGATCGTAGCCGGTATGCGACGG
5	ATGGCCGTGCTGGGGACAAGTCAA	TTGACTTGTCCCCAGCACGGCCAT
210	ACGAAAAAAGTGTGCGGATCCCCT	AGGGGATCCGCACACTTTTTTCGT
211	CCAAGTACACCGCACGCATGTTTA	TAAACATGCGTGCGGTGTACTTGG
212	ATCGTGCGTGGAGTGTCGCATCTA	TAGATGCGACACTCCACGCACGAT
213	TCCAGATACCGCCCCGAACTTTGA	TCAAAGTTCGGGGCGGTATCTGGA
214	TCTGCTGGCAGCACGTGAAGTGGC	GCCACTTCACGTGCTGCCAGCAGA
215	TTGAAATTGCTCTGCCGTCAGTCA	TGACTGACGGCAGAGCAATTTCAA
216	AGTCAGGCGAGATGTTCAGGCAGC	GCTGCCTGAACATCTCGCCTGACT
217	ACAAGCCGACGTTAAGCCCGCCCA	TGGGCGGCTTAACGTCGGCTTGT
218	CCCTAATGAGGCCAGTAACCTGCA	TGCAGGTTACTGGCCTCATTAGGG
219	GTGAGACACACCCCCCCCAATG	CATTGGAGGGGATGTGTCTCAC
220	CGACGGATGCAGAGTTCAGTGGTC	GACCACTGAACTCTGCATCCGTCG
221	CCCGCATGCCTGGCGGTATTACAA	TTGTAATACCGCCAGGCATGCGGG
222	TTAGCAAAGCGGCGCCGTTAGCAA	TTGCTAACGGCGCCGCTTTGCTAA
223	CCCGACACGGGTCAGCGTAATAAT	ATTATTACGCTGACCCGTGTCGGG
224	GCGACGGCCCTGAGGTATGTCGTC	GACGACATACCTCAGGGCCGTCGC
225	CAAAAGTGTGTTCCCTTGCGCTTG	CAAGCGCAAGGGAACACACTTTTG
226	TCTCGAAGCACAGCCCGGTTATTG	CAATAACCGGGCTGTGCTTCGAGA
227	ATGCTAACCGTTGGCCATGGAACT	AGTTCCATGGCCAACGGTTAGCAT
228	CTTGCGGAGTGTTAGCCCAGCGGT	ACCGCTGGGCTAACACTCCGCAAG
229	TGCTCCCTAGGCGCTCGGAGGAGT	ACTCCTCCGAGCGCCTAGGGAGCA

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TABLE 3-continued

Seq. ID	No. Decoder	Sequence	(5'-3')	Probe	Sequence	(5'-3')
230	CCAATGC	CTTTGAGTAA	\GCGATGG	CCATC	GCTTACTCA <i>I</i>	AAGGCATTGG
231	AGCAGAT	AACGTCCCAA	TGACGCC	GGCGT	CATTGGGACG	TTATCTGCT
232	TTGACCA	TTACGTGTTG	CGCCCAT	ATGGG	CGCAACACGT	TAATGGTCAA
233	TCGCGTA	TTTGCGGAAT	TCGTCTG	CAGAC	GAATTCCGC <i>I</i>	AATACGCGA
234	CTGCGTG	TCAACAATGI	CCCGCAG	CTGCG	GGACATTGTT	GACACGCAG
235	TCTGGTG	CCACGCAAGG	STCCACAG	CTGTG	GACCTTGCGT	GGCACCAGA
236	CTCCGGG.	AGGTCACTTA	ATTGCGG	CCGCA	ATTAAGTGAC	CTCCCGGAG
237	TTTTCGT	GATTGCCCGG	AGGAGGC	GCCTC	CTCCGGGCA	ATCACGAAAA
238	TCGGGAT	GTAGCTGGGG	CTACCGG	CCGGT	AGCCCCAGCT	PACATCCCGA
239	CGAGCCA	ACGCAAACAC	GTCCTTG	CAAGG	ACGTGTTTGC	CGTTGGCTCG
240	GCAAAGC	CTTTGTGGGG	CGGTAGT	ACTAC	CGCCCACA	AAGGCTTTGC
241	ATTCGAC	CGGAAATGAG	GTCTTCG	CGAAG	ACCTCATTTC	CCGGTCGAAT
242	TTCGCTT	GCTGAGTTGG	TCTGTTC	GAACA	GAGCAACTC <i>I</i>	AGCAAGCGAA
243	CGCGTGA	AGACCCCATT	CCCGAGT	ACTCG	GGAATGGGGT	CTTCACGCG
244						SAATACGGTT
245						GTTGGCCCC
246						GCCAGCCGAA
247						AACCACACCC
248						CGGTCCTCGC
249						ACGCGTGCGT
250						CGACCTTTTA
251 252						AGCGATCGCA
252						TGTCAGCAT
254						TTAACCACA
255						GTGTGAACG
256						CGGGATAGG
257	GTCTGCA	CTCACGCAGO	GGAGGGA	TCCCT	CCGCTGCGTG	SAGTGCAGAC
258	GCACGAG	TTGGTGCTCG	GCAGATT	AATCT	GCCGAGCAC	CAACTCGTGC
259	AACGTCG	CACGACACAC	GTTCGTC	GACGA	ACGTGTGTC	TGCGACGTT
260	ATGCGCG	CTTATCCTAG	CATGGTC	GACCA!	IGCTAGGAT <i>I</i>	AAGCGCGCAT
261	TCACGTT	TTCGTCTCGA	CATGAGG	CCTCA	rgtcgagaco	SAAAACGTGA
262	TGTGCCT	CATCCTTAGG	SATACGGC	GCCGT	ATCCTAAGG	ATGAGGCACA
263	AGGTGGT	GTGGGTCAAC	CGCTTTA	TAAAG	CGGTTGACCC	CACACCACCT
264	CTGGATC	GAAGGGACTG	CAAGCTC	GAGCT'	IGCAGTCCCI	TTCGATCCAG
265	TAGATCA	ACTCGCGTAC	GCATGGA	TCCAT	GCGTACGCG <i>I</i>	AGTTGATCTA
266	GATCCTG	CGGAGAAGAG	SAGTGCAG	CTGCA	CTCTCTTCTC	CCGCAGGATC

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TABLE 3-continued

Seq. ID	No.Decoder	Sequence	(5'-3')	Probe	Sequence	(5'-3')
267	TACGTGT	GGAGATGCCC	CGAACCG	CGGTT	CGGGGCATCT	CCACACGTA
268	GCGCTATO	GTCAATCGTG	GGCGTAG	CTACG	CCCACGATTO	ACATAGCGC
269	AGCGAGG'	ITTCTAGCGT	CGACACC	GGTGT	CGACGCTAG	AACCTCGCT
270	ACCCAGG!	ITTTGCCGTT	GTGGAAT	ATTCC	ACAACGGCAA	AAACCTGGGT
271	CCCTGTT	AACGGCTGCG	TAGTCTC	GAGAC'	racgcagcco	STTAACAGGG
272	AGGCCGA	FTTCACCCGC	CAATTGC	GCAAT	rggcgggtg <i>i</i>	AAATCGGCCT
273	GAGCCCT	CACTCCTTGC	CCTTTGA	TCAAA	GGCAAGGAG	STGAGGGCTC
274	GGGTGGA	CATCCGCCTC	GCAGTCA	TGACT	GCGAGGCGG <i>I</i>	ATGTCCACCC
275	GATGGCT	GAGAACCGTG	CTACGAT	ATCGT	AGCACGGTTC	CTCAGCCATC
276	TCGACGT	PAGGAGTGCT	GCCAGAA	TTCTG	GCAGCACTCC	CTAACGTCGA
277	CGAATGG	GTCTGGACCT	TGCATAG	CTATG	CAAGGTCCAG	ACCCATTCG
278	GTGCACC	AGACATTCGA	ACTCGGA	TCCGA	GTTCGAATGT	CTGGTGCAC
279	AGAGGCC	CCGTATATCC	CATCCAT	ATGGA:	rgggatatac	CGGGGCCTCT
280	AACGCCT	GTTCAGAGCA	TCAGCGG	CCGCT	GATGCTCTG <i>I</i>	AACAGGCGTT
281						STTGAGCCTT
282						AACACGGACT
283						CATGGGACAT
284						CAGACTCCAT
285						TGGAGGCCG
286						CACGGCTCTG
287						ATTCAAATGA
288 289						CCGGTACGTC
290						CCTCACTCT
291						TACGGTGCG
292						CAAAGGTTCA
293	TCCGCCT	TTTTGGTTAC	CTCGAAG	CTTCG	AGGTAACCA <i>I</i>	AAAGGCGGA
294	GAACGCC	AACGGCACTA	ACACATC	GATGT	GTTAGTGCCC	TTGGCGTTC
295	CCGACAG	CAGCCAAGAC	GTCCCAG	CTGGG	ACGTCTTGGC	TGCTGTCGG
296	САТАААА	AAACCTGGGG	CTCTGCG	CGCAG	AGCCCCAGGT	TTTTTTATG
297	TGCCAAC	IGTGCAGACC	GGACTTA	TAAGT	CCGGTCTGC	ACAGTTGGCA
298	GGCGAAA	GAGCGAAACC	GGCTCGT	ACGAG	CCGGTTTCGC	CTCTTTCGCC
299	GGGATGC	GTATTTTAGO	GAACACG	CGTGT'	ICGCTAAAAT	TACGCATCCC
300	TGGGATT	CAGCGACCAG	TACGCGA	TCGCG'	TACTGGTCGC	CTGAATCCCA
301	CCCGATA	TTCGCCCGGC	CTATTCG	CGAAT	AGGCCGGGC	SAATATCGGG
302	CGAGAAGA	ATGCCTCACG	CAACCAA	TTGGT'	IGCGTGAGGC	CATCTTCTCG
303	AACCTTG	ACCCGTGGAT	GACGCTA	TAGCG	ICATCCACG(	GTCAAGGTT

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TABLE 3-continued

Seq. ID	No.Decoder Sequence (5'-3')	Probe Sequence (5'-3')
6	TTGCAACGGGCTGGTCAACGTCAA	TTGACGTTGACCAGCCCGTTGCAA
7	CGCATAGGTTGCCGATTTCGTCAA	TTGACGAAATCGGCAACCTATGCG
306	GCTTCCGGATGAACGGGATGGTTG	CAACCATCCCGTTCATCCGGAAGC
307	CCCTCCATGTTCTTCGAACGGTTT	AAACCGTTCGAAGAACATGGAGGG
308	TTGATGGGCGGCAATGCTCTTGCT	AGCAAGAGCATTGCCGCCCATCAA
309	ATTGTGAGATGCGCCAAATTCCCC	GGGGAATTTGGCGCATCTCACAAT
310	TCAGCACAGCCAGACGGTCAACTT	AAGTTGACCGTCTGGCTGTGCTGA
311	ACTCCACTCCTCGGTGGCAAACTA	TAGTTTGCCACCGAGGAGTGGAGT
312	TCTGGGCATGCCTGGACGGAGACG	CGTCTCCGTCCAGGCATGCCCAGA
313	TCTCAACTCCGGTACGACGAAACA	TGTTTCGTCGTACCGGAGTTGAGA
314	TTGCGTGGTCAAAGGCGCAACGTG	CACGTTGCGCCTTTGACCACGCAA
315	AGACAGCGATCCGCGGCTCATGAT	ATCATGAGCCGCGGATCGCTGTCT
316	CGCGTCTCTAACTGAGAGCAGCCA	TGGCTGCTCTCAGTTAGAGACGCG
317	AGGCGCACATGTACGGACATTCAG	CTGAATGTCCGTACATGTGCGCCT
318	GATGAGTGGCACGTCGGTGTGTAA	TTACACACCGACGTGCCACTCATC
319	TGATCCATATTGTCGGACGTTGCG	CGCAACGTCCGACAATATGGATCA
320	ACCTGCCGGGAGTTCATAGGCTAG	CTAGCCTATGAACTCCCGGCAGGT
321	AGCATTGGCGTTTTTCCGCAACGA	TCGTTGCGGAAAAACGCCAATGCT
322	GGTAATATTCAGCGCGACCGCTCA	TGAGCGGTCGCGCTGAATATTACC
323	ATAGCGTACGACGAGGTGACGCGC	GCGCGTCACCTCGTCGTACGCTAT
324	TAGGTCACGATGCGTTTGACGCTA	TAGCGTCAAACGCATCGTGACCTA
325	ACTGCCCGTACCTCTGGTTCTGGC	GCCAGAACCAGAGGTACGGCAGT
326		GCTACGACAACTTCAGGCCAAAGG
327		TACAACGATACGCTCGTGGGGCAC
328		TTGCTCCAGGCCCACGTAGCGCCT
329		CGGACTAATGCAATGGTAGCACCC
330	ACCACGCGCGTACGTGTAACCGAG	
331		CTAAATGCACCCAATGCATCATGG
332		TCGAACGTTTCGTAGGGCCGGACC TCACACGAATCTCCAGCCACACGG
333	GTTAGGGCGACGCATATTGGCACA	
335 336		GATCCTAACGCACCTGACTGACCC TCGATCTGCATTCGACTTCACGGC
337		TACCTGAATGCACTGGGTGGTGGC
338		GCCCGATGACCGCAAACTAAGCTC
339		GTTACTCCCTAATGGCGGCAAACA
340		CTAAACCGGCACATCCAGCGGAGC
340	SOLOGOTOMICIOCOGITIAG	

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TABLE 3-continued

	TABLE 3-conc	
Seq. ID	No.Decoder Sequence (5'-3')	Probe Sequence (5'-3')
341	CGGTAGCATGCGAGATCCCTGTTA	TAACAGGGATCTCGCATGCTACCG
342	CTACGCTCTACCAGTTGCCTGCGA	TCGCAGGCAACTGGTAGAGCGTAG
343	GTGCCTCCTGCTGTATTTGCCAAG	CTTGGCAAATACAGCAGGAGGCAC
344	TTGCGACTCGACTTGGACGAGTAG	CTACTCGTCCAAGTCGAGTCGCAA
345	TCTGGGAGCTGTTTACTCCAGCCA	TGGCTGGAGTAAACAGCTCCCAGA
346	TGGACGCGGAACTCCCTTTAGCAT	ATGGTAAAGGGAGTTCCGCGTGCA
347	TGGCAGCAAATGAATCGAAAGCAC	GTGCTTTCGATTCATTTGCTGCCA
348	AACTGGTGACGCGGTACAGCGAAG	CTTCGCTGTACCGCGTCACCAGTT
349	AGACGATTACGCTGGACGCCGTCG	CGACGGCGTCCAGCGTAATCGTCT
350	ATGCCCTCCTTCATGGAAAGGGTT	AACCCTTTCCATGAAGGAGGGCAT
351	ATTCTCGGAGCGTATGCGCCAGAA	TTCTGGCGCATACGCTCCGAGAAT
352	ATAGCGGAGTTTGGGTACGCGAAC	GTTCGCGTACCCAAACTCCGCTAT
353	ACCTACGCATACCGCTTGGCGAGG	CCTCGCCAAGCGGTATGCGTAGGT
354	GATTACCTGAATGGCCAAGCGAGC	GCTCGCTTGGCCATTCAGGTAATC
355	CCTGTTAGCATCACGGCGCTTAGG	CCTAAGCGCCGTGATGCTAACAGG
356	CGGAATGATGCGCTCGACAACGCT	AGCGTTGTCGAGCGCATCATTCCG
357	TGAGAGAGGCGTTGGTTAAGGCAA	TTGCCTTAACCAACGCCTCTCTCA
358	AAGCAGGCGAAGGGATACTCCTCG	CGAGGAGTATCCCTTCGCCTGCTT
359	TCACGACAGACGGGCCGAGATTAC	GTAATCTCGGCCCGTCTGTCGTGA
360	AAGCAATTTGGCCTCGTTTTGTGA	TCACAAAACGAGGCCAAATTGCTT
361	GCTGGTTGCGGTAGGATCGCATAT	ATATGCGATCCTACCGCAACCAGC
362	TTGTGAATCCGTTCTGTCCCCGAC	GTCGGGGACAGAACGGATTCACAA
363	TGGGCTCCTCTGAGGCGAGATGGC	GCCATCTCGCCTCAGAGGAGCCCA
364	GGATAGAGTGAATCGACCGGCAAC	GTTGCCGGTCGATTCACTCTATCC
365	TGCACCGAACGTGCACGAGTAATT	AATTACTCGTGCACGTTCGGTGCA
366	GCCAGTATTCTCGGGTGTTGGACG	CGTCCAACACCCGAGAATACTGGC
367	TCGCTACCTAAGACCGGGCCATAC	GTATGGCCCGGTCTTAGGTAGCGA
368	TGGCATTGACGAGCAGCAGTCAGT	ACTGACTGCTGCTCGTCAATGCCA
369	CGCGTCCCAGCGCCCTTGGAGTAT	ATACTCCAAGGGCGCTGGGACGCG
370	ATGAAGCCTACCGGGCGACTTCGT	ACGAAGTCGCCCGGTAGGCTTCAT
371	CCAGACAGATGGCCTGGAACCATG	CATGGTTCCAGGCCATCTGTCTGG
372	TGGCGTGGGACCATCTCAAAGCTA	TAGCTTTGAGATGGTCCCACGCCA
373	CCGCATGGGAACACGTGTCAAGGT	ACCTTGACACGTGTTCCCATGCGG
374	GCCCACTCGTCAGCTGGACGTAAT	ATTACGTCCAGCTGACGAGTGGGC
375	ATTACGGTCGTGATCCAGAAAGCG	CGCTTTCTGGATCACGACCGTAAT
376	TGCGAGGTGAGCACCTACGAGAGA	TCTCTCGTAGGTGCTCACCTCGCA
377	GGGCCGCATTCTTGATGTCCATTC	GAATGGACATCAAGAATGCGGCCC

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TABLE 3-continued

Seq. ID	No.Decoder Sequence (5'-3')	Probe Sequence (5'-3')
378	CCTCGGATGTGGGCTCTCGCCTAG	CTAGGCGAGAGCCCACATCCGAGG
379	TAGGCATGTTGGCGTGAGCGCTAT	ATAGCGCTCACGCCAACATGCCTA
380	CGATACGAACGAGGATGTCCGCCT	AGGCGGACATCCTCGTTCGTATCG
381	TACGCCGGTTAGCACGGTGCGCTA	TAGCGCACCGTGCTAACCGGCGTA
382	CATACGATGTCCGGGCCGTGTCGC	GCGACACGGCCCGGACATCGTATG
383	ATCCGCAGTTGTATGGCGCGTTAT	ATAACGCGCCATAGAACTGCGGAT
384	GGGTAAGGGACAAAGATGGGATGG	CCATCCCATCTTTGTCCCTTACCC
385	ATTGGAGTGTTTTGGTGAATCCGC	GCGGATTCACCAAAACACTCCAAT
386	GAACCGAGCCAACGTATGGACACG	CGTGTCCATACGTTGGCTCGGTTC
387	GCCGTCAAGCTTAAGGTTTTGGGC	GCCCAAAACCTTAAGCTTGACGGC
388	ACCTGCTTTTGGGTGGGTGATATG	CATATCACCCACCCAAAAGCAGGT
389	AATCGTGGGCGCAGCAAACGTATA	TATACGTTTGCTGCGCCCACGATT
390	GTCGCCGGATTGCTCAGTATAAGC	GCTTATACTGAGCAATCCGGCGAC
391	ACCCGTCGATGCTTCCTCCTCAGA	TCTGAGGAGGAAGCATCGACGGGT
392	ATCCGGGTGGGCGATACAAGAGAT	ATCTCTTGTATCGCCCACCCGGAT
393	TTCCGCATGAGTCAGCTTTGAAAA	TTTTCAAAGCTGACTCATGCGGAA
394	GCAAAGTCCCACTGGCAAGCCGAT	ATCGGCTTGCCAGTGGGACTTTGC
395	CGACCTCGGCTTCATCGTACACAT	ATGTGTACGATGAAGCCGAGGTCG
396	CTCATGAGCGCAGTTGTGCGTGAG	CTCACGCACAACTGCGCTCATGAG
397	CAGATGAAGGATCCACGGCCGGAG	CTCCGGCCGTGGATCCTTCATCTG
398	TCAAAGGCTCTTGGATACAGCCGT	ACGGCTGTATCCAAGAGCCTTTGA
399	TCCGCTAATTTCCAATCAGGGCTC	GAGCCCTGATTGGAAATTAGCGGA
8	CCGTTTGCGGTCGTCCTTGCTCAA	TTGAGCAAGGACGACCGCAAACGG
9	TTCGCTTTCGTGGCTGCACTTCAA	TTGAAGTGCAGCCACGAAAGCGAA
402	CTTAGTTGGGGCGCGGTATCCAGA	TCTGGATACCGCGCCCCAACTAAG
403	GCTCTAATGCCGTGGAGTCGGAAC	GTTCCGACTCCACGGCATTAGAGC
404	CCGATTACAAATTGACTGACCGCA	TGCGGTCAGTCAATTTGTAATCGG
405	AGACGTACGTGAGCCTCCCGTGTC	GACACGGGAGGCTCACGTACGTCT
406	AATGGAGCGATACGATCCAACGCA	TGCGTTGGATCGTATCGCTCCATT
407	GGAGGCGCTGTACTGATAGGCGTA	TACGCCTATCAGTACAGCGCCTCC
408	TGTTTTTGAATTGACCACACGGGA	TCCCGTGTGGTCAATTCAAAAACA
409	CATGTCTGGATGCGCTCAATGAAG	CTTCATTGAGCGCATCCAGACATG
410	GCCCGCTAATCCGACACCCAGTTT	AAACTGGGTGTCGGATTAGCGGGC
411	CCATTGACAGGAGAGCCATGAGCC	GGCTCATGGCTCTCCTGTCAATGG
412	GAATCACCGAATCACCGACTCGTT	AACGAGTCGGTGATTC
413	AACCAGCCGCAGTAGCTTACGTCG	CGACGTAAGCTACTGCGGCTGGTT
414	TTTTCTGAGGGACACGCGGGCGTT	AACGCCCGCGTGTCCCTCAGAAAA

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TABLE 3-continued

Seq. ID	No. Decoder	Sequence	(5'-3')	Probe	Sequence	(5'-3')
415	GGTGCTC	CGTTTGATCG	SATCCTCC	GGAGG	ATCGATCAA <i>I</i>	ACGGAGCACC
416	CCGCTTA	GGCCATACTC	CTGAGCCA	TGGCT	CAGAGTATGO	CCTAAGCGG
417	TAAGACA	TACCGACGCC	CCTTGCCT	AGGCA	AGGGCGTCGG	STATGTCTTA
418	GTTCCCG	ACGCCAGTCA	ATTGAGAC	GTCTC	AATGACTGGC	CGTCGGGAAC
419	TAAAAGT	TTCGCGGAGG	STCGGGCT	AGCCC	GACCTCCGC	SAAACTTTTA
420	CGGTCCA	GACGAGCTGA	AGTTCGGC	GCCGA	ACTCAGCTC	TCTGGACCG
421	CGGCGTA	GCGGCTACGG	SACTTAAA	TTTAA	GTCCGTAGCC	CGCTACGCCG
422	GCTTGGA	TGCCCATGCG	GCAAGGT	ACCTT	GCCGCATGG	GCATCCAAGC
423	AGCGGGA	TCCCAGAGTT	TCGAAAA	TTTTC	GAAACTCTGG	GATCCCGCT
424	GAGCTTG.	AGAGCGAGGT	CATCCTC	GAGGA'	rgacctcgc1	CTCAAGCTC
425	GCATCGG	CCGTTTTGAC	CATATTC	GAATA'	rggtcaaaac	CGGCCGATGC
426	CATAGCG	CTGCACGTTT	CGACCGC	GCGGT	CGAAACGTGC	CAGCGCTATG
427	ACCCGAC	AACCACCAAT	TCAAAAA	TTTTT	GAATTGGTG	TTGTCGGGT
428	GCGAACA	CTCATAAGAG	CGCCCTG	CAGGG	CGCTCTTATO	SAGTGTTCGC
429		GTGTAGAGAG				
430		GGAGCCGGAA				
431		GACTCGGCGA				
432		TATACTGACT				
433		AACCCGAGTT				
434		ACTCCGCGAA				
435		TGTCGCGTCA				
436 437		CGCGAAGTCG GGACTGGGCC				
437		AGACTTGCAT				
439		CCAGTCCGAA				
440		CTGCATCTCG				
441						SATGCGGTCT
442	AGAGGCT	TGGCAAGTAG	GGACCCT	AGGGT	CCCTACTTGO	CAAGCCTCT
443	GCAATGG.	ACGCCAGACG	SATACCGG	CCGGT	ATCGTCTGGC	CGTCCATTGC
444	GCTGGAC	TTAGTCGTGT	TCGGCGG	CCGCC	GAACACGACT	PAAGTCCAGC
445	AGGCATC	GTGCCGGATT	GCTCCCT	AGGGA	GCAATCCGGC	CACGATGCCT
446	TGCGCAT	GTCGACGTTG	SAACAAAG	CTTTG	TTCAACGTC	GACATGCGCA
447	TTCGGGT	CACATCCGAT	GCCATAC	GTATG	GCATCGGAT	STGACCCGAA
448	ACCCATC	GCCGGAAAGC	GATGTTG	CAACA!	rcgctttcc0	GCGATGGGT
449	AAGCGCT	GACTCGGCTA	AGAATCA	TGATT	CTTAGCCGAG	TCAGCGCTT
450	ACTTCCA	AGTCCTTGAC	CCGTCCGA	TCGGA	CGGTCAAGG	ACTTGGAAGT
451	TCTCAAT	ATTCCCGTAG	TCGCCCA	TGGGC	GACTACGGG <i>I</i>	AATATTGAGA

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TABLE 3-continued

Seq. ID	No.Decoder Sequence (5'-3')	Probe Sequence (5'-3')
452	AACAGTTCCTCTTTTTCCTGGCGC	GCGCCAGGAAAAAGAGGAACTGTT
453	CGTCCTCCATGTTGTCACGAACAG	CTGTTCGTGACAACATGGAGGACG
454	TGCGCAGACCTACCTGTCTTTGCT	AGCAAAGACAGGTAGGTCTGCGCA
455	ATGGACGGCTTCGCAGTCCTCCTT	AAGGAGGACTGCGAAGCCGTCCAT
456	TGAACGCTTTCTATGGGCCACGTA	TACGTGGCCCATAGAAAGCGTTCA
457	TGAACCCTGCCGCGAGCGATAACC	GGTTATCGCTCGCGGCAGGGTTCA
458	GTTCTTGCGCGATGAATCAGGACC	GGTCCTGATTCATCGCGCAAGAAC
459	AGGGTACGTGTCGCAGCTTCGCGT	ACGCGAAGCTGCGACACGTACCCT
460	ACCCTTGCTCCGCCATGTCTCTCA	TGAGAGACATGGCGGAGCAAGGGT
461	GGGACAAGGATTGAAGCTGGCGTC	GACGCCAGCTTCAATCCTTGTCCC
462	TGTCGTTGCTCCCGAGTACCATTG	CAATGGTACTCGGGAGCAACGACA
463	GTTGTCCGAGACGTTTGTGTCAGC	GCTGACACAAACGTCTCGGACAAC
464	GCTGGTGAACACTCACGAACCGCT	AGCGGTTCGTGAGTGTTCACCAGC
465	GCAGACAGGGCAAATCGGTGCAAA	TTTGCACCGATTTGCCCTGTCTGC
466	CCCATCACAACGAGTGGCGACTTT	AAAGTCGCCACTCGTTGTGATGGG
467	GCTTCTACAGCTGGCGTGCTAGCG	CGCTAGCACGCCAGCTGTAGAAGC
468	GAATGTGTGCCGACCATTCTAGCC	GGCTAGAATGGTCGGCACACATTC
469	CCAGCGGAAGTTAGAGCTCTGTGG	CCACAGAGCTCTAACTTCCGCTGG
470	TTTTTACCGACCACTCCATGTCGG	CCGACATGGAGTGGTCGGTAAAAA
471	GCGGCTATGTGATGACGGCCTAGC	GCTAGGCCGTCATCACATAGCCGC
472	AGTACACGGGCGTGTTAGCGCTCC	GGAGCGCTAACACGCCCGTGTACT
473	TCCTGTGTGGTGGCGCACTCCCAC	GTGGGAGTGCGCCACACACAGGA
474		TCATCCGCGCGATTGGTTAGTTGG
475		TTGCTCCTGCCTTGGTCACTCACT
476		CCGCAATAAACTCCGCGAAAGATG
477		TGCTGTCGCACTAACCGGACGAAG
478		ATTTCGGGCCCACGTTTTCGTGAG
479		CAATGCTAGAGTTCAGCTGCTGCG
480		GCACCATTTGGGCGTATGTCTCCT CAAACTCCCGCACGAGTTCTCAAT
481 482		TGCTCCTCTGGGCCTACAAAGAG
483		
483	GCCGCAGGGTCGATAATTGGTCTA	CCCAATAGTCTCAGGGCGGCGTTT
485		AGTCCAACGTTCCAGGCAACTCAG
486		ATCCCATACTCTGCAACCCATCCG
487		ACCGCACTAACCCCCAAAGGTCAG
488		CGCTGGGGTAAGGTTCTCATTTCC
400	John T. C.	

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TABLE 3-continued

	TABLE 3-CONT	Inuea
Seq. ID	No.Decoder Sequence (5'-3')	Probe Sequence (5'-3')
489	AACGCATCGTCCGTCAACTCATCA	TGATGAGTTGACGGACGATGCGTT
490	TGGAGAGAGACTTCGGCCATTGTT	AACAATGGCCGAAGTCTCTCTCCA
491	TTGCGCTCATTGGATCTTGTCAGG	CCTGACAAGATCCAATGAGCGCAA
492	AGCGCGTTAAAGCACGGCAACATT	AATGTTGCCGTGCTTTAACGCGCT
493	AGCCAGTAAACTGTGGGCGGCTGT	ACAGCCGCCCACAGTTTACTGGCT
494	CGACTGATGTGCAACCAGCAGCTG	CAGCTGCTGGTTGCACATCAGTCG
495	GGTTGCTCATACGACGAGCGAGTG	CACTCGCTCGTCGTATGAGCAACC
10	GTCCAACGCGCAACTCCGATTCAA	TTGAATCGGAGTTGCGCGTTGGAC
11	TTGCCGCACCGTCCGTCATCTCAA	TTGAGATGACGGACGGTGCGGCAA
498	AGAACCTCCGCGCCTCCGTAGTAG	CTACTACGGAGGCGCGGAGGTTCT
499	AAAGGAGCTTTCGCCCAACGTACC	GGTACGTTGGGCGAAAGCTCCTTT
500	AGTGATTGTGCCACTCCACAGCTC	GAGCTGTGGAGTGGCACAATCACT
501	GCGATCGTCGAGGGTTGAGCTGAA	TTCAGCTCAACCCTCGACGATCGC
502	GGGAGACAGCCATTATGGTCCTCG	CGAGGACCATAATGGCTGTCTCCC
503	GAGACGCTGTCACTCCGGCAGAAC	GTTCTGCCGGAGTGACAGCGTCTC
504	CCACCGGTCGCTTAAGATGCACTT	AAGTGCATCTTAAGCGACCGGTGG
505	CGGCATAACGTCCAGTCCTGGGAC	GTCCCAGGACTGGACGTTATGCCG
506	AAGCGGAACGGGTTATACCGAGGT	ACCTCGGTATAACCCGTTCCGCTT
507	TGCACACTAGGTCCGTCGCTTGAT	ATCAAGCGACGGACCTAGTGTGCA
508	AGGGAACCGCGTTCAAACTCAGTT	AACTGAGTTTGAACGCGGTTCCCT
509	GAATTACAACCACCCGCTCGTGTT	AACACGAGCGGGTGGTTGTAATTC
510	TTCAGTGCTCACGAAGCATGGATT	AATCCATGCTTCGTGAGCACTGAA
511	TTAGTTTGGCGTTGGGACTTCACC	GGTGAAGTCCCAACGCCAAACTAA
512	AATGCGACCTCGACGAGCCTCATA	TATGAGGCTCGTCGAGGTCGCATT
513	CCGAAACCGTTAACGTGGCGCACA	TGTGCGCCACGTTAACGGTTTCGG
514	TAAAGTAACAAGGCGACCTCCCGC	GCGGGAGGTCGCCTTGTTACTTTA
515	TAATGATTTTAGTCGCGGGGTGGG	CCCACCCGCGACTAAAATCATTA
516	GGCTACTCTAAGTGCCCGCTCAGG	CCTGAGCGGGCACTTAGAGTAGCC
517	TGGCGGACGACTCAATATCTCACG	CGTGAGATATTGAGTCGTCCGCCA
518	GGGCGTTAGGCGTAATAGACCGTC	GACGGTCTATTACGCCTAACGCCC
519	GCCACCTTTAGACGGCGGCTCTAG	CTAGAGCCGCCGTCTAAAGGTGGC
520	GAGATGTGTAAACGTGCAGGCACC	GGTGCCTGCACGTTTACACATCTC
521	TAGCTCGTGGCCCTCCAAGCGTGT	ACACGCTTGGAGGGCCACGAGCTA
522	GTGTCGGCGCTATTTGGCCTTACC	GGTAAGGCCAAATAGCGCCGACAC
523	CCAGGGAAGCAACTGGTTGCCATT	AATGGCAACCAGTTGCTTCCCTGG
524	TTCCGAAACTAAGCCAGAACCGCT	AGCGGTTCTGGCTTAGTTTCGGAA
525	GCAAACCCGGTAACCCGAGAGTTC	GAACTCTCGGGTTACCGGGTTTGC

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TABLE 3-continued

Seq. ID	No.Decoder Sequence (5'-3')	Probe Sequence (5'-3')
526	GCAAATGGCGTCATGCACGAACGT	ACGTTCGTGCATGACGCCATTTGC
527	AGTACTTTCGCGCCCAGTTTAGGG	CCCTAAACTGGGCGCGAAAGTACT
528	AAGATCTGCGAGGCATCCCGGCTT	AAGCCGGGATGCCTCGCAGATCTT
529	GCAAGTGTATCGCACAGTGCGATT	AATCGCACTGTGCGATACACTTGC
530	CCGACAAGGCCTCAATTCATTCTG	CAGAATGAATTGAGGCCTTGTCGG
531	GTCTCGTCTCAACTTTAAGGCGCG	CGCGCCTTAAAGTTGAGACGAGAC
532	ATCCAGAGATCCGTTTTGCAGCGT	ACGCTGCAAAACGGATCTCTGGAT
533	GTCACCAGGAGGGAAGTTTCACCC	GGGTGAAACTTCCCTCCTGGTGAC
534	TTCCGTCAGGCGGATCAACGGAAT	ATTCCGTTGATCCGCCTGACGGAA
535	ATGCCGGACACGCATTACACAGGC	GCCTGTGTAATGCGTGTCCGGCAT
536	TGGGCCGCTTGGCGCTTTCATAGA	TCTATGAAAGCGCCAAGCGGCCCA
537	CCTAGCGCGAGCTTTACTGACCAG	CTGGTCAGTAAAGCTCGCGCTAGG
538	TTGGCCAGGAATATGGTCTCGAGA	TCTCGAGACCATATTCCTGGCCAA
539	GTCTGCGGCCGACTTGCTATGCAT	ATGCATAGCAAGTCGGCCGCAGAC
540	AACTTGCTCATTCTCAAGCCGACG	CGTCGGCTTGAGAATGAGCAAGTT
541	ACGTCAGCGATTGTGGCGAAATAT	ATATTTCGCCACAATCGCTGACGT
542	ACGGCCTGCGTCAGCACATGCATC	GATGCATGTGCTGACGCAGGCCGT
543	ATACCTCCGCAGAACCATTCCGTT	AACGGAATGGTTCTGCGGAGGTAT
544	AGTTCGCGGTCCCACGATTCACTT	AAGTGAATCGTGGGACCGCGAACT
545	TGCTCAATTTGTGCAGAAAACGCC	GGCGTTTTCTGCACAAATTGAGCA
546	TTATCGCGAGAGACGACCGTGTCC	GGACACGGTCGTCTCTCGCGATAA
547	GACGCGACGTGAGTAGTGGAAGCG	CGCTTCCACTACTCACGTCGCGTC
548	ATGGTAGGGGCATTGGGCTTTCCT	AGGAAAGCCCAATGCCCCTACCAT
549	CCAAATATAGCCGCGCGGAGACAT	ATGTCTCCGCGCGGCTATATTTGG
550	GCAAACCCTGATTGAATCGTGCCC	GGGCACGATTCAATCAGGGTTTGC
551	TAGCGTCTTGCGTGAAACCATGGG	CCCATGGTTTCACGCAAGACGCTA
552	CCACCCGACAGCGCTGGACTCTT	AAGAGTCCAGCGCTGTCGGGGTGG
553	ACGAGCACTGAAGGCTGCTTTACG	CGTAAAGCAGCCTTCAGTGCTCGT
554	CATATCAGCGTCGTCTAGCTCGCG	CGCGAGCTAGACGACGCTGATATG
555	TGATCCCGGACCGGCTAGACTAAT	ATTAGTCTAGCCGGTCCGGGATCA
556	GGCCCCGACACTACAGGGTAATCA	TGATTACCCTGTAGTGTCGGGGCC
557	GGCTCCAGGGCGAGATTATGAATG	CATTCATAATCTCGCCCTGGAGCC
558	CAAAATCCGATGGGCGGAAAATTA	TAATTTTCCGCCCATCGGATTTTG
559	CACAGGCGCATAGGGAGCAAGCTA	TAGCTTGCTCCCTATGCGCCTGTG
560	TAGCTATTGCCCCGATGGGCTACT	AGTAGCCCATCGGGGCAATAGCTA
561	TGGTACGCGGTCCATAGCAAGTCG	CGACTTGCTATGGACCGCGTACCA
562	GACGCTGTGGCTCGGAAACTGTTC	GAACAGTTTCCGAGCCACAGCGTC

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TABLE 3-continued

Seq. ID	No.Decoder Sequence (5'-3')	Probe Sequence (5'-3')
563	CCTGGGTTCGCCGCGTGGTAACTG	CAGTTACCACGCGGCGAACCCAGG
564	TTCCCGCGTAGCCCAACAGCTATA	TATAGCTGTTGGGCTACGCGGGAA
565	TTCGCGGATTGCTGCCGCATAACA	TGTTATGCGGCAGCAATCCGCGAA
566	AAAAATGGCACCGAAGTTGAGGCA	TGCCTCAACTTCGGTGCCATTTTT
567	CATTCCGCGCGAGTTGAAATCCAG	CTGGATTTCAACTCGCGCGGAATG
568	ACGCACGTTTTTTGGCACGGTTAA	TTAACCGTGCCAAAAAACGTGCGT
569	TGTCCATGACGTCGTTTCTCTGGT	ACCAGAGAAACGACGTCATGGACA
570	TCTCAGTCGGACTCGTATGCCAGA	TCTGGCATACGAGTCCGACTGAGA
571	CTCCAAACGCACACATCAAGCATC	GATGCTTGATGTGTGCGTTTGGAG
572	TTCAACCAAGCGGGGTGTTCGTGA	TCACGAACACCCCGCTTGGTTGAA
573	GGTGTCGGAGGGTGGTGACCTCGA	TCGAGGTCACCACCCTCCGACACC
574	AGCGCTTTTGGTCATGATTTGCAA	TTGCAAATCATGACCAAAAGCGCT
575	CCGAGGACTTACGTCTGCCCAGGA	TCCTGGGCAGACGTAAGTCCTCGG
576	GCCCAATCCAGTTCTTATGCGCCC	GGGCGCATAAGAACTGGATTGGGC
577	CGGGTTAACCCACGCAAGTTATGA	TCATAACTTGCGTGGGTTAACCCG
578	TGATTAGCGCTCAATACACGCGTG	CACGCGTGTATTGAGCGCTAATCA
579	AAGGGCAGACCTTTGGTTCGACTG	CAGTCGAACCAAAGGTCTGCCCTT
580	GCGCCACAAGATTCACATGTCATT	AATGACATGTGAATCTTGTGGCGC
581	GCCATGTTCAAGGGCCTTTCGAAG	CTTCGAAAGGCCCTTGAACATGGC
582	CGCGGTGTTTTGTCTAGGTGCCGG	CCGGCACCTAGACAAAACACCGCG
583	CAACATTGTGGTGGCACTCCATCC	GGATGGAGTGCCACCACAATGTTG
584	CGATACGCGCCGGTTTGTTAAATC	GATTTAACAAACCGGCGCGTATCG
585		GGAGCAGTCCGCACGTTTATAGCC
586		AACCGCGCAATAGTGATTTACCCA
587		TAGCTTGCGCGGGCCGATGAAGAC
588		GCATCAGAGTACAGGGTGTGTCGC
589		GCTTGGTCTTGCGGACCCTGCTAC
590		ATGGCAGTTACCCTGCGTTGGCGA
591		TCGTGCCGCTCGAAGCTTCGGAGT TTGATCCCATCGAAAGGGACGATG
12		TTGACACGTCGTCAGCTCCCGTGC
594		
594		CTCTTCACTCTGCCGTGGGATGAT CGACTCGGATAGGCCAGTCCAGCG
595		TTTGCGACAGTGTTGCTGAGACCG
597		GGCCATTACATCGGAGAACGTTCG
598		TCAGAGGGGCTTGTCGCACGGTAT
599		GGTGTTCCGTCTCGGGAATGAGCT
3,7,	110101111000mineoumenee	11111111111111111111111111111111111111

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TABLE 3-continued

600 TTTCATGCGGCCTTGCAAATCAT ATGATTTGCAACGGCCGCATGAAA 601 ACTCGAACGGACGTTCAATTCCCA TGGGAATTGAACGTCCGTTCGAGT 602 CTGCATGGTGGGTGGAGACTCCC GGGAGTCTCACCCACACCATGCAG 603 CCGCGAGTGTGGATGGCGGGTG TCAACACGCCATCCACACTCGCGG 604 AATGTGTCGGTCCTAAGCCGGGTG CACCCGGCTTAGGACCGACACATT 605 TAAGACGAGCCTGCACAGCTTGCG CGCAAGCTGTAGCACGCACACATT 606 GGCGTGGGAGGATAGACGATGTC GACACTGTCCTCCCACCCCC 607 TGCTCCATGTTAGGAACGACCAC GTGGTGCGTTCATACATGGAGCA 608 CGGTGTGTGCGGACAGCTGC CAGTCGTCAACATGGAGCA 609 CCGCGCGTATCTATCAGACTGACC 609 CCGCGCGTATCTATCAGATCTGG CCCAGATCTGATAGATACGCCGCG 610 AAAGCATGCTCCACCTGGAGCGAC 611 ACTTGCATCGTCGGACTAGACTAC CAGTCGTCCAACACCG 612 TGCTTACGCACGGGTTAGATCCGC 613 ATGCAGATGAACAAATCGCCGAAT ATTCGGCGATTTCATCAGATT 614 GCAATTCTGGGCCATGTATTCCTC GACGAATCCACTGCGTAAGCA 615 AGGGTTCTTACGCGTCGAATATCCTC GACGAATTCACTGCATTGCAT	Seq. II	No.	Decoder	Sequence	(5'-3')	Probe	Sequence	(5'-3')
CTGCATGGATGGATCAATTCCCA TGGGATTGAACGTCCGTTCGAGT CTGCATGGTGTGGGTGAGACTCCC GGGAGTCTCACCACCACCATCCAG CCGCGAGTGTGGATGGCGTGTTGA TCAACACGCCATCCACACCACCACCACCACCACCACCACCACCACCAC	600		TTTCATG	CGGCCGTTGC	CAAATCAT	ATGAT	TTGCAACGG(	CCGCATGAAA
CCGCGGGTTGGATGGCGTGTTGA TCAACACGCCATCCACACTCGCGG AATGTCGCGTCCTAAGCCGGGTG CACCCGGCTTAGGACCGACTT CTAAGACGAGCCTGCACAGCTTGCG CGCAAGCTGTCCAGCCTGTCTTA CGGCGTGGGAGGATAAGACGATGTC GACATCGTCTTATCCTCCCAGCC CGGCGTTGGTCGGACTGACAGCTTCG CGCAAGCTGTCTAACATGGAGCA CGGTGTTGGTCGGACTGACGACTG CAGTCGTCAGTCCGACCAACACCG CCGCGCGTATCTATCAGAATCTGGG CCAGATCTGATAGATACGCGCGG CCGCGCGTATCTATCAGAATCTGGG CCCAGATCTGATAGATACGCGCGG AAAGCATGCTCCACCTGGAGCGAG CTCGCTCCAGCGAGCAACACCG CCGCGCGTATCTATCAGATCCGG CCGGATCTACCCAGCGAGCAAGCACGG AAAGCATGCTCCACCTGGAGCGAG CTCGCTCAGGTGGAGCATGCTTT ACTTGCATCGCTGGGTGGATCCGG CCGGATCTACCCAGCGATGCAAGT TGCTTACGCAGTGGATTGGTCAGA TCTGACCAATCCACTGCGTAAGCA ATGCAGATCAACAAATCGCCCAAT ATTCGGCGATTTGTTCATCTCCAT AGGGTTCCTTACGCGTCGACATG CCATTCTGACCAATCCACTGCGTAAGCA ATGCAGATCATCTGGCGCAATGATCC GACGAATACATGGCCCAGAATTGC CGGACTCATACCCGGCAATGATCC GACGAATACATGGCCCAGAATTGC CTGTGGTCCTACCCGGCAATGATCC GGAACATTGCCCGCGTAAGCACCT TCGTAGTCTCACCGGCAATGATCC GGAACATTGCCGCGTAAGCACCCT CCGCAGACCTTATCCGCGTCGACTAGA TCTGAGGCTCGCGATTAGCTCCAC CGAACAGTGCTGTCCGCTCAA TTGAGGCTCGCGAATTGCTCCAC CGAACAGTGCTGTCCGTCCCTCAA TTGAGGCTCGCACTGCTTAAA CGAACAGTGCTGTCCGTCCCTCAA TTGAGGCACGGCACACTGTTTC CCCCGTGGACTGTTTAGACGCTAA TAACGGTCTACACGCCGGGA CTCCCCGTGGACTGTTTAGACGCTAA TAACGGTCTACACGCCGGGA CTCCCCGTGGACTGTTAGACTGT ACAGTTACCGACAGCGGGCTAATG CCATTAGCCCGCTGTGCGAAACAGCCCTAA CAGTTTCCCTGCTCGAGCGGCTAATG CCATCGCTGGACAGGAGAATCCT ACAGTTACCGACAGGGGCTAATG CCATCGCTGGACAGGAGAATCCT ACAGTTACCGACAGGGGCTAATG CCATCGCTGGAACCAGCGCAATC CATCACGCGGGTGAAACAAGAGGATCACT TATGGAAAGGCCATCAAGGCCCGTATAC GATTACCGGCTGGTTTCCTTCCATA CTGTGGTTCATGGGGCAACACGCCTATAC GTATACGGGCCTGATGCCC CATGGTTGATGGAACCAAGCGCTATC GATTACCGCCTGGGTTTCCATCAACACCAG ACTCGCTGAACCACGCGTTACC GTTCAGCCCAAATTCCAACCACG CCGGCATAGGGCCAAAAACACGCCTTACAC GTTTAACCGCCTTTCCACCACG CAGGCCCGAACCACGCGGTTACCA CTTTAACCGCCGTGTTTCCGCC GGCCAATGGGCCAATAAACACCAC GTTTCAGCCCAATCCACCACC GGCCAATGGGCCAATAAAATACTA TAGTATTTATGCGCCCATTCCCC AGGCCCAATGCGCCAATAAATACTA TAGTATTTATGCGCCCATTCCCCCACCACC AGGCCCAATGGGCCAATAAATACCAC GCGGAAGGGCTCCACACCCAACCCA								
AATGTGTCGGTCCTAAGCCGGGTG CACCCGGCTTAGGACCGACACATT  TAAGACGAGCCTGCACAGCTTGCG CGCAAGCTGTGCAGGCTCGTCTTA  GGCGTGGGAGGATAAGACGATGTC GACATCGTCTTATCCTCCACCGCC  GGCGTGGGAGGATAAGACGACGAC GTGGTGCGTTCCTAACATGGAGCA  GGCGTGTTGGTCGGACCGACCAC GTGGTGCGTTCCTAACATGGAGCA  CGGTGTTGGTCGGACTGACGACTG CAGTCGTCCTAACATCGACCACCG  GGCGTGTTGGTCGACCTGGAGCGAC CAGTCGTCCAGCTCAACACCG  GGCGTATCTATCAGATCTGGG CCCAGATCTGATAGATACGCGCGG  AAAGCATGCTCCACCTGGAGCGAG CTCGCTCCAGGTGGAGCATGCTTT  G11 ACTTGCATCGCTGGGTAGATCCGG CCGGATCTACCCAGCGATGCAAGT  G12 TGCTTACGCAGTGGATTGGTCAGA TCTGACCAATCCACTGCGTAAGCA  ATGCAGATGAACAAATCGCCGAAT ATTCGGCGATTTGTTCATCTGCAT  G14 GCAATTCTGGGCCATGTATTCGTC GACGAATACCACTGCCGTAAGCA  G15 AGGGTTCCTTACGCGTCGACATGG CCATGTCGACGCGATTAGCCCAC  G16 GTGGAGCTAATCGCGGACCTCAGA TCTGAGCGATTAGCTCCAC  G17 TCGTAGTCTCACCGGCAATGATCC GGATCATTCCCGGTGAGAACCCT  G18 TTATAGCAGTGCGCCAATGCTTCG CGAAGCATTGCCCACCGGGA  G19 CGAACAGTGCTGTCCTCACA TTGAGCGACAGCACTGCTATAA  G19 CGAACAGTGCTGCTCACAATGCTTCG CGAAGCATTGCCCACCGGGA  G20 TCCGCGTGGACTGTTAGACGCTAA ATAGCGTCTAACAGCACACTGCTACACA  G21 CATTAGCCCGCTGTCGCTCAA TTGAGCGACAGCGACACTGCTACAA  G22 GGAAAGAAACTCAGACGGGCAATG CATTGCCGACGGGACAATGC  G23 CGACTCCCTGGTTAACATGT ACAGTTACCGACAGCGGCTAATG  G24 CATGATCCTCTGTTTCACCCGCG CCGCGGGTGAAACAGCGGCTAATG  G25 GGCGTAGCCCTTAAAAGCTTCG CCGAAGCTTTTTGAGCGCTACACC  G26 AGTGATGCCATCAGGCCCGTATAC GTATACCGGCCTGAGGATCACC  G26 AGTGATGCCATCAGGCCCGTATAC GTATACCGGCCTGATGCCCC  G26 AGTGATGCCATCAGGCCCGTATAC GTATACCGGCCTGATGCCCTTCCACC  G26 ACTCGCTGGAACAGCCCGTATAC GTATACCGGCCTGATGCCCTTCCACC  G26 ACTCGCTGGAATTGCGCCGACCCGTATAC GTATACCGGCCTGATGCCCTTCCACC  G27 ACTCGCTGGAATTTCGCCTGACC GTGTCACCCCTTCCACCACCACG  G31 GGCCCAAACCACCGCGTTACAG CTGTACCCCCTGATCCCCCTGACCCTTCCACCACCAC  G32 GGTCAATTCCGCGTACACGCGTTACAC CTGTGCACCCATC  G33 GATGGTGGACTGAGGCCCTTCCGC GCGGAAGGCCTCAACCCACC  G34 GATGGTGGACTGAGGCCCTTCCGC GCGGAAGGGCTCCAGTCCACCATC  CCGCGCATAGCGCATAAATACTA TAGTATTTATGCGCCCATTCCACCACC  G34 GATGGTGGACTGGAGCCCTTCCGC GCGGAAGGGCTCCAGTCCACCATC  CCGCGCATAGCGCATAAATAGCGCACCCAAC TCCCCCTATTGCGCCGAACGCCAAGAGAGACACCACCAACACCACCACACCAC	602		CTGCATG	GTGTGGGTG#	AGACTCCC	GGGAG'	ICTCACCCAC	CACCATGCAG
605 TAAGACGAGCCTGCACAGCTTGCG CGCAAGCTGTGCAGGCTCGTCTTA 606 GGCGTGGGAGGATAAGACGACTG GACATCGTCTTATCCTCCACCCC 607 TGCTCCATGTTAGGAACGCACCAC GTGGTGCGTTCCTAACATGGAGCA 608 CGGTGTTGGTCGGACTGACGACTG CAGTCGTCAGTCCGACCAACACCG 609 CCGCGGCGTATCTATCAGATCTGG CCCAGATCTGATAGATACGCGCGG 610 AAAGCATGCTCCACCTGGAGCGAG CTCGCTCCAGGTGGAGCAACACCG 611 ACTTGCATCGCTGGGTAGATCCGG CCGGATCTACCCAGCGATCGATGCAAGT 612 TGCTTACGCAGTGGATTGGTCAGA TCTGACCAATCCACTGCGTAAGCA 613 ATGCAGATGAACAAATCGCCGAAT ATTCGGCGATTTGTTCATCTGCAT 614 GCAATTCTGGGCCATGTATTCGTC GACGAATACATGCCCAGAATTGC 615 AGGGTTCCTTACGCGTCGACATG CCATGTCGACGGTAAGGAACCCT 616 GTGGAGCTAATCGCGGAATTATCCGC GAATCACCAGCGTAAGGAACCCT 617 TCGTAGTCTCACCGGCAATGATCC GGATCATTGCCGGTAGGACCACCAC 618 TTATAGCAGTGCGCCAATGATCC GGATCATTGCCGGTAGACCACACAC 619 CGAACAGTGCTGCTCGACAAT ATAGCGCTCTACACAGA 610 CGAACAGTGCTGCTCGACAAT ATAGCGCTCACACACACAC 620 TCCGCGTGGACTGTTAGACGCTAA TAGAGCATTAGCCACCACGCGGA 621 CATTAGCCCGCTGTCGGTCAA TTGAGCGCACAGCACTGCTTCG 622 GGAAAGAAACTCAGACGGCCAATG CATTTCCGACAGCGGCACATGCTTC 623 CGACTCGCTGGGTAACTGT ACAGTTACCACAGCGGGCTAATG 624 CATGATCCTCTGTTTCACCCCCG CCGCGGGTCAAACAGAGCACTCTTCC 625 GGCGTAGCGCTCTAAAAGCTTCG CCGAAGCTTTTAGAGCGCTACCC 626 AGTGATCCCTTGTTTCACCCCCG CCGCGGTCAAACAGAGGATCATC 627 TATGGAAAGGGCAACAGCCGTATC GATACCGCCTGAACCACCC 626 AGTGATCCCTTGTTCACCCCCG CCGCGGTGAAACAGAGGATCATC 627 TATGGAAAGGGCAACAGCCGTATC GATACCGCCTGATGGCCTTCCATC 628 CTGTGGTTGATGAGGCCTATC GATACCGCCTGATTCCACCACAG 629 ACTCGCTGGAACAGCGCTATC GATACCGCCTGAATCCCCCTTCCATC 621 CAGGCCCAAACACACCGCGTATAC GTGTCACCCCTTTCCATA 622 CTGTGGTTGATGTGAGCCTATCAC GTGTAACCCCCTGATTCCCCCTTCCATC 623 GGCCAATGGGCCCTACAC GTGTGGATCCTCCATCAACCACAG 629 ACTCGCTGGAATTTCCGCCGAACCACCCTTCCCC 631 GGCGCAATGGGCCCTACAC CTGTAACCCCTGGTCCCCTTTCCATC 632 GGCCAATGGGCCAATAATACTA TAGTATTTATGCGCCCATTCCGCC 633 GATGGTGGACTGAGCCCTTCCCC GCGGGAAGGCCTCCACCACC 634 CCGCGCATAAGCGCAATAAGGGAGA TCTCCCCTATTGCGCCAACCATC 635 GTCAATTCCGCCTACATCCCCTA TAGGGCCTGATCGCCCAACCACACCAACACCCCAACACCCCCAACCCCAACCCC	603		CCGCGAG'	IGTGGATGGC	GTGTTGA	TCAAC	ACGCCATCC <i>I</i>	ACACTCGCGG
GGCGTGGGAGGATAAGACGACCAC GTGGTGCGTTCCTAACATGGACCA  TGCTCCATGTTAGGAACGACCAC GTGGTGCGTTCCTAACATGGACCA  GGCGTGTTGGTCGGACTGACGACTG CAGTCGTCAGTCCGACCAACACCG  CGGGCGTATCTATCAGATCTGG CCCAGATCTGATAGATACGCCGGG  AAAGCATGCTCCACCTGGAGCGAG CTCGCTCCAGGTGGAGCATGCTTT  G11 ACTTGCATCGCTGGGTAGATCCGG CCGGATCTACCAGCGAGTGCAAGT  G12 TGCTTACGCAGTGGATTGGTCAGA TCTGACCAATCCACTGCGTAAGCA  G13 ATGCAGATGAACAAATCGCCGAAT ATTCGGCGATTGTTCATCTGCAT  G14 GCAATTCTGGGCCATGTATTCGTC GACGAATACATGGCCCAGATTGC  G15 AGGGTTCCTTACGCGTCGACATG CCATTGCGCGATTAGCTCCAC  G16 GTGGAGCTAATCGCGGAATGATCC GCAATACACAGGCCCAGAATTGC  G17 TCGTAGTCTCACCGGCAATGATCC GGATCATTGCCGGTAAGGAACCCT  G18 TTATAGCAGTGCGCCAATGATCC GGATCATTGCCGGTAGGACCACTGCTT  G19 CGAACAGTGCTCCTCAGCTCAA TTGAGCGCTCAGCACTGCTATAA  G19 CGAACAGTGCTGCTCACATTTTGACCGGTAAGGACACTGTTCG  G20 TCCGCGTGGACTGTTAGACGCTAA ATAGCGTCTACAGCAGCACTGTTCG  G21 CATTAGCCCGCTGTCGGTCAAA TTGAGCGCACACGCACTGCTATAA  G19 CGAACAGTGCTGCTCAGATTATCCGACGGGACACCACTGTTCG  G20 TCCGCGTGGACTGTTAGACGCTAAT ATAGCGTCTACAGCAGCACACTGTTCC  G21 CATTAGCCCGCTGTCGGTAACTGT ACAGTTACCACAGCGGGA  G21 CATTAGCCCGCTGTCGGTAACTGT ACAGTTCCCACGCGGA  G22 GGAAAGAAACTCAGACGGCCAATG CATTGCGCGTTGAGTTTCTTTCC  G23 CGACTCGCTGGACAGGGAGAATCGT ACGATTCCCTGTGCAGCGGATCG  G24 CATGATCCTCTGTTTCACCCCCGG CCGCGGGTGAAACAGAGGATCATG  G25 GGCGTAGCGCTCTAAAAGCTTCGG CCGAAGCTTTTAGAGCGCTACCCC  G26 AGTGATCCCATCAGGCCCGTATAC GTATACCGGCCTGATGGCATCACC  G27 TATGGAAAGGGCAACAGCGCTATC GATAGCGCTGATGGCCTTCCATA  G28 CTGTGGTTGATGAGGAGAACACCCGTATCACCACAG  G29 ACTCGCTGGAATTTGCGCTGACAC GTGTAACCGCTGAATTCCAGCGAG  G31 GGCCCAAACACACGGGTACAC GTGTAACCGCTGGTTCCCCTTTCCATA  G31 GGCGCAATGGGCCATACAAC CTGTAACCCCTGGGCCTAGCCC  G31 GGCGCAATGGGCCCATACAAC CTGTAACCGCTGGTTCCGCC  G32 GGTCAATTCCGCCTACATGCCCTA TAGGGCCTGATTGCGCC  G33 GATGGTGGACTGCACCTTCCCC GCGGGAAGGCCTACACCACC  G33 GATGGTGGACTGCCCTA TAGGGCATTTAGCGCCAACCACC  G34 GATGGTGGACTGCACCCTACATCCCCTATTCCGCC  G33 GATGGTGGACTGCACCCCAATAATACCAA TAGGGCATTATGCGCCAACCAAC  G34 GATGGTGGACTGAGCCCTACATCCCCTA TAGGGCCTATCCGCCAACCAACACCAAC  G34 GATGGTGGACTGAGCCCTACAACCCCAACCCAACACCAACACCAACACCAACACCA	604		AATGTGTG	CGGTCCTAAG	CCGGGTG	CACCC	GGCTTAGGA	CCGACACATT
GOTTCCATGTTAGGAACGCACCAC GTGGTGCGTTCCTAACATGGAGCA GOS CGGTGTTGGTCGACTGACGACTC CAGTCGTCAGTCCGACCAACACCG GOG CCGCGCGTATCTATCAGATCTGGG CCCAGATCTGATAGATACGCGCGG GOO CCGCGCGTATCTATCAGATCTGGG CCCAGATCTGATAGATACGCGCGG GOO AAAGCATGCTCCACCTGGAGCGAG CTCGCTCCAGGTGGAGCATGCTTT GOTTACGCAGTGGATTGGTCAGA TCTGACCAATCCACTGCGTAAGCA GOO ATTCGAGCAGTGGATTGGTCAGA TCTGACCAATCCACTGCGTAAGCA ATGCAGATGAACAAATCGCCGAAT ATTCGGCGATTTGTTCATCTGCAT GOAATTCTGGGCCATGTATTCGTC GACGAATACAATGGCCCAGAATTGC GTGGAGCTAATCGCGGAGCCTCAGA TCTGAGCGCGTAAGGAACCCT GOTGAGACTAATCGCGGAGCCTCAGA TCTGAGGCTCGGCGTAAGGAACCCT GTGAGACTTACCGCGCAATGATCC GGATCATTGCCGGTGAGACTACGA TTATAGCAGTGCGCCAATGCTTCG CGAAGCATTGCCGGTGAGACTACGA GOO TCCGCGTGGACTGTTAGACGCTAA TTGAGCGACAGCACTGTTTCG CGAACAGTGCTGCTCGACTATA ATAGCGTCTAACAGTCCACGCGGA CCATTAGCCCGCTGTCGGTCAAT ATAGCGTCTAACAGTCCACGCGGA CCATTAGCCCGCTGTCGGTAACTGT ACAGTTACCGACAGCGGGTAATG CCATTAGCCCGCTGTCGGTAACTGT ACAGTTACCGACAGCGGGCTAATG CCATTAGCCCGCTGTCGGTAACTGT ACAGTTACCGACAGCGGGCTAATG CCATCACTGGACAGGAGAAACTCCAGACGCGCAATG CATTGCCGTCTAACAGTCCACCGCGGA CCATGATCCTCTGTTTCACCCGCGG CCGCGGGTGAAACAGGGGTCACGC CATGATCCTCTGTTTCACCCGCGG CCGCGGGTGAAACAGAGGATCATG CCATGATCCCTCTGTTTCACCCGCGG CCGCGGGTGAAACAGAGGATCATG CATTAGGAAAGGGCAACAGCGCCTATC GTATACCGGCCTACGCC AGGCTAACGCCTCTAAAAGCTTCG CCGAAGCTTTTAGAGCGCTACCCC CCGAAGCTTTTAGAGCGCCTACCAC GTGTGGATCCTCCTCCATCA CCGCGTAGAGCACACACGCGTTAC GTATACCGGCCTATGCCCTTCCATCA CAGCCCGAACCACGCGGTTACAC GTGTGAGCCCTATCACCACAG CAGCCCGAACCACGCGGTTACAC GTGTGAGCCCTATCACCACAG CAGCCCGAACCACGCGGTTACAC GTGTGAGCCCAAATTCCAGCGCC GOG GGCCAATGCGCCTAAAAATACTA TAGTATTTATGCGCCCATTCCGCC GGCGCAATGCGCCTAAAAATACTA TAGTATTTATGCGCCCATTGCCCC GGCGCAATGCGCCTAAAAATACTA TAGTATTTATGCGCCCATTGCCCC GGCGCAATGCGCCAATAACACAC GCGGAAGGGCTCCAGCCCACCACC GGCGCAATGCGCCAATAACACAC GCGGAAGGGCTCCAGCCCACCACC GGCGCAATGCGCCAAAAATACCAC GCGGAAGGGCTCCAGCCCACCACC GGCGCAATGCGCCAATAAGGGGAGA TCCCCCTATTGCGCCCATTCCGCC GGCGCAATGCGCCAATAGGGCAAATACCACCAG GCGGAAGGCCCAATTGCCCCAACCACCAGAGAGCCCAATAGCGCCAATAGGGCCAAATAGGGCAAATAGGGCACACACA	605		TAAGACG	AGCCTGCACA	AGCTTGCG	CGCAA	GCTGTGCAG	CTCGTCTTA
CGGTGTTGGTCGGACTGACGACTG CAGTCGTCAGTCCGACCAACACCG CCGCGCGTATCTATCAGATCTGGG CCCAGATCTGATAGATACGCGCGG AAAGCATGCTCCACCTGGAGCGAG CTCGCTCCAGGTGGAGCATGCTTT ACTTGCATCGCTGGGTAGATCCGG CCGGATCTACCCAGCGATGCAAGT TGCTTACGCAGTGGATTGGTCAGA TCTGACCAATCCACTGCGTAAGCA ATGCAGATGAACAAATCGCCGAAT ATTCGGCGATTTGTTCATCTGCAT GCAATTCTGGGCCATGTATTCGTC GACGAATACCACTGCCTAAGCA AGGGTTCCTTACGCGTCGACATGG CCATGTCGACGCGTAAGGAACCCT GGGGGGTAATCGCGGAATGATCC GACGAATACCACTGCCGAAATTGC GTGGAGCTAATCGCGGCACATGG CCATGTCGACGCGTAAGGAACCCT TCGTAGTCTCACCGGCAATGATCC GGATCATTGCCGGTGAGACCCCT GTGAGCTTACCACGGCAATGCTTCG CGAAGCATTGCCGCACTGCTATAA CTGTAGTCTCACCGGCAATGCTTCG CGAAGCATTGCCGCACTGCTATAA CGGACAGTGCTGCGTCGACTGCTCAA TTGAGCGACGGCACACTGCTTCG CGAACAGTGCTGTCGGTCGATCAT TAGACGGACAGCACTGTTCG CGAACAGTGCTGTCGGTCAACTGT ACAGTTACCGACAGCGGGCTAATG CATTAGCCCGCTGTCGGTAACTGT ACAGTTACCGACAGCGGGCTAATG CATTAGCCCGCTGTCGGTAACTGT ACAGTTACCGACAGCGGGATAGG CAGACCGCTGGACAGGAGAATCCT ACGATTCCCTGTCCAGCGAGTCG CAACAGTCCTCTGTTTCACCCGCGG CCGCGGGTGAAACAGAGGATCATG CAGATCCCTCTGTTTCACCCGCGG CCGCGGGTGAAACAGAGGATCATG CAGGCCGAACCACGAGCACACACGCGCTATAC GTATAGCGCCTGACTTTCCATA CAGTTCCTCTGTTTCACCCGCGG CCGGAGCTTTTTAGAGCGCTACACC CAGGCCTGAACCACAGCGCCTATAC GTATAGCGCCTGATGCACCCC AGTGATCCCTTTAAAAGCTTCGG CCGAAGCTTTTAGAGCGCTACCCC CAGGCCTGAACCACCGCGTTACAC GTGTGAGCCTTACACCACAG CAGGCCCGAACCACCAGCGCTATAC GTATACCGCGAAATTCCACCACAG CAGGCCCGAACCACCGCGTTACAC CTGTAACCGCGTGTTCCCCTTTCCATA CAGGCCCGAACCACCGCGTTACAC CTGTAACCGCGTGGTTCCGCCTGCCC CAGGCCCGAACCACCGCGTTACAC CTGTAACCGCGTGGTTCCGCCCTGCCCCACCACCGCGCTTACACCACCAGCGCTACACCCCGCCGAACCACCGCGGTTACAC CTGTAACCGCGTGGTTCCGCCCACCACCGCCGAACCACCGCGAACCACCGCGGTTACAC CTGTAACCGCGTGGTTCCGCCCACCACCGCCGAACCACCGCGAACCACCGCGAACCACC	606		GGCGTGG	GAGGATAAGA	ACGATGTC	GACAT	CGTCTTATC	CTCCCACGCC
609 CCGCGCGTATCTATCAGATCTGGG CCCAGATCTGATAGATACGCGCGG 610 AAAGCATGCTCCACCTGGAGCGAG CTCGCTCCAGGTGGAGCATGCTTT 611 ACTTGCATCGCTGGGTAGATCCGG CCGGATCTACCCAGCGATGCAAGT 612 TGCTTACGCAGTGGATTGGTCAGA TCTGACCAATCCACTGCGTAAGCA 613 ATGCAGATGAACAAATCGCCGAAT ATTCGGCGATTTGTTCATCTGCAT 614 GCAATTCTGGGCCATGTATTCGTC GACGAATACATGGCCCAGAATTGC 615 AGGGTTCCTTACGCGTCGACATGG CCATGTCGACGCGTAAGGAACCCT 616 GTGGAGCTAATCGCGGAACATGG CCATGTCGACGCGTAAGGAACCCT 617 TCGTAGTCTCACCGGCAATGATCC GGATCATTGCCGGTGAGACTACGA 618 TTATAGCAGTGCGCAATGATCC CGAAGCATTGGCGGACACGCACTGTTCG 620 TCCGCGTGGACTGTTCGGTCACAT ATTGGGGACGGCACTGCTTCG 621 CATTAGCCCGCTGTCGGTCACAT ATAGCGTCTAACAGTCCACGCGGA 622 GGAAAGAAACTCAGACGCCAATG CATTGCCGGTGAGACACTGTTCC 623 CGACTCGCTGGGACAGCACTGT ACAGTTACCGACAGCGGGCTAATG 624 CATGATCCTCTGTTTCACCCGCGG CCGCGGGTGAAACAGAGGGTCACTG 625 GGCGTAGCGCTCTAAAAGCTTCG CCGAAGCTTTTAGAGCGCTACCCC 626 AGTGATGCCATCAGACCCGTATAC GTATACCGGCTAACACCCC 627 TATGGAAAGGGCAACAGCCCTATAC GTATACCGGCCTACCCC 628 AGTGATGCCATCAGGCCCGTATAC GTATACCGGCCTACCCCC 629 ACTCGCTGGAACAACGCCCTATAC GTATACCGGCCTATCCCACCACG 629 ACTCGCTGGAATTTGCGCTGACCCCTACCCCCCACACCCCGGG 631 CAGGCCCGAACCACCGCGTTACAC CTGTAACCGCTGTTCCCATCACCACAG 632 GGCCAATGGGCCATAAAATACTA TAGTATTTATGCGCCCATTCCGCC 633 GATGGTGGACTGAGCCCTTCCGC GCGGAAGGCTTATGCCCCACATC 634 CCGCGCATAGCGCTACATGCCCTA TAGGGCATGTAGCCCACATC 635 TCTTCTGGCTGCACACCCGAA TCCCCCTATTGCGCCTATCCACCACACCCCCACCCCCACCCCCACCCCCACCCCCACCCC	607		TGCTCCA	IGTTAGGAAC	CGCACCAC	GTGGT	GCGTTCCTA	ACATGGAGCA
AAAGCATGCTCCACCTGGAGCGAG CTCGCTCCAGGTGGAGCATGCTTT 611 ACTTGCATCGCTGGGTAGATCCGG CCGGATCTACCCAGCGATGCAAGT 612 TGCTTACGCAGTGGATTGGTCAGA TCTGACCAATCCACTGCGTAAGCA 613 ATGCAGATGAACAAATCGCCGAAT ATTCGGCGATTTGTTCATCTGCAT 614 GCAATTCTGGGCCATGTATTCGTC GACGAATACATGGCCCAGAATTGC 615 AGGGTTCCTTACGCGTCGACATGG CCATGTCGACCGGTAAGGAACCCT 616 GTGGAGCTAATCGCGGAGCCTCAGA TCTGAGCGCGTAAGGAACCCT 617 TCGTAGTCTCACCGGCAATGATCC GGATCATTGCCGGTGAGAACCACGA 618 TTATAGCAGTGCGCCAATGATCC GGATCATTGCCGGTGAGACTACGA 619 CGAACAGTGCTGCCCAA TTGAGCGCGACACGCCTATAA 619 CGAACAGTGCTGTCCGTCCAA TTGAGCGACAGCACTGTTCG 620 TCCGCGTGGACTGTTAGACGCTAT ATAGCGTCTAACAGTCCACCGCGGA 621 CATTAGCCCGCTGTCGGTAACTGT ACAGTTACCGACAGCGGGA 622 GGAAAGAAACTCAGACGGCAATG CATTGCGCGTCTGAGTTTCTTTCC 623 CGACTCGCTGGACAGGAGAATCGT ACAGTTACCAGCGGACTCG 624 CATGATCCTCTGTTTCACCCGCGG CCGCGGGTGAAACAGAGGATCATG 625 GGCGTAGCGCTCTAAAAGCTTCGG CCGAAGCTTTTAGAGCGCTACGCC 626 AGTGATGCCATCAAAAGCTTCGG CCGAAGCTTTTAGAGCGCTACCC 627 TATGGAAAGGGCAACAGCGCTATC GATAACGGGCCTAGCCC 628 CTGTGGTTGATGGAGCCCGTATAC GTATACGGGCCTAGGCATCACC 629 ACTCGCTGGAATTTGCGCTGACAC GTGTGGACCCTATCCATCA 629 ACTCGCTGGAATTTGCGCTGACAC GTGTGAGCCCTATCCACCAC 629 ACTCGCTGGAATTTGCGCTGACAC GTGTGAGCCCTATCCACCACG 630 CAGGCCCGAACCACCGCGTTACAC CTGTTAACCGCCGTGGTTCGGCCTG 631 GGCGCAATGGGCCATAAATACTA TAGTATTTATGCGCCCATTGCGCC 632 GGTCAATTCGCCTGACAC GTGTTACCGCGGAATTGACC 633 GATGGTGGACTGGACCCTA TAGGGCATGATGACCCACAC 634 CCGCCCAACCACCGCGTTACAG CTGTAACCGCGGAATTGACC 635 GATGGTGGACTGGAGCCCTTCCGC GCGGAAGGGCTCCAGCCACCAC 636 GATGGTGGACTGGAGCCCTTCCGC GCGGAAGGGCTCCAGCCACCACC 637 GATGGTGGACCCAATAGGGGAA TCTCCCCTATTGCGCCAACCACC 634 CCGCCCAATAGCGCAATAGGGGAA TCTCCCCTATTGCGCCAACCACCGCG 635 TCTTCTGGCTGCCCGAACCCCGAA TTCCGCCTATTGCGCCGGAACCACCGCGTTCCACCACCAC 636 CCGCGCATAGCCCAATAGGGGAAA TCTCCCCTATTGCGCCAACCACCACCACCACCACCACCACCACCACCACCA	608		CGGTGTT	GGTCGGACTG	GACGACTG	CAGTC	GTCAGTCCG <i>I</i>	ACCAACACCG
611 ACTTGCATCGCTGGGTAGATCCGG CCGGATCTACCCAGCGATGCAAGT 612 TGCTTACGCAGTGGATTGGTCAGA TCTGACCAATCCACTGCGTAAGCA 613 ATGCAGATGAACAAATCGCCGAAT ATTCGGCGATTTGTTCATCTGCAT 614 GCAATTCTGGGCCATGTATTCGTC GACGAATACATGGCCCAGAATTGC 615 AGGGTTCCTTACGCGTCGACATGG CCATGTCGACCGGTAAGGAACCCT 616 GTGGAGCTAATCGCGGACCTCAGA TCTGAGGCTCGCGATTAGCTCCAC 617 TCGTAGTCTCACCGGCAATGATCC GGATCATTGCCGGTGAGACTACGA 618 TTATAGCAGTGCGCCAATGCTTCG CGAAGCATTGGCGCACTGCTATAA 619 CGAACAGTGCTGCTCAA TTGAGCGACGGACAGCACTGTTCG 620 TCCGCGTGGACTGTTAGACGCTAA ATAGCGTCTAACAGTCCACCGGGA 621 CATTAGCCCGCTGTCGGTAACTGT ACAGTTACCGACAGCGGGATAGG 622 GGAAAGAAACTCAGACGCGAATG CATTGCGCGTTAGATTGCC 623 CGACTCGCTGGACAGGAGAATCGT ACAGTTACCGACAGCGGACTAG 624 CATGATCCTCTGTTTCACCCGCGG CCGCGGGTGAAACAGAGGGATCATG 625 GGCGTAGCGCTTAAAAGCTTCG CCGAAGCTTTTAGACGGCTACGC 626 AGTGATGCCATCAAAACCTTCG CCGAAGCTTTTAGACCGCTACCC 627 TATGGAAAGGGCCAATAC GTATACGGGCCTGATGCATCACC 628 CTGTGGTTGATGGAGGACACACCGTATC 628 CTGTGGTTGATGGAGGACACACCGTATC 629 ACTCCCTGAAATTCGCCCGTATAC GTATACGGCCTGATGCACTCATA 628 CTGTGGTTGATGGAGGATCACAC GTGTCAGCCAAATTCCAGCAGG 630 CAGGCCCGAACCACCGCGTTACA CTGTTAACCGCCGAAATTCCACCACAG 621 GGCCCAAACCACCGCGTTACA TAGGGCTGTTGCCCTTTCCATA 631 GGCGCAATGGGCCAATAAATACTA TAGTATTTATGCGCCCAATTGCGCC 632 GGTCAATTCGCCTGACAC GTGTAACCGCGTGGTTCGGCCTGCCC 633 GATGGTGGACTGGAGCCCTTCCGC GCGGAAGGGCTCCAGCCCATCCACCAC 634 CCGCCCAATGCGCCAATAAATACTA TAGGGCTGTTAGCGCCAATTGCCCC 635 GATGGTGGACTGGAGCCCTTCCGC GCGGAAGGGCTCCAGCCACCACC 636 GATGGTGGACTGGAGCCCTTCCGC GCGGAAGGGCTCCAGCCACCACC 637 GATGGTGGACTGGAGCCCTTCCGC GCGGAAGGGCTCCAGCCACCACC 638 CCCGCCAATGCGCCAATAGGGGAGA TCTCCCCTATTGCGCCAACCACCACCACCACCACCACCACCACCACCACCA	609		CCGCGCG'	TATCTATCAG	SATCTGGG	CCCAG	ATCTGATAG <i>I</i>	ATACGCGCGG
ATGCAGATGACAATCCCGAAT ATTCGGCGATTGTTCATCTGCAT GCAATTCTGGCCATGTATTCGTC GACGAATACAATGCCCAAATTGC GCAATTCTGGGCCATGTATTCGTC GACGAATACATGGCCCAGAATTGC AGGGTTCCTTACGCGTCGACATGG CCATGTCGACGCGTAAGGAACCCT GTGGAGCTAATCGCGGACCTCAGA TCTGAGGCTCGCGATTAGCTCCAC GTGGAGCTAATCGCGGCAATGATCC GGATCATTGCCGCGTGAGAACCCT TCGTAGTCTCACCGGCAATGATCC GGATCATTGCCGGTGAGACTACGA TTATAGCAGTGCGCCAATGCTTCG CGAAGCATTGGCGCACTGCTATAA CGAACAGTGCTGTCCGTCGCTCAA TTGAGCGACGGCACAGCACTGTTCG CATTAGCCCGCTGTTAGACGCTAT ATAGCGTCTAACAGTCCACCGCGA CATTAGCCCGCTGTTAGACGCTAT ATAGCGTCTAACAGTCCACGCGGA CATTAGCCCGCTGTCGGTAACTGT ACAGTTACCGACAGCGGGCTAATG CGAACAGAACACCAGAGAGAAACCCAATG CATTGCGCGTCAGCTTTCTTTCC GCAGCTCGCTGGACAGGAGAATCGT ACAGTTACCGACAGCGGGCTAATG CATGATCCTCTCTTTTCACCCCGCG CCGCGGGTGAAACAGAGGATCATG CATGATCCTCTCTTTTCACCCCGCG CCGCGGGTGAAACAGAGGATCATG GCAGCCGAACCACTCCGTAACAGCCCGTATAC GTATACGGGCCTGATGCACCACGC AGTGATGCCATCAGGCCCGTATAC GTATACGGGCCTGATGCACTACACCACAG CTGTGGTTGATGGAGGACACACCGGTTACAG GTGTCAGCGCAAATTCCAGCACAG CTGTGGTTGATGGAGGACACACCGGTTACAG CTGTTAACCGCCTATCACCACAG CAGGCCCGAACCACCACGCGTTACAG CTGTTAACCGCCGTGGTTCGGCCTG GGCGCAATGGGCCCATAAATACTA TAGTATTTATGCGCCCATTCCACCACCAC GGCGCAATGGGCCCATACACCCCTA TAGGGCATGTAGCCCCATTCCGCC GGTCAATTCGCGCTACACTCCCCTA TAGGGCATGAACCACCACCACCACCACCACCACCACCACCACCACCAC	610		AAAGCAT	GCTCCACCTG	GAGCGAG	CTCGC'	TCCAGGTGG <i>I</i>	AGCATGCTTT
ATGCAGATGAACAAATCGCCGAAT ATTCGGCGATTTGTTCATCTGCAT  614 GCAATTCTGGGCCATGTATTCGTC GACGAATACATGGCCCAGAATTGC  615 AGGGTTCCTTACGCGTCGACATGG CCATGTCGACGCGTAAGGAACCCT  616 GTGGAGCTAATCGCGAGCCTCAGA TCTGAGGCTCGCGATTAGCTCCAC  617 TCGTAGTCTCACCGGCAATGATCC GGATCATTGCCGGTGAGACTACGA  618 TTATAGCAGTGCGCCAATGCTTCG CGAAGCATTGCCGCACTGCTATAA  619 CGAACAGTGCTGTCCGTCCAA TTGAGCGACGGACAGCACTGTTCG  620 TCCGCGTGGACTGTTAGACGCTAT ATAGCGTCTAACAGTCCACCGCGA  621 CATTAGCCCGCTGTCGGTAACTGT ACAGTTACCGACAGCGGACTATGC  622 GGAAGAAACTCAGACGCGCAATG CATTGCGCGTCTGAGTTTCTTCC  623 CGACTCGCTGGACAGGAGAATCGT ACAGTTCCTGTCCACGCGGACCGCCCGACCCCTGCTTCCACCACCACCGCGACCCCCCCC	611		ACTTGCA	ICGCTGGGTA	AGATCCGG	CCGGA'	ICTACCCAGO	CGATGCAAGT
614 GCAATTCTGGGCCATGTATTCGTC GACGAATACATGGCCCAGAATTGC 615 AGGGTTCCTTACGCGTCGACATGG CCATGTCGACGCGTAAGGAACCCT 616 GTGGAGCTAATCGCGAGCCTCAGA TCTGAGGCTCGCGATTAGCTCCAC 617 TCGTAGTCTCACCGGCAATGATCC GGATCATTGCCGGTGAGACTACGA 618 TTATAGCAGTGCGCCAATGCTTCG CGAAGCATTGCCGGTCATATAA 619 CGAACAGTGCTGTCCGTCGAA TTGAGCGACAGCACTGCTATAA 619 CGAACAGTGCTGTAGACGCTAA ATAGCGTCTAACAGTCCACGCGGA 621 CATTAGCCCGCTGTTAGACGCTAT ATAGCGTCTAACAGTCCACGCGGA 622 GGAAAGAAACTCAGACGCGCAATG CATTGCGCGTCTGAGTTTCTTCC 623 CGACTCGCTGGACAGGAGAATCGT ACGATTCCTGTCCAGCGAGTCG 624 CATGATCCTCTGTTTCACCCGCGG CCGCGGGTGAAACAGAGGATCATG 625 GGCGTAGCGCTCTAAAAGCTTCGG CCGAAGCTTTTAGAGGCGCTACGCC 626 AGTGATGCCATCAGGCCCGTATAC GTATACCGGCCTGATGCACCAC 627 TATGGAAAGGGCAACAGCGCTATC GATAGCGGCTGATGCACCACAG 628 CTGTGGTTGATGGAGGATCCACAC GTGTGGATCCTCCATCAACCACAG 629 ACTCGCTGGAATTTGCGCTGACAC GTGTCAGCGCAAATTCCAGCGAGT 630 CAGGCCCGAACCACGCGGTTACAG CTGTAACCGCGAAATTCCAGCGAGT 631 GGCGCAATGGGCCATACATA TAGTATTTATGCGCCCATTGCGCC 632 GGTCAATTCGCGCTACATGCCCTA TAGGGCATGTAGCCCACTC 633 GATGGTGGACCGCTACATGCCCTA TAGGGCATGTAGCCCACATC 634 CCGCGCATAGCGCCAATAGGGGAGA TCCCCCTATTGCGCCGGAAGGCTCCACCACTC 635 TCTTCTGGCTGTCCGGCAACCCCGAA TTCCGCTATTGCGCCGG 636 TCTTCTGGCTGTCCGGCAACCCCGAA TTCCGCTATTGCGCCGGACAGCCAGAAGA	612		TGCTTAC	GCAGTGGATT	GGTCAGA	TCTGA	CCAATCCACT	GCGTAAGCA
AGGGTTCCTTACGCGTCGACATGG CCATGTCGACGCGTAAGGAACCCT G16 GTGGAGCTAATCGCGAGCCTCAGA TCTGAGGCTCGCGATTAGCTCCAC G17 TCGTAGTCTCACCGGCAATGATCC GGATCATTGCCGGTGAGACTACGA G18 TTATAGCAGTGCGCCAATGCTTCG CGAAGCATTGCCGCACTGCTATAA G19 CGAACAGTGCTGTCCGTCCACA TTGAGCGACAGCACTGCTTCG G20 TCCGCGTGGACTGTTAGACGCTAT ATAGCGTCTAACAGTCCACGCGGA G21 CATTAGCCCGCTGTCGGTAACTGT ACAGTTACCGACAGCGGGCTAATG G22 GGAAAGAAACTCAGACGCGCAATG CATTGCGCGTCTGAGTTTCTTCC G23 CGACTCGCTGGACAGGAGAATCGT ACGATTCTCCTGTCCAGCGAGTCG G24 CATGATCCTCTGTTTCACCCCGCG CCGCGGGTGAAACAGAGGATCATG G25 GGCGTAGCGCTCTAAAAGCTTCGG CCGAAGCTTTTAGAGCGCTACACC G26 AGTGATGCCATCAGGCCCGTATAC GTATACCGGCCTGATGCACCC G27 TATGGAAAGGGCAACAGCGCTATC GATAGCGCTGATGCCCTTTCCATA G28 CTGTGGTTGATGGAGGATCCACC GTGTGGATCCTCCATCAACCACAG G29 ACTCGCTGGAACTTTCGCCTGACAC GTGTGGATCCTCCATCAACCACAG G29 ACTCGCTGGAATTTCGCTGACAC GTGTGAGCGCAAATTCCAGCGAGT G30 CAGGCCCGAACCACGCGGTTACAG CTGTAACCGCGTGGTTCGGCCTG G31 GGCGCAATGGGCCGATAAATACTA TAGTATTTATGCGCCCATTGCGCC G32 GGTCAATTCGCGCTACATGCCCTA TAGGGCATGTAGCGCAATTGACC G33 GATGGTGGACCTGCACATC GCGGAAGGGCTCCAGTCCACCATC CCGCCGATAGCGCATAAGAGCCCTTACCG CCGGAAGGGCTCCAGTCCACCATC CCGCGCATAGCGCAATAGGGGAAA TCCCCCTATTGCGCCGGGACACCCCACAC CCGCGCATAGCGCAATAGGGGAAA TCCCCCTATTGCGCCGGACACCCACCACC CCGCGCATAGCGCAATAGGGGAAA TCCCCCTATTGCGCCGGACACCACCACCACCACCACCACCACCACCACCA	613		ATGCAGA	IGAACAAATO	CGCCGAAT	ATTCG	GCGATTTGTT	CATCTGCAT
616 GTGGAGCTAATCGCGAGCCTCAGA TCTGAGGCTCGCGATTAGCTCCAC 617 TCGTAGTCTCACCGGCAATGATCC GGATCATTGCCGGTGAGACTACGA 618 TTATAGCAGTGCGCCAATGCTTCG CGAAGCATTGGCGCACTGCTATAA 619 CGAACAGTGCTGTCCGTCGCTCAA TTGAGCGACAGCAGCACTGTTCG 620 TCCGCGTGGACTGTTAGACGCTAT ATAGCGTCTAACAGTCCACGCGGA 621 CATTAGCCCGCTGTCGGTAACTGT ACAGTTACCGACAGCGGGCTAATG 622 GGAAAGAAACTCAGACGCGCAATG CATTGCGCGTCTGAGTTTCTTCC 623 CGACTCGCTGGACAGGAGAATCGT ACGATTCTCCTGTCCAGCGAGTCG 624 CATGATCCTCTGTTTCACCCGCGG CCGCGGGTGAAACAGAGGATCATG 625 GGCGTAGCGCTCTAAAAGCTTCGG CCGAAGCTTTTAGAGCGCTACGCC 626 AGTGATGCCATCAGGCCCGTATAC GTATACCGGCCTGATGGCATCACT 627 TATGGAAAGGGCAACAGCGCTATC GATAGCGCTTGTCCCTTTCCATA 628 CTGTGGTTGATGGAGGATCCACAC GTGTGGATCCTCCATCAACCACAG 629 ACTCGCTGGAACCACGCGTTACAG CTGTAACCGCGAGTT 630 CAGGCCCGAACCACGCGGTTACAG CTGTAACCGCGTGTTCGGCCTG 631 GGCGCAATGGGCCCTATAATACTA TAGTATTTATGCGCCCATTGCGCC 632 GGTCAATTCGCGCTACATGCCCTA TAGGGCATGTAGCCCATC 633 GATGGTGGACTGGAGCCCTTCCGC GCGGAAGGGCTCCACCATC 634 CCGCGCATAGCGCAATAGGGGAGA TCTCCCCTATTGCGCTATGCGCGG 635 TCTTCTGGCTGCCCGAACCCCGAA TTCCGGGTGCCAGACAAGAGA 635 TCTTCTGGCTGTCCGGCACCCCGAA TTCCGGCTGGCCAGAAGAGA	614		GCAATTC	TGGGCCATGT	ATTCGTC	GACGA	ATACATGGC	CCAGAATTGC
TCGTAGTCTCACCGGCAATGATCC GGATCATTGCCGGTGAGACTACGA TTATAGCAGTGCGCCAATGCTTCG CGAAGCATTGGCGCACTGCTATAA CGAACAGTGCTGTCCGTCCGTCAA TTGAGCGACGGACAGCACTGTTCG TCCGCGTGGACTGTTAGACGCTAT ATAGCGTCTAACAGTCCACGCGGA CATTAGCCCGCTGTCGGTAACTGT ACAGTTACCGACAGCGGGCTAATG GCGGAAAGAAACTCAGACGCGCAATG CATTGCGCGTCTGAGTTTCTTCC CGACTCGCTGGACAGGAGAATCGT ACGATTCCCTGTCCAGCGAGTCG CGACTCGCTGGACAGGAGAATCGT ACGATTCTCTTCCAGCGAGTCG CGACTCGCTGGACAGGAGAATCGT ACGATTCTCCTGTCCAGCGAGTCG CATGATCCTCTGTTTCACCCGCGG CCGCGGGTGAAACAGAGGATCATG GCGCTAGCGCTCTAAAAGCTTCGG CCGAAGCTTTTAGAGCGCTACGCC AGTGATGCCATCAGGCCCGTATAC GTATACGGGCCTGATGCACTACACCACAG ACTGGTTGATGGAGAGAGACCCCGTATC GATAGCGCTGTTGCCCTTTCCATA CTGTGGTTGATGGAGGATCCACAC GTGTGGATCCTCCATCAACCACAG ACTCGCTGGAATTTGCGCTGACAC GTGTCAGCGCAAATTCCAGCAGGT CAGGCCCGAACCACGCGGTTACAG CTGTAACCGCGTGGTTCGGGCCTG GGCGCAATGGGCGCATAAATACTA TAGTATTTATGCGCCCATTGCGCC GGTCAATTCGCGCTACATGCCCTA TAGGGCATGTAGCCCATTCACCACACCA	615		AGGGTTC	CTTACGCGTC	CGACATGG	CCATG	TCGACGCGT	AAGGAACCCT
TTATAGCAGTGCGCCAATGCTTCG CGAAGCATTGGCGCACTGCTATAA  CGAACAGTGCTGTCCGTCGCTCAA TTGAGCGACGGACAGCACTGTTCG  CGAACAGTGCTGTCCGTCGCTCAA TTGAGCGACAGCACTGTTCG  TCCGCGTGGACTGTTAGACCGCTAT ATAGCGTCTAACAGTCCACGCGGA  CATTAGCCCGCTGTCGGTAACTGT ACAGTTACCGACAGCGGGCTAATG  CATTAGCCCGCTGTCGGTAACTGT ACAGTTACCGACAGCGGGCTAATG  CATTAGCCCGCTGTCGGTAACTGT ACAGTTACCGACAGCGGGCTAATG  CGACTCGCTGGACAGGAGAATCGT ACGATTCTCCTGTCCAGCGAGTCG  CGACTCGCTGGACAGGAGAATCGT ACGATTCTCCTGTCCAGCGAGTCG  CATGATCCTCTGTTTCACCCGCGG CCGCGGGTGAAACAGAGGGATCATG  GCGCTAGCGCTCTAAAAGCTTCGG CCGAAGCTTTTAGAGCGCTACGCC  AGTGATGCCATCAGGCCCGTATAC GTATACCGGGCCTGATGCATCACT  TATGGAAAGGGCAACAGCGCTATC GATAGCGCCTGTTGCCCTTTCCATA  CTGTGGTTGATGGAGGATCCACAC GTGTGGATCCTCCATCAACCACAG  ACTCGCTGGAATTTGCGCTGACAC GTGTCAGCGCAAATTCCAGCGAGT  CAGGCCCGAACCACGCGGTTACAG CTGTAACCGCGTGGTTCGGCCC  GGGCAATGGGCCCATAAATACTA TAGTATTTATGCGCCCATTGCGCC  GGTCAATTCGCGCTACATGCCCTA TAGGGCATGAGCGCAATTGACC  GATGGTGGACTGGAGCCCTTCCGC GCGGAAGGGCTCCACCATC  CCGCGCATAGCGCCAATAGGGGAA TCTCCCCTTATTGCGCTATCCCCTC  CCGCGCATAGCGCCAATAGGGGAA TCTCCCCTTATTGCGCTATGCGCGG  TCTTCTGGCTGTCCGGCACCCGAA TTCCGCTGGACAGCCAGAAGA	616		GTGGAGC'	FAATCGCGAG	GCCTCAGA	TCTGA	GGCTCGCGAT	TAGCTCCAC
CGAACAGTGCTGTCCGTCGCTCAA TTGAGCGACGGACAGCACTGTTCG  TCCGCGTGGACTGTTAGACGCTAT ATAGCGTCTAACAGTCCACGCGGA  CATTAGCCCGCTGTCGGTAACTGT ACAGTTACCGACAGCGGGCTAATG  G22 GGAAAGAAACTCAGACGCGCAATG CATTGCGCGTCTGAGTTTCTTTCC  CGACTCGCTGGACAGGAGAATCGT ACGATTCTCCTGTCCAGCGAGTCG  CATGATCCTCTGTTTCACCCGCGG CCGCGGGTGAAACAGAGGATCATG  CATGATCCTCTGTTTCACCCGCGG CCGCAGGTGAAACAGAGGATCATG  G25 GGCGTAGCGCTCTAAAAGCTTCGG CCGAAGCTTTTAGAGCGCTACGCC  AGTGATGCCATCAGGCCCGTATAC GTATACGGGCCTGATGGCATCACT  TATGGAAAGGGCAACAGCGCTATC GATAGCGCTGTTGCCCTTTCCATA  CTGTGGTTGATGGAGGATCCACAC GTGTCAGCCCAAACTCCACCAG  ACTCGCTGGAATTTGCGCTGACAC GTGTCAGCGCAAATTCCAGCGAGT  G30 CAGGCCCGAACCACGCGGTTACAG CTGTAACCGCGTGGTTCGGCCTG  G31 GGCGCAATGGGCCATAAATACTA TAGTATTTATGCGCCCATTGCGCC  G33 GATGGTGGACTGGAGCCCTTCCGC GCGGAAGGGCTCCAGTCCACCATC  CCGCGCATAGCGCAATAGGGGAGA TCTCCCCTATTGCGCTATGCGCG  G34 CCGCGCATAGCGCAATAGGGGAGA TCTCCCCTATTGCGCCTATGCGCG  TCTTCTGGCTGTCCGGCACCCGAA TTCGGGTGCCGGACAGCCAGAAGA	617							
TCCGCGTGGACTGTTAGACGCTAT ATAGCGTCTAACAGTCCACGCGGA CATTAGCCCGCTGTCGGTAACTGT ACAGTTACCGACAGCGGGCTAATG G22 GGAAAGAAACTCAGACGCGCAATG CATTGCGCGTCTGAGTTTCTTTCC CGACTCGCTGGACAGGAGAATCGT ACGATTCTCCTGTCCAGCGAGTCG CATGATCCTCTGTTTCACCCGCGG CCGCGGGTGAAACAGAGGATCATG G24 CATGATCCTCTGTTTCACCCGCGG CCGCGGGTGAAACAGAGGATCATG G25 GGCGTAGCGCTCTAAAAGCTTCGG CCGAAGCTTTTAGAGCGCTACGCC AGTGATGCCATCAGGCCCGTATAC GTATACGGGCCTGATGGCATCACT TATGGAAAGGGCAACAGCGCTATC GATAGCGCTGTTGCCCTTTCCATA CTGTGGTTGATGGAGGATCCACAC GTGTGGATCCTCCATCAACCACAG ACTCGCTGGAATTTGCGCTGACAC GTGTCAGCGCAAATTCCAGCGAGT G30 CAGGCCCGAACCACGCGGTTACAG CTGTAACCGCGTGTTCGGCCTG G31 GGCGCAATGGGCCATAAATACTA TAGTATTTATGCGCCCATTGCGCC GGTCAATTCGCGCTACATGCCCTA TAGGGCATGAGCGCAATTGACC GATGGTGGACTGGAGCCCTTCCGC GCGGAAGGGCTCCAGTCCACCATC CCGCGCATAGCGCAATAGGGGAGA TCTCCCCTATTGCGCTATGCGCG TCTTCTGGCTGTCCGGCACCCGAA TTCCGGGTGCCGGACAGCCAGAAGA								
621 CATTAGCCCGCTGTCGGTAACTGT ACAGTTACCGACAGCGGGCTAATG 622 GGAAAGAACTCAGACGCGCAATG CATTGCGCGTCTGAGTTTCTTTCC 623 CGACTCGCTGGACAGGAGAATCGT ACGATTCTCCTGTCCAGCGAGTCG 624 CATGATCCTCTGTTTCACCCGCGG CCGCGGGTGAAACAGAGGATCATG 625 GGCGTAGCGCTCTAAAAGCTTCGG CCGAAGCTTTTAGAGCGCTACGCC 626 AGTGATGCCATCAGGCCCGTATAC GTATACGGGCCTGATGGCATCACT 627 TATGGAAAGGGCAACAGCGCTATC GATAGCGCTGTTGCCCTTTCCATA 628 CTGTGGTTGATGGAGGATCCACAC GTGTGGATCCTCCATCAACCACAG 629 ACTCGCTGGAATTTGCGCTGACAC GTGTCAGCGCAAATTCCAGCGAGT 630 CAGGCCCGAACCACGCGGTTACAG CTGTAACCGCGTGGTTCGGCCTG 631 GGCGCAATGGGCCATAAATACTA TAGTATTTATGCGCCCATTGCGCC 632 GGTCAATTCGCGCTACATGCCCTA TAGGGCATGTAGCGCGAATTGACC 633 GATGGTGGACTGGAGCCCTTCCGC GCGGAAGGGCTCCAGTCCACCATC 634 CCGCGCATAGCGCAATAGGGGAGA TCTCCCCTATTGCGCTATGCGCG								
GGAAAGAAACTCAGACGCGCAATG CATTGCGCGTCTGAGTTTCTTCC  CGACTCGCTGGACAGGAGAATCGT ACGATTCTCCTGTCCAGCGAGTCG  CATGATCCTCTGTTTCACCCGCGG CCGCGGGTGAAACAGAGGATCATG  GCGCGTAGCGCTCTAAAAGCTTCGG CCGAAGCTTTTAGAGCGCTACGCC  AGTGATGCCATCAGGCCCGTATAC GTATACGGGCCTGATGGCATCACT  TATGGAAAGGGCAACAGCGCTATC GATAGCGCCTGTTGCCCTTTCCATA  CTGTGGTTGATGGAGGATCCACAC GTGTGGATCCTCCATCAACCACAG  ACTCGCTGGAATTTGCGCTGACAC GTGTCAGCGCAAATTCCAGCGAGT  CAGGCCCGAACCACGCGGTTACAG CTGTAACCGCGTGTTCGGCCTG  GGCGCAATGGGCCATAAATACTA TAGTATTTATGCGCCCATTGCGCC  GGTCAATTCGCGCTACATGCCCTA TAGGGCATGTAGCGCGAATTGACC  GATGGTGGACTGGAGCCCTTCCGC GCGGAAGGGCTCCAGTCCACCATC  CCGCGCATAGCGCAATAGGGGAGA TCTCCCCTATTGCGCTATGCGCG  TCTTCTGGCTGTCCGGCACCCGAA TTCGGGTGCCGGACAGCCAGAAGA								
CGACTCGCTGGACAGGAGAATCGT ACGATTCTCCTGTCCAGCGAGTCG CATGATCCTCTGTTTCACCCGCGG CCGCGGGTGAAACAGAGGATCATG GCGGTAGCGCTCTAAAAGCTTCGG CCGAAGCTTTTAGAGCGCTACGCC AGTGATGCCATCAGGCCCGTATAC GTATACGGGCCTGATGGCATCACT TATGGAAAGGGCAACAGCGCTATC GATAGCGCTGTTGCCCTTTCCATA CTGTGGTTGATGGAGGATCCACAC GTGTGGATCCTCCATCAACCACAG ACTCGCTGGAATTTGCGCTGACAC GTGTCAGCGCAAATTCCAGCGAGT CAGGCCCGAACCACGCGGTTACAG CTGTAACCGCGTGTTCGGCCTG GGCGCAATGGGCCCATAAATACTA TAGTATTTATGCGCCCATTGCGCC GGTCAATTCGCGCTACATGCCCTA TAGGGCATGTAGCGCGAATTGACC GATGGTGGACTGGAGCCCTTCCGC GCGGAAGGGCTCCAGTCCACCATC CCGCGCATAGCGCAATAGGGGAGA TCTCCCCTATTGCGCTATGCGCG TCTTCTGGCTGTCCGGCACCCGAA TTCGGGTGCCGGACAGCCAGAAGA								
624 CATGATCCTCTGTTTCACCCGCGG CCGCGGGTGAAACAGAGGATCATG 625 GGCGTAGCGCTCTAAAAGCTTCGG CCGAAGCTTTTAGAGCGCTACGCC 626 AGTGATGCCATCAGGCCCGTATAC GTATACGGGCCTGATGGCATCACT 627 TATGGAAAGGGCAACAGCGCTATC GATAGCGCTGTTGCCCTTTCCATA 628 CTGTGGTTGATGGAGGATCCACAC GTGTGGATCCTCCATCAACCACAG 629 ACTCGCTGGAATTTGCGCTGACAC GTGTCAGCGCAAATTCCAGCGAGT 630 CAGGCCCGAACCACGCGGTTACAG CTGTAACCGCGTGGTTCGGGCCTG 631 GGCGCAATGGGCGCATAAATACTA TAGTATTTATGCGCCCATTGCGCC 632 GGTCAATTCGCGCTACATGCCCTA TAGGGCATGTAGCGCGAATTGACC 633 GATGGTGGACTGGAGCCCTTCCGC GCGGAAGGGCTCCAGTCCACCATC 634 CCGCGCATAGCGCAATAGGGGAGA TCTCCCCTATTGCGCTATGCGCG 635 TCTTCTGGCTGTCCGGCACCCGAA TTCGGGTGCCGGACAGCCAGAAGA								
GGCGTAGCGCTCTAAAAGCTTCGG CCGAAGCTTTTAGAGCGCTACGCC  AGTGATGCCATCAGGCCCGTATAC GTATACGGGCCTGATGGCATCACT  TATGGAAAGGGCAACAGCGCTATC GATAGCGCTGTTGCCCTTTCCATA  CTGTGGTTGATGGAGGATCCACAC GTGTGGATCCTCCATCAACCACAG  ACTCGCTGGAATTTGCGCTGACAC GTGTCAGCGCAAATTCCAGCGAGT  CAGGCCCGAACCACGCGGTTACAG CTGTAACCGCGTGTTCGGCCTG  GGCGCAATGGGCGCATAAATACTA TAGTATTTATGCGCCCATTGCGCC  GGTCAATTCGCGCTACATGCCCTA TAGGGCATGTAGCGCGAATTGACC  GATGGTGGACTGGAGCCCTTCCGC GCGGAAGGGCTCCAGTCCACCATC  CCGCGCATAGCGCAATAGGGGAGA TCTCCCCTATTGCGCTATGCGCG  TCTTCTGGCTGTCCGGCACCCGAA TTCGGGTGCCGGACAGCCAGAAGA								
AGTGATGCCATCAGGCCCGTATAC GTATACGGGCCTGATGGCATCACT TATGGAAAGGGCAACAGCGCTATC GATAGCGCTGTTGCCCTTTCCATA CTGTGGTTGATGGAGGATCCACAC GTGTGGATCCTCCATCAACCACAG ACTCGCTGGAATTTGCGCTGACAC GTGTCAGCGCAAATTCCAGCGAGT CAGGCCCGAACCACGCGGTTACAG CTGTAACCGCGTGGTTCGGGCCTG GGCGCAATGGGCGCATAAATACTA TAGTATTTATGCGCCCATTGCGCC GGTCAATTCGCGCTACATGCCCTA TAGGGCATGTAGCGCGAATTGACC GATGGTGGACTGGAGCCCTTCCGC GCGGAAGGGCTCCAGTCCACCATC CCGCGCATAGCGCAATAGGGGAGA TCTCCCCTATTGCGCTATGCGCG TCTTCTGGCTGTCCGGCACCCGAA TTCGGGTGCCGGACAGCCAGAAGA								
TATGGAAAGGGCAACAGCGCTATC GATAGCGCTGTTGCCCTTTCCATA  CTGTGGTTGATGGAGGATCCACAC GTGTGGATCCTCCATCAACCACAG  ACTCGCTGGAATTTGCGCTGACAC GTGTCAGCGCAAATTCCAGCGAGT  CAGGCCCGAACCACGCGGTTACAG CTGTAACCGCGTGTTCGGGCCTG  GGCGCAATGGGCGCATAAATACTA TAGTATTTATGCGCCCATTGCGCC  GGTCAATTCGCGCTACATGCCCTA TAGGGCATGTAGCGCGAATTGACC  GATGGTGGACTGGAGCCCTTCCGC GCGGAAGGGCTCCAGTCCACCATC  CCGCGCATAGCGCAATAGGGGAGA TCTCCCCTATTGCGCTATGCGCG  TCTTCTGGCTGTCCGGCACCCGAA TTCGGGTGCCGGACAGCCAGAAGA								
CTGTGGTTGATGGAGGATCCACAC GTGTGGATCCTCCATCAACCACAG ACTCGCTGGAATTTGCGCTGACAC GTGTCAGCGCAAATTCCAGCGAGT CAGGCCCGAACCACGCGGTTACAG CTGTAACCGCGTGGTTCGGGCCTG GGCGCAATGGGCGCATAAATACTA TAGTATTTATGCGCCCATTGCGCC GGTCAATTCGCGCTACATGCCCTA TAGGGCATGTAGCGCGAATTGACC GATGGTGGACTGGAGCCCTTCCGC GCGGAAGGGCTCCAGTCCACCATC CCGCGCATAGCGCAATAGGGGAGA TCTCCCCTATTGCGCTATGCGCG TCTTCTGGCTGTCCGGCACCCGAA TTCGGGTGCCGGACAGCCAGAAGA								
ACTCGCTGGAATTTGCGCTGACAC GTGTCAGCGCAAATTCCAGCGAGT  CAGGCCCGAACCACGCGGTTACAG CTGTAACCGCGTGGTTCGGGCCTG  GGCGCAATGGGCGCATAAATACTA TAGTATTTATGCGCCCATTGCGCC  GGTCAATTCGCGCTACATGCCCTA TAGGGCATGTAGCGCGAATTGACC  GATGGTGGACTGGAGCCCTTCCGC GCGGAAGGGCTCCAGTCCACCATC  CCGCGCATAGCGCAATAGGGGAGA TCTCCCCTATTGCGCTATGCGCGG  TCTTCTGGCTGTCCGGCACCCGAA TTCGGGTGCCGGACAGCCAGAAGA								
GGCGCAATGGGCGCATAAATACTA TAGTATTTATGCGCCCATTGCGCC GGTCAATTCGCGCTACATGCCCTA TAGGGCATGTAGCGCGAATTGACC GATGGTGGACTGGAGCCCTTCCGC GCGGAAGGGCTCCAGTCCACCATC CCGCGCATAGCGCAATAGGGGAGA TCTCCCCTATTGCGCTATGCGCGG TCTTCTGGCTGTCCGGCACCCGAA TTCGGGTGCCGGACAGCCAGAAGA	629		ACTCGCT	GGAATTTGCG	CTGACAC	GTGTC	AGCGCAAATT	CCAGCGAGT
GGTCAATTCGCGCTACATGCCCTA TAGGGCATGTAGCGCGAATTGACC GATGGTGGACTGGAGCCCTTCCGC GCGGAAGGGCTCCAGTCCACCATC CCGCGCATAGCGCAATAGGGGAGA TCTCCCCTATTGCGCTATGCGCGG TCTTCTGGCTGTCCGGCACCCGAA TTCGGGTGCCGGACAGCCAGAAGA	630		CAGGCCC	GAACCACGCG	GTTACAG	CTGTA	ACCGCGTGGT	TCGGGCCTG
GATGGTGGACTGGAGCCCTTCCGC GCGGAAGGGCTCCAGTCCACCATC  CCGCGCATAGCGCAATAGGGGAGA TCTCCCCTATTGCGCTATGCGCGG  TCTTCTGGCTGTCCGGCACCCGAA TTCGGGTGCCGGACAGCCAGAAGA	631		GGCGCAA!	TGGGCGCATA	AATACTA	TAGTA	TTATGCGC	CATTGCGCC
634 CCGCGCATAGCGCAATAGGGGAGA TCTCCCCTATTGCGCTATGCGCGG 635 TCTTCTGGCTGTCCGGCACCCGAA TTCGGGTGCCGGACAGCCAGAAGA	632		GGTCAAT	TCGCGCTAC <i>A</i>	ATGCCCTA	TAGGG	CATGTAGCG	CGAATTGACC
635 TCTTCTGGCTGTCCGGCACCCGAA TTCGGGTGCCGGACAGCCAGAAGA	633		GATGGTG	GACTGGAGCC	CCTTCCGC	GCGGA	AGGGCTCCAC	FTCCACCATC
	634		CCGCGCA	TAGCGCAATA	AGGGGAGA	TCTCC	CCTATTGCG	CTATGCGCGG
636 GCGTTCGCAATTCACGGGCCCTTA TAAGGGCCCGTGAATTGCGAACGC	635		TCTTCTG	GCTGTCCGGC	CACCCGAA	TTCGG	GTGCCGGAC <i>I</i>	AGCCAGAAGA
	636		GCGTTCG	CAATTCACGG	GCCCTTA	TAAGG	GCCCGTGAA	TTGCGAACGC

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TABLE 3-continued

Seq. ID	No.Decoder	Sequence	(5'-3')	Probe	Sequence	(5'-3')
637	TCGTTTCO	GCCTTGGAG	SAGTATCG	CGATA	CTCTCCAAGG	CCGAAACGA
638	AGGTGCAA	AGTGCAAGGC	GAGAGGC	GCCTC	ICGCCTTGC <i>I</i>	ACTTGCACCT
639	CGCCAGTT	TTCGATGGCT	GACGTTT	AAACG'	rcagccatco	GAAACTGGCG
640	GCTTTACC	CGCCGATCCC	AGATATC	GATAT	CTGGGATCG	CGGTAAAGC
641	GTGCTTG <i>I</i>	ACGAAGAGGC	GAAATGT	ACATT	rcgcctcttc	CGTCAAGCAC
642	CAGTCCGT	TGCGCTTCAT	GTCCTCA	TGAGG	ACATGAAGC	CACGGACTG
643	TACGCGT	AAGAGCCTAC	CCTCGCG	CGCGA	GGTAGGCT	CTTACGCGTA
644	GGCGAGTC	CTTGTGGGGA	CATGTGT	ACACA!	IGTCCCCAC <i>I</i>	AGACTCGCC
645	CCAAAGCC	GAAGCGAGCG	TGTCTAT	ATAGA	CACGCTCGCT	TCGCTTTGG
646	GCCGTAGC	TTGCTCTTC	ACCGAAC	GTTCG	GTGAAGAGC <i>I</i>	AACCTACGGC
647	AAATCCGC	CGATGTGCCG	TGAGGCT	AGCCT	CACGGCACAT	CGCGGATTT
648	GGCTTCGC	CACCCGTACC	AATTTAG	CTAAA	TTGGTACGGC	STGCGAAGCC
649	TGTAGAGT	CCCACGTAG	CCGGCAT	ATGCC	GGCTACGTGG	GACTCTACA
650						CAGACTAGTG
651						CCGAGTACA
652						ATACCCGTT
653						GGCAGTCCG
654						CTGAACGAT
655						TCGATGCAT
656						ATGCCTGGAA
657 658						GACGATGAG
659						AAGTGCCATT
660						CTCCCACGG
661						ACGAGAATTT
662						TAAGAGCAA
663	TTAAGGAT	CAGGCGGAG	CTTGCAG	CTGCA	AGCTCCGCCT	GATCCTTAA
664	CGCGACT	AGGTGCTGC	CAACTCGA	TCGAG'	TTGCAGCAC	CTTAGTCGCG
665	GCTCGATT	TCACGGCCC	GTTGTTC	GAACA	ACGGGCCGT	GAAATCGAGC
666	AGCAGAGT	TGCGTTGCAG	SAGGCTAA	TTAGC	CTCTGCAAC	CACTCTGCT
667	TGGAGGTO	GAGGACGACG	TGCACTA	TAGTG	CACGTCGTC	TCACCTCCA
668	AACCGTTT	TAGGGTACAT	TCGCGGT	ACCGC	GAATGTACCO	CTAAACGGTT
669	TATGATCO	GCTCGGCTCA	CAGTTTG	CAAAC	IGTGAGCCG <i>I</i>	AGCGATCATA
670	GACTTTT	GCGGAAACG	TCATGGT	ACCATO	GACGTTTCC	CAAAAAGTC
671	TGTCGGTT	TATTCCACCT	GCAAGGA	TCCTT	GCAGGTGGAA	ATAACCGACA
672	CTATGGTT	TTGCACTGCG	CCGTCGA	TCGAC	GCGCAGTGC	CAAACCATAG
673	AGCAGGG	AATTCAATC	GTTCGCA	TGCGA	ACGATTGAAT	TTTCCCTGCT

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TABLE 3-continued

	TABLE 3-conci	
Seq. ID	No.Decoder Sequence (5'-3')	Probe Sequence (5'-3')
674	CCTAACCGAGCGCTTAGCATTTCC	GGAAATGCTAAGCGCTCGGTTAGG
675	CCCGACCCTAACTCGCATTGAATA	TATTCAATGCGAGTTAGGGTCGGG
676	TTGCTTAATGGTGACGCCACGGAT	ATCCGTGGCGTCACCATTAAGCAA
677	GATGCTCGCCGTGTTTAGTTCACG	CGTGAACTAAACACGGCGAGCATC
678	TCGGATGACGAGTTTCCATGACGG	CCGTCATGGAAACTCGTCATCCGA
679	ATGCGGTCTACTTTCTCGATCGGG	CCCGATCGAGAAAGTAGACCGCAT
680	TTGCGAGGCTAAGCACACGGTAAA	TTTACCGTGTGCTTAGCCTCGCAA
681	AACTTAATTACCGCCTCTGGCGCC	GGCGCCAGAGGCGGTAATTAAGTT
682	GTGACCGCGAACTTGTTCCGACAG	CTGTCGGAACAAGTTCGCGGTCAC
683	TGCGGATTACCGATTCGCTCTTAA	TTAAGAGCGAATCGGTAATCCGCA
684	TGATAGGGGGCCACGTTGATCAGA	TCTGATCAACGTGGCCCCCTATCA
685	TCGCTCCGTAGCGATTCATCGTAG	CTACGATGAATCGCTACGGAGCGA
686	TGTCAGCTGGTAGCCTCCGTTTGA	TCAAACGGAGGCTACCAGCTGACA
687	AGCGTCGCATGACGCTTACGGCAC	GTGCCGTAAGCGTCATGCGACGCT
14	AGACGCACCGCAACAGGCTGTCAA	TTGACAGCCTGTTGCGGTGCGTCT
15	CGTGTAGGGGTCCCGTGCTGTCAA	TTGACAGCACGGGACCCCTACACG
690	GTCGCATTCTGCACTGGCTTCGCC	GGCGAAGCCAGTGCAGAATGCGAC
691	TGATTAGGTGCGGTCCCGTAGTCC	GGACTACGGGACCGCACCTAATCA
692	AAGGGACCTTGGGTGACGGCGAGA	TCTCGCCGTCACCCAAGGTCCCTT
693	TCAAATGGCCACCGCGTGTCATTC	GAATGACACGCGGTGGCCATTTGA
694	CTCCGACGACCAATAAATAGCCGC	GCGGCTATTTATTGGTCGTCGGAG
695	GGCTATTCCCGTAGAGAGCGTCCA	TGGACGCTCTCTACGGGAATAGCC
696	TGGATAACCTCTCGGTCCATCCAC	GTGGATGGACCGAGAGGTTATCCA
697	GACCGCTGTACGGGAGTGTGCCTT	AAGGCACACTCCCGTACAGCGGTC
698	GCCACAGAGTTTTAGCAGGGACCC	GGGTCCCTGCTAAAACTCTGTGGC
699	CCCACGCTTTCCGACCACTGACCT	AGGTCAGTGGTCGGAAAGCGTGGG
700	CATTGACACAATGCGGGGACTGAT	ATCAGTCCCCGCATTGTGTCAATG
701	AGCCACTCGACAGGGTTCCAAAGC	GCTTTGGAACCCTGTCGAGTGGCT
702	CAGGATGAGCAAAGCGACTCTCCA	TGGAGAGTCGCTTTGCTCATCCTG
703	CAAGGTATGGTCTGGGGCCTAAGC	GCTTAGGCCCCAGACCATACCTTG
704	GGTGTTCGGCCTAAACTCTTTCGG	CCGAAAGAGTTTAGGCCGAACACC
705	TTTAGTCGGACCCTGTGGCAATTC	GAATTGCCACAGGGTCCGACTAAA
706	CACACGTTTCCGACCAGCCTGAAC	GTTCAGGCTGGTCGGAAACGTGTG
707	CTGGACGAACTGGCTTCCTCGTAC	GTACGAGGAAGCCAGTTCGTCCAG
708	TTCACAATCCGCCGAAAACTGACC	GGTCAGTTTTCGGCGGATTGTGAA
709	AACAGGATATCCGCGATCACGACA	TGTCGTGATCGCGGATATCCTGTT
710	TACGTCGGATCCATTGCGCCGAGT	ACTCGGCGCAATGGATCCGACGTA

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TABLE 3-continued

Seq.	ID I	No.	Decoder	Sequence	(5'-3')	Probe	Sequence	(5'-3')
7	11		CATGGATO	CTCTCGGTTT	GATCGCC	GGCGA'	rcaaaccgag	SAGATCCATG
	12							CGCCTGGCT
7	13		ATTTGGC	ACGTGTCGTG	CCATGTT	AACATO	GGCACGACAC	CGTGCCAAAT
7	14		CCGCGTTC	GCACCACTTI	GAGGTGC	GCACC'	ICAAAGTGG1	GCAACGCGG
7	15		TTGGACG	IGACAAGCAT	GGCGCTC	GAGCG	CCATGCTTGT	CACGTCCAA
7	16		CTGAATC	GCGCAAGTAA	ATGGGGG	ccccc	ATTTACTTGO	CGCGATTCAG
7	17		GATAAGG	ICCACCAGAT	TGCGCGC	GCGCG	CAATCTGGT	GACCTTATC
7	18		CTAACAA	FTGCCAACCG	GGACGGC	GCCGT	CCCGGTTGGC	CAATTGTTAG
7	19		GGTAACC	rgggtgctte	GCAGGTTA	TAACC	IGCAAGCACO	CCAGGTTACC
7	20		ATCGGAG	CCACCATTCC	CATTGGG	CCCAA	rgcgaatgg1	GGCTCCGAT
7	21		GTGAACTO	GCTTGCCC	CAGGATTA	TAATC	CTGGGGCAAC	CCAGTTCAC
7.	22		AGGCGATA	AGCATGGTCC	CCATATGA	TCATA	rgggaccat(	CTATCGCCT
7.	23		AACGGTA	rcgtggcta#	ATGCACGA	TCGTG	CATTAGCCAC	CGATACCGTT
7.	24		AGTAGTG	GTCCTCCAGA	ATCGGCAA	TTGCC	GATCTGGAGG	ACCACTACT
7.	25		CCGTTGA	ATTGGACGGG	SAGGTTAG	CTAAC	CTCCCGTCC	AATTCAACGG
7.	26		GCATAAG	IGCGGCATCG	GCGAAGGG	CCCTT	CGCGATGCC	CACTTATGC
7.	27		CGACAAGA	ATGCAGCTGC	CTACATGC	GCATG'	PAGCAGCTGC	CATCTTGTCG
7.	28		TCGCAGT	GATTCCCGAC	CCGATAAG	CTTAT	CGGTCGGGAI	ATCACTGCGA
7.	29		CAAGGCGA	AGTCCACTCG	SAGGGGAC	GTCCC	CTCGAGTGG	ACTCGCCTTG
7	30		GCAACTTO	GCACGGCATA	AAGTGGCC	GGCCA	CTTATGCCGT	GCAAGTTGC
7	31							CAAGCTCGGA
	32							SCCCAGCGCT
7.	33							GACATGAA
	34							PAGCGGTTCG
	35							ACCTTCCGTG
7.	36							CCATCTGTG
7.	37							FTTGCGAAAA
	38							AACGTAACGT
	39							CAATCCGATA
	40							ATTGTGGAAG
	41							CCTTTGTGCA
	42							GGCATCGGA ACGGTTTCAG
	43							CGGAACACCG
	45							CCTGCTAGA
	46							AGGTGACTC
	47							GACAGAAGA
,	21		1011010.	. 0111001001	LOUNGERI	.113010	JUIGUNGGAI	CHOMOMOM

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TABLE 3-continued

		D 1 0 151 0/1
Seq. ID	No.Decoder Sequence (5'-3')	Probe Sequence (5'-3')
748	GCGGATGAAACCTGAAAGGGGCCT	AGGCCCCTTTCAGGTTTCATCCGC
749	GGGGCCCCAAACTGGTATCAAGCC	GGCTTGATACCAGTTTGGGGCCCC
750	GCATTGGCTTCGGATTCTCCTACA	TGTAGGAGAATCCGAAGCCAATGC
751	AGGCGGCCCAACTGTGAGGTCTTG	CAAGACCTCACAGTTGGGCCGCCT
752	ACACCATGTGCTCCGCGCTGCAGT	ACTGCAGCGCGGAGCACATGGTGT
753	ACGATGAACATGAATCGGGAGTCG	CGACTCCCGATTCATGTTCATCGT
754	CTGCATCCCTGTAGCAGCGCTCCG	CGGAGCGCTGCTACAGGGATGCAG
755	GTGCCGTATTTCGACCTGTGCGTT	AACGCACAGGTCGAAATACGGCAC
756	GCAGTGCGCACTTCAGTTCAAAAG	CTTTTGAACTGAAGTGCGCACTGC
757	GCGATTTTAAGCGATGCCTTGACG	CGTCAAGGCATCGCTTAAAATCGC
758	TAGGTGACCTAGGCTTGCTTGCGG	CCGCAAGCAAGCCTAGGTCACCTA
759	CTGGATACCTTGCCTGTGCGGCGC	GCGCCGCACAGGCAAGGTATCCAG
760	CCCCTTACGGCTCGTCGTCTATGC	GCATAGACGACGAGCCGTAAGGGG
761	GCGCTTGCCCGATGCGATGCATTA	TAATGCATCGCATCGGGCAAGCGC
762	TTTCTGTAAGCGGCCTGGGGTTCA	TGAACCCCAGGCCGCTTACAGAAA
763	GGCTGAGGTGAGCGGTAAGGATGA	TCATCCTTACCGCTCACCTCAGCC
764	TCTTGGCCTCCCCGATCTAATTTG	CAAATTAGATCGGGGAGGCCAAGA
765	GGAGGTAACGCCGTGTACGTAGGA	TCCTACGTACACGGCGTTACCTCC
766	GTAATCCATTTGTGGCTGCGTCAA	TTGACGCAGCCACAAATGGATTAC
767	CAAACCCATTCCAGCAGACGCCTG	CAGGCGTCTGCTGGAATGGGTTTG
768	TAGGAGGAATTTGGCATGCGGGCG	CGCCCGCATGCCAAATTCCTCCTA
769	ATAGGTAGGATGTGCCCGGCGTTG	CAACGCCGGGCACATCCTACCTAT
770	GCAAGTGCTTAGCTCGTCAGCCTC	GAGGCTGACGAGCTAAGCACTTGC
771	CTGGCTGTGTCGCATCTCGTTAAC	GTTAACGAGATGCGACACAGCCAG
772	CTAACGTCGTCTCGCGCAATCACT	AGTGATTGCGCGAGACGACGTTAG
773	TTTTCATAAACGTTGTCCCCGAGC	GCTCGGGGACAACGTTTATGAAAA
774	AGCAGGAGGACGAACCTCCGCTCC	GGAGCGGAGGTTCGTCCTCCTGCT
775	TTCAAGCACCATCGTGCAATCCAA	TTGGATTGCACGATGGTGCTTGAA
776	AGCGTCGCCAGTGATCGCTAGTGG	CCACTAGCGATCACTGGCGACGCT
777	TACATTCCCTGCCTCCGTGGGCTT	AAGCCCACGGAGGCAGGGAATGTA
778	CGCTTCGCGTATTCAGTAGCGGTT	AACCGCTACTGAATACGCGAAGCG
779	TCGGACGCGTCGACACTCATTATA	TATAATGAGTGTCGACGCGTCCGA
780	TCTGAGCAGGCCAGCGCTCCAGCT	AGCTGGAGCGCTGGCCTGAGA
781	TTGAATTGCCAAGCCCTGAAAGCC	GGCTTTCAGGGCTTGGCAATTCAA
782	AGTTTTCGCCTTGATGCGTCGGTG	CACCGACGCATCAAGGCGAAAACT

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TABLE 3-continued

Seq. ID	No.Decoder Sequence (5'-3') Probe Sequence (5'-3')
783	GTTTCATAGGCCACGCGTGCTAAA TTTAGCACGCGTGGCCTATGAAAC
16	CATCGCTGCAAGTACCGCACTCAA TTGAGTGCGGTACTTGCAGCGATG

[0209]

## TABLE 4

	111555	<u> </u>
Seq. II	No.Decoder Sequence (5'-3') + 5'	T Probe Sequence (5'-3') + 5' T
17	TTTCGCCGTCGTGTAGGCTTTTCAA	TTTGAAAAGCCTACACGACGGCGAA
18	TGTTCCCAGTGAAGCTGCGATCTGG	TCCAGATCGCAGCTTCACTGGGAAC
19	TTACTTGGCATGGAATCCCTTACGC	TGCGTAAGGGATTCCATGCCAAGTA
20	TACTAGCATATTTCAGGGCACCGGC	TGCCGGTGCCCTGAAATATGCTAGT
21	TGAACGGTCAATGAACCCGCTGTGA	TTCACAGCGGGTTCATTGACCGTTC
22	TGCGGCCTTGGTTCAATATGAATCG	TCGATTCATATTGAACCAAGGCCGC
23	TGATCGTTAGAGGGACCTTGCCCGA	TTCGGGCAAGGTCCCTCTAACGATC
24	TTGGACCTAGTCCGGCAGTGACGAA	TTTCGTCACTGCCGGACTAGGTCCA
25	TATAAACTACCCAGGACGGGCGGAA	TTTCCGCCCGTCCTGGGTAGTTTAT
26	TCATCGGTTCGCGCCAATCCAGATA	TTATCTGGATTGGCGCGAACCGATG
27	TGTCGGGCATAGAGCCGACCACCCT	TAGGGTGGTCGGCTCTATGCCCGAC
28	TCTTGGGTCATGATTCACCGTGCTA	TTAGCACGGTGAATCATGACCCAAG
29	TTGCCTAACGTGCTAATCAGCAGCG	TCGCTGCTGATTAGCACGTTAGGCA
30	TCGCATGTTGGAGCATATGCCCTGA	TTCAGGGCATATGCTCCAACATGCG
31	TAGCCACTGCATCAGTGCTGTTCAA	TTTGAACAGCACTGATGCAGTGGCT
32	TGGTTGTTTTGAGGCGTCCCACACT	TAGTGTGGGACGCCTCAAAACAACC
33	TTCGACCAAGAGCAAGGGCGGACCA	TTGGTCCGCCCTTGCTCTTGGTCGA
34	TGACATCGCTATTGCGCATGGATCA	TTGATCCATGCGCAATAGCGATGTC
35	TGAAATACGAAGTCTGCGGGAGTCG	TCGACTCCCGCAGACTTCGTATTTC
36	TTGTCATGAATGATTGATCGCGCGA	TTCGCGCGATCAATCATTCATGACA
37	TATATCGGGATTCGTTCCCGGTGAA	TTTCACCGGGAACGAATCCCGATAT
38	TGCGAGCGTACCGAAGGGCCTAGAA	TTTCTAGGCCCTTCGGTACGCTCGC
39	TTTACCGGCAGCGGACTTCCGAATT	TAATTCGGAAGTCCGCTGCCGGTAA
40	TGTAATCGAGAGCTGCGCGCCGTCT	TAGACGGCGCGCAGCTCTCGATTAC
41	TCCTGTTAGCGTAGGCGAGTCGATC	TGATCGACTCGCCTACGCTAACAGG
42	TTAGCGGACCGGCAGAATGAGTTCC	TGGAACTCATTCTGCCGGTCCGCTA
43	TGGTACATGCACTACGCGCACTCGG	TCCGAGTGCGCGTAGTGCATGTACC
4 4	TAATTCATCTCGGACTCCCGCGGTA	TTACCGCGGGAGTCCGAGATGAATT
45	TGCCAAATCTGGATTGGCAGGAATG	TCATTCCTGCCAATCCAGATTTGGC
46	TTGCATTTTCGGTTGAGGCACATCC	TGGATGTGCCTCAACCGAAAATGCA

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TABLE 4-continued

Seq. II	No.Decoder Sequence (5'-3') + 5'	T Probe Sequence (5'-3') + 5' T
47	TCCGCTCAATTCACCATGCTTCGCT	TAGCGAAGCATGGTGAATTGAGCGG
48	TCTCGGAAAGGTGCAACTTTGGTGT	TACACCAAAGTTGCACCTTTCCGAG
49	TAATTCGACCAGCAGAACGTCGCAT	TATGGGACGTTCTGCTGGTCGAATT
50	TGCCAGAGTCTCAACCTCACGGGAT	TATCCCGTGAGGTTGAGACTCTGGC
51	TCCAACAACTGGAACGGGAACCCGC	TGCGGGTTCCCGTTCCAGTTGTTGG
52	TGAGAACTGATCGCTGAGGGGCATG	TCATGCCCCTCAGCGATCAGTTCTC
53	TGGCACACTAGACTTGTGGCACCGA	TTCGGTGCCACAAGTCTAGTGTGCC
54	TTCACATCCAAATATGGTCCGCGAA	TTTCGCGGACCATATTTGGATGTGA
55	TGTCTGCCGGTGTGACCGCTTCATT	TAATGAAGCGGTCACACCGGCAGAC
56	TCATCGCAGAGCATAAACACCCTCA	TTGAGGGTGTTTATGCTCTGCGATG
57	TGTTGGTATCTATGGCAGAGGCGGA	TTCCGCCTCTGCCATAGATACCAAC
58	TACGAGGTGCCGCTGAGGTTCCATT	TAATGGAACCTCAGCGGCACCTCGT
59	TGGAATGAGTGGACCCAGGCACATT	TAATGTGCCTGGGTCCACTCATTCC
60	TTGTCAATATGCGTCCGTGTCGTCT	TAGACGACACGGACGCATATTGACA
61	TTGATGAGCCTCAGGGTACGAGGCA	TTGCCTCGTACCCTGAGGCTCATCA
62	TCACCGCGGTGTTCCTACAGAATGA	TTCATTCTGTAGGAACACCGCGGTG
63	TTTGTTGCCAATGGTGTCCGCTCGG	TCCGAGCGGACACCATTGGCAACAA
64	TTTAACCTGCGTCTGCCCCTTTCCT	TAGGAAAGGGCAGACGCAGGTTAA
65	TAGGCGCGTTCCTGCCTTAGTGACG	TCGTCACTAAGGCAGGAACGCGCCT
66	TTAGGGCGATGGCACGAAGCTTCAA	TTTGAAGCTTCGTGCCATCGCCCTA
67	TTGCATAGAGCCAAAGTCGGCGATG	TCATCGCCGACTTTGGCTCTATGCA
68	TTTGAGAGGCAGGTGGCCACACGGA	TTCCGTGTGGCCACCTGCCTCTCAA
69	TTCCGCATTGTGAGAAAAACGAGC	TGCTCGTTTTTTCTCACAATGCGGA
70	TGGCGGTTTCCGTAGCTATAGGTGC	TGCACCTATAGCTACGGAAACCGCC
71	TGGTGAAAATTTCGTAGCCACGGGC	TGCCCGTGGCTACGAAATTTTCACC
72	TCCGACGGAGGATGAAGACAATCAC	TGTGATTGTCTTCATCCTCCGTCGG
73	TCCAGTTTGGCCCAATTCGCCAAAA	TTTTTGGCGAATTGGGCCAAACTGG
7 4	TGGATCTATTAGGCCGTGCGCACAG	TCTGTGCGCACGGCCTAATAGATCC
75	TCGGATGTCACCGTTTGGACTTTCA	TTGAAAGTCCAAACGGTGACATCCG
76	TATCGCAAATCCTGCTCGTCCCTAA	TTTAGGGACGAGCAGGATTTGCGAT
77	TCAGGGCATGCAATAATCGAGGTTC	TGAACCTCGATTATTGCATGCCCTG
78	TCATGCGTTGATATATGGGCCCAAG	TCTTGGGCCCATATATCAACGCATG
79	TCAGCTGCAGCTTGTGACCAACCAC	TGTGGTTGGTCACAAGCTGCAGCTG
80	TTTGTATGTCTGCCGACCGGCGACC	TGGTCGCCGGTCGGCAGACATACAA
81	TGATGGCGCCCGTTGATAGGTATGG	TCCATACCTATCAACGGGCGCCATC
82	TATGAGAATCGCCGGCAATCTGCTA	TTAGCAGATTGCCGGCGATTCTCAT
83	TATTTGCACTGACCGCAGGCTCGTG	TCACGAGCCTGCGGTCAGTGCAAAT

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Seq. ID	No.Decoder Sequence (5'-3') + 5'	T Probe Sequence (5'-3') + 5' T
84	TCAGGGAGAACGGTTAAGTTCCCGT	TACGGGAACTTAACCGTTCTCCCTG
85	TAGGCCGGCGATCGAGGAGTTTGGT	TACCAAACTCCTCGATCGCCGGCCT
86	TACACGGTGGTCTCTGATAGCGACC	TGGTCGCTATCAGAGACCACCGTGT
87	TGTGCAACGCCGAGGACTTCCATCA	TTGATGGAAGTCCTCGGCGTTGCAC
88	TTCGGTGCCTGATAGCCATTCCGAT	TATCGGAATGGCTATCAGGCACCGA
89	TTGAAATACCACACAGCCAATTGGC	TGCCAATTGGCTGTGTGTATTTCA
90	TGCATCGTGTACATGACTGCCGCGA	TTCGCGGCAGTCATGTACACGATGC
91	TCAGTGTTCTAACGGCGCGCGTGAA	TTTCACGCGCGCCGTTAGAACACTG
92	TCGCTTGCAACGTTGCACCTACTCT	TAGAGTAGGTGCAACGTTGCAAGCG
93	TCGAAAAACTAGTGGGCTCGCCGCG	TCGCGGCGAGCCCACTAGTTTTTCG
94	TCTTTCAGGGGAACTGCCGGAGTCG	TCGACTCCGGCAGTTCCCCTGAAAG
95	TTTGTGGCCTTCTTGTAAAGGCACG	TCGTGCCTTTACAAGAAGGCCACAA
96	TTCCACGAACGGCGACCCGTTGTCT	TAGACAACGGGTCGCCGTTCGTGGA
97	TCGACCTTGCACGAAACCTAACGAG	TCTCGTTAGGTTTCGTGCAAGGTCG
98	TGTGCAGCTTCACGAGCCAGCCTGA	TTCAGGCTGGCTCGTGAAGCTGCAC
99	TCGCTTTCGTGCGAATAGACGATGA	TTCATCGTCTATTCGCACGAAAGCG
100	TTGCGCTTACAGGCTCCTAGTGGTC	TGACCACTAGGAGCCTGTAAGCGCA
101	TCACGCGCTTAGTCGCGATCGCATA	TTATGCGATCGCGACTAAGCGCGTG
102	TCGGAGGGAGGGAGCTAGCCTTCGA	TTCGAAGGCTAGCTCCCTCCCTCCG
103	TGCATCCGGCCTGTTGATGACGCCT	TAGGCGTCATCAACAGGCCGGATGC
104	TAGGCCAATCGATCTTATTGCCGAG	TCTCGGCAATAAGATCGATTGGCCT
105	TCCTTCCAATGATTGCATACGCCCA	TTGGGCGTATGCAATCATTGGAAGG
106	TAACACTTGATCAGGCGGGTCGTCT	TAGACGACCCGCCTGATCAAGTGTT
107	TTGGAATCAAGGCCGTAAAGGACAG	TCTGTCCTTTACGGCCTTGATTCCA
108	TGCTCCCGTAACCTGTCCACCAGTG	TCACTGGTGGACAGGTTACGGGAGC
109	TAGTGGTGAATGGCCGCTACCCTGA	TTCAGGGTAGCGGCCATTCACCACT
110	TTGTTGAAGCGAGCTAAAACGGCCA	TTGGCCGTTTTAGCTCGCTTCAACA
111	TCAGCGCTCCAGAATTGACAGCAAT	TATTGCTGTCAATTCTGGAGCGCTG
2		TTTGAAAAGGGACGTGCGCTTCGAA
3		TTTGATGTCCCATTCCCCACGCGTT
114		TCCACCCTTACGCCGGTATCTCGTG
115		TACCCATTCCACACGTTTGCCGTAG
116		TGTAGTTCGCCCGTCATCGCCCTAC
117		TTGCGAATGTGTGCGGAGGTCGATT
118		TGAATCTCCGCCGCCATGCTGACTC
119		TCCCGTGTTGCCAGCGTCTTTATCT
120	TGGTACCTCAACGCGAACCACTTGT	TACAAGTGGTTCGCGTTGAGGTACC

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TABLE 4-continued

			TABLE 4-CONC	- 11.	iueu			
Seq.	ID	No.Decoder Seque	nce (5'-3') + 5'	Т	Probe	Sequence	(5'-3')	+ 5' T
	121	TAAGCGATGGCTA	CCCAAGAGCGAT		TATCGC	TCTTGGGT <i>I</i>	AGCCATCG	CTT
	122	TAGAGCTTATGCA	GAACCAGGCGCC		TGGCGC	CTGGTTCTG	CATAAGC	TCT
	123	TATCGGTCTCACG	CAGGGTTGGATA		TTATCO	AACCCTGCG	TGAGACC	GAT
	124	TTAGGTTGCCCGC	CAGAAGAAACAT		TATGTI	TCTTCTGGC	GGGCAAC	CTA
	125	TCGGTGCTGTTGC	AAAAGCCTGTAG		TCTACA	AGGCTTTTGC	CAACAGCA	CCG
	126	TTGATGAAAGTTT	GCGGCAGGACAC		TGTGTC	CTGCCGCA	ACTTTCA	TCA
	127	TGTTGAGTGCAGG	ATGCAGCGATAG		TCTATO	GCTGCATCC	TGCACTC.	AAG
	128	TAACATTGCGCGG	TCCACCAGGGTT		TAACCC	TGGTGGACC	GCGCAAT	GTT
	129	TGGGCAGTTAGAG	AGGGCCAGAAGT		TACTTO	TGGCCCTCT	CTAACTG	ccc
	130	TTCGAGCTGGTCC	CCGTGAACGTGT		TACACO	TTCACGGGG	GACCAGCT	CGA
	131	TGTCTTGGGGGCC	GCTTAGTGAAAA		TTTTTC	ACTAAGCGG	CCCCCAA	GAC
	132	TACTGTTGGCTTG	CTCTCATGTCCA		TTGGAC	ATGAGAGCA	AGCCAAC.	AGT
	133	TAGGACCATTCGG	AAGGCGAAGATA		TTATCI	TCGCCTTCC	GAATGGT	CCT
	134	TCTTGGGAGGCAT	CCGCTATAAGGA		TTCCTT	'ATAGCGGAT	GCCTCCC.	AAG
	135	TAATAAACGGAAC	GCACCGCTACAG		TCTGTA	GCGGTGCG1	TCCGTTT.	ATT
	136	TTTGTACGTGCGG	TCCCCATAAGCA		TTGCTT	'ATGGGGACC	GCACGTA	CAA
	137	TCGCACCAAACTG	AGTTTCCCAGAC		TGTCTG	GGAAACTCA	GTTTGGT	GCG
	138	TACCTGATCGTTC	CCCTATTGGGAA		TTTCCC	CAATAGGGGA	ACGATCA	GGT
	139	TGGAACAGAGGCG	AGGGGACTGAGC		TGCTCA	GTCCCCTCG	CCTCTGT	TCC
	140	TCCCTGCCTTGGC	GTGTCGGCTTAT		TATAAG	CCGACACGC	CAAGGCA	GGG
	141	TACTCTGACACGC	CAACTCCGGAAG		TCTTCC	GGAGTTGGC	GTGTCAG.	AGT
	142	TCTGACGGTTTTC	ATTCGGCGTGCC		TGGCAC	GCCGAATGA	AAACCGT	CAG
	143	TTGCGGTGGTTCA	TTGGAGCTGGCC		TGGCCA	GCTCCAATG	SAACCACC	GCA
	144	TGCATGGCCAACT	AGTGACTCGCAA		TTTGCG	AGTCACTAG	TTGGCCA	TGC
	145	TAGGCCGTAAAGC	GAATCTCACCTG		TCAGGT	GAGATTCGC	TTTACGG	CCT
	146	TCGAATATTATGC	CGAGAATCCGCG		TCGCGG	SATTCTCGGC	TATAATA	TCG
	147	TACAGACGAGCTC	CCAACCACATGA		TTCATO	TGGTTGGG	AGCTCGTC	TGT
	148	TGGACGGTTTGTG	CTGGATTGTCTG		TCAGAC	CAATCCAGCA	CAAACCG	TCC
	149	TAAAGGCTATTGA	GTTGGTTGGGCG		TCGCCC	CAACCAACTO	CAATAGCC	TTT
	150	TGATGGCCTATTC	GGAGATCGGGCC		TGGCCC	GATCTCCGA	ATAGGCC.	ATC
	151	TGATCCAGTAGGC	AGCTTCATCCCA		TTGGGA	TGAAGCTGC	CTACTGG.	ATC
	152	TAATAACTCGCGC	GGGTATGCTTCT		TAGAAG	CATACCCGC	GCGAGTT.	ATT
	153	TGGAGGAGGTTTG	TCTCGGAAAGCA		TTGCTT	TCCGAGAC <i>I</i>	AACCTCC	TCC
	154	TCTTTGGTATGGC	ACATGCTGCCCG		TCGGGC	CAGCATGTGC	CCATACCA	AAG
	155	TAGAAAGGCTCGA	GCAACGGGAACT		TAGTTO	CCGTTGCTC	GAGCCTT	TCT
	156	TAATCTACCGCAC	TGGTCCGCAAGT		TACTTO	CGGACCAGI	GCGGTAG.	ATT
	157	TCGTGGCGGCCAC	AGTTTTTGGAGG		TCCTCC	CAAAAACTGI	GGCCGCC.	ACG

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TABLE 4-continued

	TABLE 4-COIL	.inded
Seq. ID	No.Decoder Sequence (5'-3') + 5'	T Probe Sequence (5'-3') + 5'
158	TTTGCAGTTCAATCCATACGCACGT	TACGTGCGTATGGATTGAACTGCAA
159	TGGCCCAAAGCCCCAGACCATTTTA	TTAAAATGGTCTGGGGCTTTGGGCC
160	TCGCCTGTCTTTGTCTCCGGACAAT	TATTGTCCGGAGACAAAGACAGGCG
161	TTGAGGCAACAGGGGCCAAAAACTA	TTAGTTTTTGGCCCCTGTTGCCTCA
162	TAGCGGAAGTAGTCCTCGGCTCGTC	TGACGAGCCGAGGACTACTTCCGCT
163	TGGCCCCAAGGCTTAGAGATAGTGG	TCCACTATCTCTAAGCCTTGGGGCC
164	TGCACGTGAAGTTTAACCGCGATTC	TGAATCGCGGTTAAACTTCACGTGC
165	TAGCGGCAGAAACGTTCCTTGACGG	TCCGTCAAGGAACGTTTCTGCCGCT
166	TTCGTCGAGCAGACGAGATTGCACG	TCGTGCAATCTCGTCTGCTCGACGA
167	TTCTTTGCCGCGTAACTGACTGCTT	TAAGCAGTCAGTTACGCGGCAAAGA
168	TTTTATGTGCCAAGGGGTTAACCGA	TTCGGTTAACCCCTTGGCACATAAA
169	TTGTTACTGTGGTTCACGGCAGTCC	TGGACTGCCGTGAACCACAGTAACA
170	TCGCGCCTCGCTAGACCTTTTATTG	TCAATAAAAGGTCTAGCGAGGCGCG
171	TACAAATGCGTGAGAGCTCCCAACT	TAGTTGGGAGCTCTCACGCATTTGT
172	TCGCGCAGATTATAGACCCGAATGT	TACATTCGGGTCTATAATCTGCGCG
173	TCAAATAACGCCGCTGAATCGGCGT	TACGCCGATTCAGCGGCGTTATTTG
174	TCCTTCGTGCATCGGTGATGATGTT	TAACATCATCACCGATGCACGAAGG
175	TTGAACACGAGCAACACTCCAACGC	TGCGTTGGAGTGTTGCTCGTGTTCA
176	TCAGCAGATCCTTCGTAGCGGTCGT	TACGACCGCTACGAAGGATCTGCTG
177	TGGAACCTGGTGAGTTGTGCCTCAT	TATGAGGCACAACTCACCAGGTTCC
178	TTCATAAGCGACAATCGCGGGCTTA	TTAAGCCCGCGATTGTCGCTTATGA
179	TCCCAACGTCACTGAAGCTCACAGT	TACTGTGAGCTTCAGTGACGTTGGG
180	TTGTCAGAGCCCGCGACTCAGACGG	TCCGTCTGAGTCGCGGGCTCTGACA
181	TTACACGAAGCCTCTCCGTGGTCCA	TTGGACCACGGAGAGGCTTCGTGTA
182	TCTCAGAAGTCCTCGGCGAACTGGG	TCCCAGTTCGCCGAGGACTTCTGAG
183	TATCCTTTATCTACTCCGCGGCGA	TTCGCCGCGGAGTAGATAAAAGGAT
184	TAGGCGTGCAGCAACAGGATAAACC	TGGTTTATCCTGTTGCTGCACGCCT
185	TACTCTCGAGGGAGTCTCTGGCACA	TTGTGCCAGAGACTCCCTCGAGAGT
186	TTTGCCAGGTCCATCGAGACCTGTT	TAACAGGTCTCGATGGACCTGGCAA
187	TTCCACTATAACTGCGGGTCCGTGT	TACACGGACCCGCAGTTATAGTGGA
188	TGCCCAGTCGGCTCTAACAAGTTCG	TCGAACTTGTTAGAGCCGACTGGGC
189	TCGGAACGGATAATCGGCGTCAGGT	TACCTGACGCCGATTATCCGTTCCG
190	TTAAAATAAGCGCCTGGCGGAGGA	TTCCTCCCGCCAGGCGCTTATTTTA
191	TGCGCACTCGTGAAACCTTTCTCGC	TGCGAGAAAGGTTTCACGAGTGCGC
192	TAGTTTGCCAGGTACTGGCAAGTGC	TGCACTTGCCAGTACCTGGCAAACT
193	TACAACGAGGGATGTCCAGCGGCAT	TATGCCGCTGGACATCCCTCGTTGT
194	TTTCGCAGCACCCGCTAGGTACAGT	TACTGTACCTAGCGGGTGCTGCGAA

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TABLE 4-continued

	TABLE 4-COILC	Indea
Seq. II	D No.Decoder Sequence (5'-3') + 5'	T Probe Sequence (5'-3') + 5' T
19	5 TTAACCCGATTTTTGCGACTCTGCC	TGGCAGAGTCGCAAAAATCGGGTTA
19	6 TCGTCGCATTGCAAGCGTAGGCTTG	TCAAGCCTACGCTTGCAATGCGACG
19	7 TGAGCTGACGTCACCATCAGAGGAA	TTTCCTCTGATGGTGACGTCAGCTC
19	8 TGGAGGCTGGGGGTCGCGCTTAAGT	TACTTAAGCGCGACCCCCAGCCTCC
19	9 TTTGTGGGAACCGCACTAGCTGGCT	TAGCCAGCTAGTGCGGTTCCCACAA
20	0 TCCCTCGCACTGTGTTCACGCTCTT	TAAGAGGGTGAACACAGTGCGAGGG
20	1 TTCATTGACTCGAATCCGCACAACG	TCGTTGTGCGGATTCGAGTCAATGA
20:	2 TACAGGGGTTGGCCTTCGTACGTAC	TGTACGTACGAAGGCCAACCCCTGT
20	3 TAGGCCGTGCAACATCACACAGGAT	TATCCTGTGTGATGTTGCACGGCCT
20	4 TGGGCCGTGGTCACGTAATATTGGC	TGCCAATATTACGTGACCACGGCCC
20	TGCGCGGACATGAAACGACAAGGCC	TGGCCTTGTCGTTTCATGTCCGCGC
20	6 TCTTATTGGGTGCCGGTGTCGGATT	TAATCCGACACCGGCACCCAATAAG
20	7 TGGGGCGGTTACCAAAAAATCCGAT	TATCGGATTTTTTGGTAACCGCCCC
	4 TCCGTCGCATACCGGCTACGATCAA	TTTGATCGTAGCCGGTATGCGACGG
!	5 TATGGCCGTGCTGGGGACAAGTCAA	TTTGACTTGTCCCCAGCACGGCCAT
21	0 TACGAAAAAGTGTGCGGATCCCCT	TAGGGGATCCGCACACTTTTTTCGT
21	1 TCCAAGTACACCGCACGCATGTTTA	TTAAACATGCGTGCGGTGTACTTGG
21:	2 TATCGTGCGTGGAGTGTCGCATCTA	TTAGATGCGACACTCCACGCACGAT
21	3 TTCCAGATACCGCCCGAACTTTGA	TTCAAAGTTCGGGGCGGTATCTGGA
21	4 TTCTGCTGGCAGCACGTGAAGTGGC	TGCCACTTCACGTGCTGCCAGCAGA
21	5 TTTGAAATTGCTCTGCCGTCAGTCA	TTGACTGACGGCAGAGCAATTTCAA
21	6 TAGTCAGGCGAGATGTTCAGGCAGC	TGCTGCCTGAACATCTCGCCTGACT
21	7 TACAAGCCGACGTTAAGCCCGCCCA	TTGGGCGGGCTTAACGTCGGCTTGT
21	8 TCCCTAATGAGGCCAGTAACCTGCA	TTGCAGGTTACTGGCCTCATTAGGG
21	9 TGTGAGACACACCCCCCCCAATG	TCATTGGAGGGGATGTGTGTCTCAC
22	0 TCGACGGATGCAGAGTTCAGTGGTC	TGACCACTGAACTCTGCATCCGTCG
22	1 TCCCGCATGCCTGGCGGTATTACAA	TTTGTAATACCGCCAGGCATGCGGG
22	2 TTTAGCAAAGCGGCGCCGTTAGCAA	TTTGCTAACGGCGCCGCTTTGCTAA
22	3 TCCCGACACGGGTCAGCGTAATAAT	TATTATTACGCTGACCCGTGTCGGG
22	4 TGCGACGGCCCTGAGGTATGTCGTC	TGACGACATACCTCAGGGCCGTCGC
22	5 TCAAAAGTGTGTTCCCTTGCGCTTG	TCAAGCGCAAGGGAACACACTTTTG
22	6 TTCTCGAAGCACAGCCCGGTTATTG	TCAATAACCGGGCTGTGCTTCGAGA
22	7 TATGCTAACCGTTGGCCATGGAACT	TAGTTCCATGGCCAACGGTTAGCAT
22	8 TCTTGCGGAGTGTTAGCCCAGCGGT	TACCGCTGGGCTAACACTCCGCAAG
22:	9 TTGCTCCCTAGGCGCTCGGAGGAGT	TACTCCTCCGAGCGCCTAGGGAGCA
23	0 TCCAATGCCTTTGAGTAAGCGATGG	TCCATCGCTTACTCAAAGGCATTGG
23	1 TAGCAGATAACGTCCCAATGACGCC	TGGCGTCATTGGGACGTTATCTGCT

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TABLE 4-continued

			17	DDE 4-CC	лист	iueu			
Seq. 1	ID No.	Decoder	Sequence	(5'-3') +	5' Т	Probe	Sequence	(5'-3')	+ 5' T
23	32	TTTGACCA	ATTACGTGT	IGCGCCCAT		TATGGG	GCGCAACACG	TAATGGT	CAA
23	33	TTCGCGT	ATTTGCGGA	ATTCGTCTG		TCAGAC	CGAATTCCGC	CAAATACG	CGA
23	3 4	TCTGCGT	GTCAACAAT	GTCCCGCAG		TCTGC	GGACATTGT	TTGACACG	CAG
23	35	TTCTGGT	GCCACGCAA	GGTCCACAG		TCTGT	GACCTTGCG	STGGCACC	AGA
23	36	TCTCCGG	GAGGTCACT	TAATTGCGG		TCCGC	AATTAAGTG <i>A</i>	ACCTCCCG	GAG
23	37	TTTTTCG	rgattgccc	GGAGGAGGC		TGCCTC	CCTCCGGGC <i>I</i>	ATCACGA	AAA
23	38	TTCGGGA	rgtagctgg	GGCTACCGG		TCCGGT	TAGCCCCAGC	CTACATCC	CGA
23	39	TCGAGCC	AACGCAAAC	ACGTCCTTG		TCAAGO	GACGTGTTTC	CGTTGGC	TCG
24	40	TGCAAAG	CCTTTGTGG	GGCGGTAGT		TACTAC	CCGCCCCACA	AAAGGCTT	TGC
24	41	TATTCGAC	CCGGAAATG	AGGTCTTCG		TCGAAG	GACCTCATTI	CCGGTCG	AAT
24	12	TTTCGCT	rgctgagtt	GCTCTGTTC		TGAACA	AGAGCAACTO	CAGCAAGC	GAA
24	43	TCGCGTG	AAGACCCCA'	TTCCCGAGT		TACTCO	GGAATGGGG	TCTTCAC	GCG
24	4 4	TAACCGT	ATTCGCGGT	CACTTGTGG		TCCACA	AAGTGACCGC	CGAATACG	GTT
24	45	TGGGGCC	AACCGTTTC	GAGGCGTAT		TATACO	GCCTCGAAAC	CGGTTGGC	ccc
24	46	TTTCGGC	rggcagtcc	AAACGGCTT		TAAGCO	CGTTTGGACT	TGCCAGCC	GAA
24	47	TGGGTGT	GGTTAGAAT	GCACGGTTC		TGAACO	CGTGCATTCT	TAACCACA	ccc
24	48	TGCGAGG	ACCGAACTA	GACAAACGG		TCCGTT	TTGTCTAGTT	CGGTCCT	CGC
24	19	TACGCAC	GCGTGACCG	AAGTTGCTG		TCAGCA	AACTTCGGTC	CACGCGTG	CGT
25	50	TTAAAAG	GTCGCTTTG	AAAGGGGGA		TTCCCC	CCTTTCAAAG	GCGACCTT	TTA
25	51	TTGCGAT	CGCTAACTG	CTGGGACAA		TTTGT	CCCAGCAGTT	TAGCGATC	GCA
25	52	TGGAGGT	ATAAGCGGA	GCGGCCTCA		TTGAGG	SCCGCTCCGC	CTTATACC	TCC
25	53	TATGCTG	ACATGTCGT	GCACCTCGT		TACGAG	GTGCACGAC	CATGTCAG	CAT
25	54	TTGTGGT	FAAAGCGTC	CGTTCAACG		TCGTT	GAACGGACGC	CTTTAACC	ACA
25	55	TCGTTCA	CACCGGCGT	AAGCTGCGT		TACGC	AGCTTACGCC	CGGTGTGA	ACG
25	56	TCCTATC	CCGGCGAGA	ACTTCTGTG		TCACAG	GAAGTTCTCG	GCCGGGAT	AGG
25	57	TGTCTGC	ACTCACGCA	GCGGAGGGA		TTCCCT	rccgctgcgi	GAGTGCA	GAC
25	58	TGCACGA	GTTGGTGCT	CGGCAGATT		TAATCI	rgccgagcac	CCAACTCG	TGC
25	59	TAACGTC	GCACGACAC	ACGTTCGTC		TGACGA	AACGTGTGTC	CGTGCGAC	GTT
26	5 0	TATGCGC	GCTTATCCT	AGCATGGTC		TGACCA	ATGCTAGGAT	TAAGCGCG	CAT
26	51	TTCACGT	TTTCGTCTC	GACATGAGG		TCCTC	ATGTCGAGAC	CGAAAACG	TGA
26	52	TTGTGCC	TCATCCTTA:	GGATACGGC		TGCCGT	TATCCTAAGG	SATGAGGC	ACA
26	53	TAGGTGG'	IGTGGGTCA	ACCGCTTTA		TTAAAC	GCGGTTGACC	CCACACCA	CCT
26	5 4	TCTGGAT	CGAAGGGAC'	IGCAAGCTC		TGAGCT	TTGCAGTCCC	CTTCGATC	CAG
26	55	TTAGATC	AACTCGCGT	ACGCATGGA		TTCCAT	rgcgtacgco	SAGTTGAT	CTA
26	56	TGATCCT	GCGGAGAAG	AGAGTGCAG		TCTGC	ACTCTCTTCT	CCGCAGG	ATC
26	57	TTACGTG	IGGAGATGC	CCCGAACCG		TCGGTT	CGGGGCATC	CTCCACAC	GTA
26	58	TGCGCTA	IGTCAATCG'	IGGGCGTAG		TCTACO	GCCCACGATT	TGACATAG	CGC

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TABLE 4-continued

		TABLE 4-CON	cinaea			
Seq. I	D No.Decoder S	Sequence (5'-3') + 5	' T Probe	Sequence	(5'-3')	+ 5' T
26	9 TAGCGAGG	TTTCTAGCGTCGACACC	TGGTGT	CGACGCTAG	AAACCTCG	CT
27	0 TACCCAGG	TTTTGCCGTTGTGGAAT	TATTC	CACAACGGCA	AAACCTGG	GT
27	1 TCCCTGTT	AACGGCTGCGTAGTCTC	TGAGAG	CTACGCAGCC	GTTAACAG	GG
27	2 TAGGCCGA	TTTCACCCGCCAATTGC	TGCAAT	TTGGCGGGTG	AAATCGGC	CT
27	3 TGAGCCCT	CACTCCTTGCCCTTTGA	TTCAA	AGGGCAAGGA	GTGAGGGC	CTC
27	4 TGGGTGGA	CATCCGCCTCGCAGTCA	TTGACT	rgcgaggcgg	SATGTCCAC	:cc
27	5 TGATGGCT	GAGAACCGTGCTACGAT	TATCG	TAGCACGGTT	CTCAGCCA	ATC
27	6 TTCGACGT	FAGGAGTGCTGCCAGAA	TTTCTC	GCAGCACTO	CTAACGTC	:GA
27	7 TCGAATGG	STCTGGACCTTGCATAG	TCTATO	GCAAGGTCCA	GACCCATT	'CG
27	8 TGTGCACCA	AGACATTCGAACTCGGA	TTCCG	AGTTCGAATC	TCTGGTGC	AC
27	9 TAGAGGCC	CCGTATATCCCATCCAT	TATGG	ATGGGATATA	CGGGGCCT	CT
28	0 TAACGCCT	STTCAGAGCATCAGCGG	TCCGCT	GATGCTCTG	AACAGGCG	TT
28	1 TAAGGCTCA	AACACGCCTATGTGCGC	TGCGC	ACATAGGCGT	GTTGAGCC	TT.
28	2 TAGTCCGT	STTGCCAGATTGGCTCG	TCGAGO	CCAATCTGGC	CAACACGGA	CT
28	3 TATGTCCC	ATGTAAAGACGCGTGTG	TCACAC	CGCGTCTTTA	CATGGGAC	'AT
28	4 TATGGAGT	CTGCTCACGCCCAAAGG	TCCTT	rgggcgtgag	CAGACTCC	'AT
28	5 TCGGCCTC	CAACAAGGAGCACTAAC	TGTTAC	TGCTCCTTG	TTGGAGGC	CG:
28	6 TCAGAGCC	FTGGCAACATTGCGAGC	TGCTC	GCAATGTTGC	CACGGCTC	TG
28	7 TTCATTTGA	AATGAGGTGCGCACCGG	TCCGGT	FGCGCACCTC	ATTCAAAT	'GA
28	8 TGACGTAC	CGGAAGCGCCGTATAAA	TTTTAT	PACGGCGCTT	CCGGTAC	TC
28	9 TATGCGAGG	CAATGGGATCCGGATTC	TGAATO	CCGGATCCCA	TTGCTCGC	AT
29	0 TAGAGTGAG	GCCTCCCTGACCAGTG	TCACTO	GTCAGGGAG	GCCTCACT	CT
29	1 TCGCACCG	PAAGTAGATTTGCCCGC	TGCGGC	GCAAATCTAC	TTACGGT	CG
29	2 TTGAACCT	TTGAGCACGTCGTGCGC	TGCGC	ACGACGTGCT	CAAAGGTT	CA
29	3 TTCCGCCT	TTTTGGTTACCTCGAAG	TCTTC	GAGGTAACCA	AAAAGGCG	GA
29	4 TGAACGCC	AACGGCACTAACACATC	TGATGT	TGTTAGTGCC	GTTGGCGT	TC.
29	5 TCCGACAG	CAGCCAAGACGTCCCAG	TCTGGG	GACGTCTTGG	CTGCTGTC	:GG
29	6 TCATAAAA	AAACCTGGGGCTCTGCG	TCGCAC	SAGCCCCAGG	TTTTTTT	ΤG
29	7 TTGCCAAC	TGTGCAGACCGGACTTA	TTAAGT	CCGGTCTGC	ACAGTTGG	CA
29	8 TGGCGAAA	GAGCGAAACCGGCTCGT	TACGAC	CCGGTTTCG	CTCTTTC	icc
29	9 TGGGATGC	STATTTTAGCGAACACG	TCGTGT	TTCGCTAAAA	TACGCATO	:CC
30	0 TTGGGATT	CAGCGACCAGTACGCGA	TTCGCC	STACTGGTCG	CTGAATCC	CA.
30	1 TCCCGATA	TTCGCCCGGCCTATTCG	TCGAAT	PAGGCCGGGC	GAATATCO	:GG
30	2 TCGAGAAGA	ATGCCTCACGCAACCAA	TTTGGT	TTGCGTGAGG	CATCTTCT	'CG
30	3 TAACCTTG	ACCCGTGGATGACGCTA	TTAGCO	FTCATCCACG	GGTCAAGG	TT
	6 TTTGCAAC	GGCTGGTCAACGTCAA	TTTGAG	CGTTGACCAG	CCCGTTGC	!AA
	7 TCGCATAGO	STTGCCGATTTCGTCAA	TTTGAG	CGAAATCGGC	AACCTATO	CG

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TABLE 4-continued

307 TCCCTCCATGTTCTTCGAACGGTTT TAAA	CCATCCCGTTCATCCGGAAGC CCGTTCGAAGAACATGGAGGG AAGAGCATTGCCGCCCATCAA
200	AAGAGCATTGCCGCCCATCAA
308 TTTGATGGGCGGCAATGCTCTTGCT TAGC	
309 TATTGTGAGATGCGCCAAATTCCCC TGGG	GAATTTGGCGCATCTCACAAT
310 TTCAGCACAGCCAGACGGTCAACTT TAAG	TTGACCGTCTGGCTGTGCTGA
311 TACTCCACTCCTCGGTGGCAAACTA TTAG	TTTGCCACCGAGGAGTGGAGT
312 TTCTGGGCATGCCTGGACGGAGACG TCGT	CTCCGTCCAGGCATGCCCAGA
313 TTCTCAACTCCGGTACGACGAAACA TTGT	TTCGTCGTACCGGAGTTGAGA
314 TTTGCGTGGTCAAAGGCGCAACGTG TCAC	GTTGCGCCTTTGACCACGCAA
315 TAGACAGCGATCCGCGGCTCATGAT TATC	ATGAGCCGCGGATCGCTGTCT
316 TCGCGTCTCTAACTGAGAGCAGCCA TTGG	CTGCTCTCAGTTAGAGACGCG
317 TAGGCGCACATGTACGGACATTCAG TCTG	AATGTCCGTACATGTGCGCCT
318 TGATGAGTGGCACGTCGGTGTGTAA TTTA	CACACCGACGTGCCACTCATC
319 TTGATCCATATTGTCGGACGTTGCG TCGC	AACGTCCGACAATATGGATCA
320 TACCTGCCGGGAGTTCATAGGCTAG TCTA	GCCTATGAACTCCCGGCAGGT
321 TAGCATTGGCGTTTTTCCGCAACGA TTCG	TTGCGGAAAAACGCCAATGCT
322 TGGTAATATTCAGCGCGACCGCTCA TTGA	GCGGTCGCGCTGAATATTACC
323 TATAGCGTACGACGAGGTGACGCGC TGCG	CGTCACCTCGTCGTACGCTAT
324 TTAGGTCACGATGCGTTTGACGCTA TTAG	CGTCAAACGCATCGTGACCTA
325 TACTGCCCGTACCTCTGGTTCTGGC TGCC	AGAACCAGAGGTACGGGCAGT
326 TCCTTTGGCCTGAAGTTGTCGTAGC TGCT	ACGACAACTTCAGGCCAAAGG
327 TGTGCCCCACGAGCGTATCGTTGTA TTAC	AACGATACGCTCGTGGGGCAC
328 TAGGCGCTACGTGGGCCTGGAGCAA TTTG	CTCCAGGCCCACGTAGCGCCT
329 TGGGTGCTACCATTGCATTAGTCCG TCGG	ACTAATGCAATGGTAGCACCC
330 TACCACGCGCGTACGTGTAACCGAG TCTC	GGTTACACGTACGCGCGTGGT
331 TCCATGATGCATTGGGTGCATTTAG TCTA	AATGCACCCAATGCATCATGG
332 TGGTCCGGCCCTACGAAACGTTCGA TTCG	AACGTTTCGTAGGGCCGGACC
333 TCCGTGTGGCTGGAGATTCGTGTGA TTCA	CACGAATCTCCAGCCACACGG
334 TGTTAGGGCGACGCATATTGGCACA TTGT	GCCAATATGCGTCGCCCTAAC
335 TGGGTCAGTCAGGTGCGTTAGGATC TGAT	CCTAACGCACCTGACTGACCC
336 TGCCGTGAAGTCGAATGCAGATCGA TTCG	ATCTGCATTCGACTTCACGGC
337 TGCCACCAGTGCATTCAGGTA TTAC	CTGAATGCACTGGGTGGTGGC
338 TGAGCTTAGTTTGCGGTCATCGGGC TGCC	CGATGACCGCAAACTAAGCTC
339 TTGTTTGCCGCCATTAGGGAGTAAC TGTT	ACTCCCTAATGGCGGCAAACA
340 TGCTCCGCTGGATGTGCCGGTTTAG TCTA	AACCGGCACATCCAGCGGAGC
341 TCGGTAGCATGCGAGATCCCTGTTA TTAA	CAGGGATCTCGCATGCTACCG
342 TCTACGCTCTACCAGTTGCCTGCGA TTCG	CAGGCAACTGGTAGAGCGTAG

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TABLE 4-continued

Seq. ID	No.Decoder Sequence (5'-3') + 5'	T Probe Sequence (5'-3') + 5' T
343	TGTGCCTCCTGCTGTATTTGCCAAG	TCTTGGCAAATACAGCAGGAGGCAC
344	TTTGCGACTCGACTTGGACGAGTAG	TCTACTCGTCCAAGTCGAGTCGCAA
345	TTCTGGGAGCTGTTTACTCCAGCCA	TTGGCTGGAGTAAACAGCTCCCAGA
346	TTGCACGCGGAACTCCCTTTACCAT	TATGGTAAAGGGAGTTCCGCGTGCA
347	TTGGCAGCAAATGAATCGAAAGCAC	TGTGCTTTCGATTCATTTGCTGCCA
348	TAACTGGTGACGCGGTACAGCGAAG	TCTTCGCTGTACCGCGTCACCAGTT
349	TAGACGATTACGCTGGACGCCGTCG	TCGACGGCGTCCAGCGTAATCGTCT
350	TATGCCCTCCTTCATGGAAAGGGTT	TAACCCTTTCCATGAAGGAGGGCAT
351	TATTCTCGGAGCGTATGCGCCAGAA	TTTCTGGCGCATACGCTCCGAGAAT
352	TATAGCGGAGTTTGGGTACGCGAAC	TGTTCGCGTACCCAAACTCCGCTAT
353	TACCTACGCATACCGCTTGGCGAGG	TCCTCGCCAAGCGGTATGCGTAGGT
354	TGATTACCTGAATGGCCAAGCGAGC	TGCTCGCTTGGCCATTCAGGTAATC
355	TCCTGTTAGCATCACGGCGCTTAGG	TCCTAAGCGCCGTGATGCTAACAGG
356	TCGGAATGATGCGCTCGACAACGCT	TAGCGTTGTCGAGCGCATCATTCCG
357	TTGAGAGAGGCGTTGGTTAAGGCAA	TTTGCCTTAACCAACGCCTCTCTCA
358	TAAGCAGGCGAAGGGATACTCCTCG	TCGAGGAGTATCCCTTCGCCTGCTT
359	TTCACGACAGACGGCCGAGATTAC	TGTAATCTCGGCCCGTCTGTCGTGA
360	TAAGCAATTTGGCCTCGTTTTGTGA	TTCACAAAACGAGGCCAAATTGCTT
361	TGCTGGTTGCGGTAGGATCGCATAT	TATATGCGATCCTACCGCAACCAGC
362	TTTGTGAATCCGTTCTGTCCCCGAC	TGTCGGGGACAGAACGGATTCACAA
363	TTGGGCTCCTCTGAGGCGAGATGGC	TGCCATCTCGCCTCAGAGGAGCCCA
364	TGGATAGAGTGAATCGACCGGCAAC	TGTTGCCGGTCGATTCACTCTATCC
365	TTGCACCGAACGTGCACGAGTAATT	TAATTACTCGTGCACGTTCGGTGCA
366	TGCCAGTATTCTCGGGTGTTGGACG	TCGTCCAACACCCGAGAATACTGGC
367	TTCGCTACCTAAGACCGGGCCATAC	TGTATGGCCCGGTCTTAGGTAGCGA
368	TTGGCATTGACGAGCAGCAGTCAGT	TACTGACTGCTGCTCGTCAATGCCA
369	TCGCGTCCCAGCGCCCTTGGAGTAT	TATACTCCAAGGGCGCTGGGACGCG
370	TATGAAGCCTACCGGGCGACTTCGT	TACGAAGTCGCCCGGTAGGCTTCAT
371	TCCAGACAGATGGCCTGGAACCATG	TCATGGTTCCAGGCCATCTGTCTGG
372	TTGGCGTGGGACCATCTCAAAGCTA	TTAGCTTTGAGATGGTCCCACGCCA
373	TCCGCATGGGAACACGTGTCAAGGT	TACCTTGACACGTGTTCCCATGCGG
374	TGCCCACTCGTCAGCTGGACGTAAT	TATTACGTCCAGCTGACGAGTGGGC
375	TATTACGGTCGTGATCCAGAAAGCG	TCGCTTTCTGGATCACGACCGTAAT
376	TTGCGAGGTGAGCACCTACGAGAGA	TTCTCTCGTAGGTGCTCACCTCGCA
377	TGGGCCGCATTCTTGATGTCCATTC	TGAATGGACATCAAGAATGCGGCCC
378	TCCTCGGATGTGGGCTCTCGCCTAG	TCTAGGCGAGAGCCCACATCCGAGG
379	TTAGGCATGTTGGCGTGAGCGCTAT	TATAGCGCTCACGCCAACATGGCTA

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TABLE 4-continued

Seq. ID	No.Decoder Sequence (5'-3') + 5'	T Probe Sequence (5'-3') + 5' T
380	TCGATACGAACGAGGATGTCCGCCT	TAGGCGGACATCCTCGTTCGTATCG
381	TTACGCCGGTTAGCACGGTGCGCTA	TTAGCGCACCGTGCTAACCGGCGTA
382	TCATACGATGTCCGGGCCGTGTCGC	TGCGACACGGCCCGGACATCGTATG
383	TATCCGCAGTTGTATGGCGCGTTAT	TATAACGCGCCATACAACTGCGGAT
384	TGGGTAAGGGACAAAGATGGGATGG	TCCATCCCATCTTTGTCCCTTACCC
385	TATTGGAGTGTTTTGGTGAATCCGC	TGCGGATTCACCAAAACACTCCAAT
386	TGAACCGAGCCAACGTATGGACACG	TCGTGTCCATACGTTGGCTCGGTTC
387	TGCCGTCAAGCTTAAGGTTTTGGGC	TGCCCAAAACCTTAAGCTTGACGGC
388	TACCTGCTTTTGGGTGGTGATATG	TCATATCACCCACCCAAAAGCAGGT
389	TAATCGTGGGCGCAGCAAACGTATA	TTATACGTTTGCTGCGCCCACGATT
390	TGTCGCCGGATTGCTCAGTATAAGC	TGCTTATACTGAGCAATCCGGCGAC
391	TACCCGTCGATGCTTCCTCCTCAGA	TTCTGAGGAGGAAGCATCGACGGGT
392	TATCCGGGTGGGCGATACAAGAGAT	TATCTCTTGTATCGCCCACCCGGAT
393	TTTCCGCATGAGTCAGCTTTGAAAA	TTTTTCAAAGCTGACTCATGCGGAA
394	TGCAAAGTCCCACTGGCAAGCCGAT	TATCGGCTTGCCAGTGGGACTTTGC
395	TCGACCTCGGCTTCATCGTACACAT	TATGTGTACGATGAAGCCGAGGTCG
396	TCTCATGAGCGCAGTTGTGCGTGAG	TCTCACGCACAACTGCGCTCATGAG
397	TCAGATGAAGGATCCACGGCCGGAG	TCTCCGGCCGTGGATCCTTCATCTG
398	TTCAAAGGCTCTTGGATACAGCCGT	TACGGCTGTATCCAAGAGCCTTTGA
399	TTCCGCTAATTTCCAATCAGGGCTC	TGAGCCCTGATTGGAAATTAGCGGA
8	TCCGTTTGCGGTCGTCCTTGCTCAA	TTTGAGCAAGGACGACCGCAAACGG
9	TTTCGCTTTCGTGGCTGCACTTCAA	TTTGAAGTGCAGCCACGAAAGCGAA
402	TCTTAGTTGGGGCGCGGTATCCAGA	TTCTGGATACCGCGCCCCAACTAAG
403	TGCTCTAATGCCGTGGAGTCGGAAC	TGTTCCGACTCCACGGCATTAGAGC
404	TCCGATTACAAATTGACTGACCGCA	TTGCGGTCAGTCAATTTGTAATCGG
405	TAGACGTACGTGAGCCTCCCGTGTC	TGACACGGGAGGCTCACGTACGTCT
406	TAATGGAGCGATACGATCCAACGCA	TTGCGTTGGATCGTATCGCTCCATT
407	TGGAGGCGCTGTACTGATAGGCGTA	TTACGCCTATCAGTACAGCGCCTCC
408	TTGTTTTTGAATTGACCACACGGGA	TTCCCGTGTGGTCAATTCAAAAACA
409	TCATGTCTGGATGCGCTCAATGAAG	TCTTCATTGAGCGCATCCAGACATG
410	TGCCCGCTAATCCGACACCCAGTTT	TAAACTGGGTGTCGGATTAGCGGGC
411	TCCATTGACAGGAGAGCCATGAGCC	TGGCTCATGGCTCTCCTGTCAATGG
412	TGAATCACCGAATCACCGACTCGTT	TAACGAGTCGGTGATTCGGTGATTC
413	TAACCAGCCGCAGTAGCTTACGTCG	TCGACGTAAGCTACTGCGGCTGGTT
414	TTTTTCTGAGGGACACGCGGGCGTT	TAACGCCCGCGTGTCCCTCAGAAAA
415	TGGTGCTCCGTTTGATCGATCCTCC	TGGAGGATCGATCAAACGGAGCACC
416	TCCGCTTAGGCCATACTCTGAGCCA	TTGGCTCAGAGTATGGCCTAAGCGG

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Seq. ID	No.Decoder Sequence (5'-3') + 5	'T Probe Sequence (5'-3') + 5' T
417	TTAAGACATACCGACGCCCTTGCCT	TAGGCAAGGGCGTCGGTATGTCTTA
418	TGTTCCCGACGCCAGTCATTGAGAC	TGTCTCAATGACTGGCGTCGGGAAC
419	TTAAAAGTTTCGCGGAGGTCGGGCT	TAGCCCGACCTCCGCGAAACTTTTA
420	TCGGTCCAGACGAGCTGAGTTCGGC	TGCCGAACTCAGCTCGTCTGGACCG
421	TCGGCGTAGCGGCTACGGACTTAAA	TTTTAAGTCCGTAGCCGCTACGCCG
422	TGCTTGGATGCCCATGCGGCAAGGT	TACCTTGCCGCATGGGCATCCAAGC
423	TAGCGGGATCCCAGAGTTTCGAAAA	TTTTTCGAAACTCTGGGATCCCGCT
424	TGAGCTTGAGAGCGAGGTCATCCTC	TGAGGATGACCTCGCTCTCAAGCTC
425	TGCATCGGCCGTTTTGACCATATTC	TGAATATGGTCAAAACGGCCGATGC
426	TCATAGCGCTGCACGTTTCGACCGC	TGCGGTCGAAACGTGCAGCGCTATG
427	TACCCGACAACCACCAATTCAAAAA	TTTTTTGAATTGGTGGTTGTCGGGT
428	TGCGAACACTCATAAGAGCGCCCTG	TCAGGGCGCTCTTATGAGTGTTCGC
429	TCCGCCGAGTGTAGAGAGACTCCGA	TTCGGAGTCTCTCTACACTCGGCGG
430	TGACATCGGGAGCCGGAAACATGAG	TCTCATGTTTCCGGCTCCCGATGTC
431	TTCGTGTAGACTCGGCGACAGGCGT	TACGCCTGTCGCCGAGTCTACACGA
432	TATGCGCATATACTGACTGCGCAGG	TCCTGCGCAGTCAGTATATGCGCAT
433	TACAAGCGAACCCGAGTTTTGATGA	TTCATCAAAACTCGGGTTCGCTTGT
434	TGCATGAGACTCCGCGAAGACATGT	TACATGTCTTCGCGGAGTCTCATGC
435	TTCCTACATGTCGCGTCACGATCAC	TGTGATCGTGACGCGACATGTAGGA
436	TGACCGATCGCGAAGTCGTACACAT	TATGTGTACGACTTCGCGATCGGTC
437	TGTCGCCAGGACTGGGCCGATGTGA	TTCACATCGGCCCAGTCCTGGCGAC
438	TACCGATAAGACTTGCATCCGAACG	TCGTTCGGATGCAAGTCTTATCGGT
439	TTCCATAACCAGTCCGAAGTGCCGG	TCCGGCACTTCGGACTGGTTATGGA
440	TACGCGCCCTGCATCTCGTATTTAA	TTTAAATACGAGATGCAGGGCGCGT
441	TAGACCGCATCAATTGGCGCGTACC	TGGTACGCGCCAATTGATGCGGTCT
442	TAGAGGCTTGGCAAGTAGGGACCCT	TAGGGTCCCTACTTGCCAAGCCTCT
443	TGCAATGGACGCCAGACGATACCGG	TCCGGTATCGTCTGGCGTCCATTGC
444	TGCTGGACTTAGTCGTGTTCGGCGG	TCCGCCGAACACGACTAAGTCCAGC
445	TAGGCATCGTGCCGGATTGCTCCCT	TAGGGAGCAATCCGGCACGATGCCT
446	TTGCGCATGTCGACGTTGAACAAAG	TCTTTGTTCAACGTCGACATGCGCA
447	TTTCGGGTCACATCCGATGCCATAC	TGTATGGCATCGGATGTGACCCGAA
448	TACCCATCGCCGGAAAGCGATGTTG	TCAACATCGCTTTCCGGCGATGGGT
449	TAAGCGCTGACTCGGCTAAGAATCA	TTGATTCTTAGCCGAGTCAGCGCTT
450	TACTTCCAAGTCCTTGACCGTCCGA	TTCGGACGGTCAAGGACTTGGAAGT
451	TTCTCAATATTCCCGTAGTCGCCCA	TTGGGCGACTACGGGAATATTGAGA
452	TAACAGTTCCTCTTTTTCCTGGCGC	TGCGCCAGGAAAAAGAGGAACTGTT
453	TCGTCCTCCATGTTGTCACGAACAG	TCTGTTCGTGACAACATGGAGGACG

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Seq. I	No.Decoder	Sequence	(5'-3') + 5	5' Т	Probe	Sequence	(5'-3')	+ 5' T
45	4 TTGCGCA	GACCTACCTO	STCTTTGCT		TAGCAZ	AAGACAGGT <i>A</i>	AGGTCTGCG	CA:
45	5 TATGGAC	GGCTTCGCAG	TCCTCCTT		TAAGG	AGGACTGCGA	AGCCGTCC	AT
45	5 TTGAACG	CTTTCTATGG	GCCACGTA		TTACGI	GGCCCATAG	GAAAGCGTT	!CA
45	7 TTGAACC	CTGCCGCGAG	GCGATAACC		TGGTT	ATCGCTCGCG	GCAGGGTT	!CA
45	3 TGTTCTT	GCGCGATGA	ATCAGGACC		TGGTC	CTGATTCATC	GCGCAAGA	<b>A</b> AC
45	9 TAGGGTA	CGTGTCGCAG	CTTCGCGT		TACGC	GAAGCTGCGA	CACGTACO	CT
46	) TACCCTT	GCTCCGCCAT	GTCTCTCA		TTGAGA	AGACATGGCG	GAGCAAGG	GT.
46	1 TGGGACA	AGGATTGAAG	CTGGCGTC		TGACGO	CCAGCTTCA	ATCCTTGTC	cc
46	2 TTGTCGT	TGCTCCCGAG	STACCATTG		TCAATO	GTACTCGGG	GAGCAACGA	ACA
46	3 TGTTGTC	CGAGACGTTI	GTGTCAGC		TGCTG	ACACAAACGI	CTCGGACA	<b>A</b> AC
46	4 TGCTGGT	GAACACTCAC	CGAACCGCT		TAGCG	GTTCGTGAGT	GTTCACCA	√GC
46	5 TGCAGAC	AGGGCAAATC	CGGTGCAAA		TTTTGO	CACCGATTTC	CCCTGTCT	!GC
46	TCCCATC.	ACAACGAGTO	GCGACTTT		TAAAGT	CGCCACTC	TTGTGATG	GG;
46	7 TGCTTCT.	ACAGCTGGCG	TGCTAGCG		TCGCT	AGCACGCCAG	CTGTAGA <i>A</i>	\GC
46	3 TGAATGT	GTGCCGACC	ATTCTAGCC		TGGCT	AGAATGGTCG	GCACACAT	PTC
46	9 TCCAGCG	GAAGTTAGAG	CTCTGTGG		TCCACA	AGAGCTCTA	ACTTCCGCT	!GG
47	ATTTTTT C	CCGACCACTO	CATGTCGG		TCCGA	CATGGAGTGG	TCGGTAA	\AA
47	1 TGCGGCT.	ATGTGATGAC	CGGCCTAGC		TGCTAG	GCCGTCATC	CACATAGCO	:GC
47	2 TAGTACA	CGGGCGTGTT	PAGCGCTCC		TGGAG	CGCTAACAC	CCCGTGT#	ACT
47	3 TTCCTGT	GTGGTGGCGC	CACTCCCAC		TGTGG	GAGTGCGCCA	ACCACACAG	GA:
47	4 TCCAACT.	AACCAATCGO	CGCGGATGA		TTCATO	CCGCGCGATT	GGTTAGTT	!GG
47	5 TAGTGAG	TGACCAAGGC	CAGGAGCAA		TTTGCT	CCTGCCTTC	GTCACTCA	\CT
47	5 TCATCTT	TCGCGGAGTT	TATTGCGG		TCCGC	ATAAACTCC	GCGAAAGA	\TG
47	7 TCTTCGT	CCGGTTAGT	GCGACAGCA		TTGCT	GTCGCACTA	ACCGGACGA	\AG
47	B TCTCACG.	AAAACGTGGG	GCCCGAAAT		TATTT	CGGGCCCACG	TTTTCGT	AG
47	TCGCAGC.	AGCTGAACTO	CTAGCATTG		TCAATO	GCTAGAGTTC	CAGCTGCTG	}CG
48	) TAGGAGA	CATACGCCCA	AATGGTGC		TGCAC	CATTTGGGCC	STATGTCTC	CT
48	1 TATTGAG.	AACTCGTGC	GGAGTTTG		TCAAA	CTCCCGCACG	AGTTCTCA	\AT
48	2 TCTCTTT	GTAGGCCCAG	GAGGAGCA		TTGCT	CCTCCTGGGC	CTACAAAG	AG:
48	3 TGCCGCA	GGGTCGATA	ATTGGTCTA		TTAGA	CCAATTATCO	ACCCTGCG	}GC
48	4 TAAACGC	CGCCCTGAGA	ACTATTGGG		TCCCA	ATAGTCTCAG	GGCGGCGT	PT.
48	5 TCTGAGT	TGCCTGGAAC	CGTTGGACT		TAGTCO	CAACGTTCC	AGGCAACTO	AG
48	5 TCGGATG	GGTTGCAGAG	STATGGGAT		TATCC	CATACTCTGC	CAACCCATC	:CG
48	7 TCTGACC	TTTGGGGGTT	AGTGCGGT		TACCGO	CACTAACCCC	CAAAGGTC	'AG
48	3 TGGAAAT	GAGAACCTTA	ACCCCAGCG		TCGCT	GGGTAAGGT	TCTCATTI	!CC
48	9 TAACGCA	TCGTCCGTC <i>I</i>	AACTCATCA		TTGATO	GAGTTGACGG	SACGATGCG	TT
49	) TTGGAGA	GAGACTTCGG	GCCATTGTT		TAACA	ATGGCCGAAG	TCTCTCTC	CA.

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Seq. ID	No.Decoder Sequence (5'-3') + 5'	T Probe Sequence (5'-3') + 5' T
491	TTTGCGCTCATTGGATCTTGTCAGG	TCCTGACAAGATCCAATGAGCGCAA
492	TAGCGCGTTAAAGCACGGCAACATT	TAATGTTGCCGTGCTTTAACGCGCT
493	TAGCCAGTAAACTGTGGGCGGCTGT	TACAGCCGCCCACAGTTTACTGGCT
494	TCGACTGATGTGCAACCAGCAGCTG	TCAGCTGCTGGTTGCACATCAGTCG
495	TGGTTGCTCATACGACGAGCGAGTG	TCACTCGCTCGTCGTATGAGCAACC
10	TGTCCAACGCGCAACTCCGATTCAA	TTTGAATCGGAGTTGCGCGTTGGAC
11	TTTGCCGCACCGTCCGTCATCTCAA	TTTGAGATGACGGACGGTGCGGCAA
498	TAGAACCTCCGCGCCTCCGTAGTAG	TCTACTACGGAGGCGCGGAGGTTCT
499	TAAAGGAGCTTTCGCCCAACGTACC	TGGTACGTTGGGCGAAAGCTCCTTT
500	TAGTGATTGTGCCACTCCACAGCTC	TGAGCTGTGGAGTGGCACAATCACT
501	TGCGATCGTCGAGGGTTGAGCTGAA	TTTCAGCTCAACCCTCGACGATCGC
502	TGGGAGACAGCCATTATGGTCCTCG	TCGAGGACCATAATGGCTGTCTCCC
503	TGAGACGCTGTCACTCCGGCAGAAC	TGTTCTGCCGGAGTGACAGCGTCTC
504	TCCACCGGTCGCTTAAGATGCACTT	TAAGTGCATCTTAAGCGACCGGTGG
505	TCGGCATAACGTCCAGTCCTGGGAC	TGTCCCAGGACTGGACGTTATGCCG
506	TAAGCGGAACGGGTTATACCGAGGT	TACCTCGGTATAACCCGTTCCGCTT
507	TTGCACACTAGGTCCGTCGCTTGAT	TATCAAGCGACGGACCTAGTGTGCA
508	TAGGGAACCGCGTTCAAACTCAGTT	TAACTGAGTTTGAACGCGGTTCCCT
509	TGAATTACAACCACCCGCTCGTGTT	TAACACGAGCGGGTGGTTGTAATTC
510	TTTCAGTGCTCACGAAGCATGGATT	TAATCCATGCTTCGTGAGCACTGAA
511	TTTAGTTTGGCGTTGGGACTTCACC	TGGTGAAGTCCCAACGCCAAACTAA
512	TAATGCGACCTCGACGAGCCTCATA	TTATGAGGCTCGTCGAGGTCGCATT
513	TCCGAAACCGTTAACGTGGCGCACA	TTGTGCGCCACGTTAACGGTTTCGG
514	TTAAAGTAACAAGGCGACCTCCCGC	TGCGGGAGGTCGCCTTGTTACTTTA
515	TTAATGATTTTAGTCGCGGGGTGGG	TCCCACCCGCGACTAAAATCATTA
516	TGGCTACTCTAAGTGCCCGCTCAGG	TCCTGAGCGGGCACTTAGAGTAGCC
517	TTGGCGGACGACTCAATATCTCACG	TCGTGAGATATTGAGTCGTCCGCCA
518	TGGGCGTTAGGCGTAATAGACCGTC	TGACGGTCTATTACGCCTAACGCCC
519	TGCCACCTTTAGACGGCGGCTCTAG	TCTAGAGCCGCCGTCTAAAGGTGGC
520	TGAGATGTGTAAACGTGCAGGCACC	TGGTGCCTGCACGTTTACACATCTC
521	TTAGCTCGTGGCCCTCCAAGCGTGT	TACACGCTTGGAGGGCCACGAGCTA
522	TGTGTCGGCGCTATTTGGCCTTACC	TGGTAAGGCCAAATAGCGCCGACAC
523	TCCAGGGAAGCAACTGGTTGCCATT	TAATGGCAACCAGTTGCTTCCCTGG
524	TTTCCGAAACTAAGCCAGAACCGCT	TAGCGGTTCTGGCTTAGTTTCGGAA
525	TGCAAACCCGGTAACCCGAGAGTTC	TGAACTCTCGGGTTACCGGGTTTGC
526	TGCAAATGGCGTCATGCACGAACGT	TACGTTCGTGCATGACGCCATTTGC
527	TAGTACTTTCGCGCCCAGTTTAGGG	TCCCTAAACTGGGCGCGAAAGTACT

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TABLE 4-continued

Seq. ID	No.Decoder Sequence (5'-3') + 5'	T Probe Sequence (5'-3') + 5' T
528	TAAGATCTGCGAGGCATCCCGGCTT	TAAGCCGGGATGCCTCGCAGATCTT
529	TGCAAGTGTATCGCACAGTGCGATT	TAATCGCACTGTGCGATACACTTGC
530	TCCGACAAGGCCTCAATTCATTCTG	TCAGAATGAATTGAGGCCTTGTCGG
531	TGTCTCGTCTCAACTTTAAGGCGCG	TCGCGCCTTAAAGTTGAGACGAGAC
532	TATCCAGAGATCCGTTTTGCAGCGT	TACGCTGCAAAACGGATCTCTGGAT
533	TGTCACCAGGAGGGAAGTTTCACCC	TGGGTGAAACTTCCCTCCTGGTGAC
534	TTTCCGTCAGGCGGATCAACGGAAT	TATTCCGTTGATCCGCCTGACGGAA
535	TATGCCGGACACGCATTACACAGGC	TGCCTGTGTAATGCGTGTCCGGCAT
536	TTGGGCCGCTTGGCGCTTTCATAGA	TTCTATGAAAGCGCCAAGCGGCCCA
537	TCCTAGCGCGAGCTTTACTGACCAG	TCTGGTCAGTAAAGCTCGCGCTAGG
538	TTTGGCCAGGAATATGGTCTCGAGA	TTCTCGAGACCATATTCCTGGCCAA
539	TGTCTGCGGCCGACTTGCTATGCAT	TATGCATAGCAAGTCGGCCGCAGAC
540	TAACTTGCTCATTCTCAAGCCGACG	TCGTCGGCTTGAGAATGAGCAAGTT
541	TACGTCAGCGATTGTGGCGAAATAT	TATATTTCGCCACAATCGCTGACGT
542	TACGGCCTGCGTCAGCAGATGCATC	TGATGCATGTGCTGACGCAGGCCGT
543	TATACCTCCGCAGAACCATTCCGTT	TAACGGAATGGTTCTGCGGAGGTAT
544	TAGTTCGCGGTCCCACGATTCACTT	TAAGTGAATCGTGGGACCGCGAACT
545	TTGCTCAATTTGTGCAGAAAACGCC	TGGCGTTTTCTGCACAAATTGAGCA
546	TTTATCGCGAGAGACGACCGTGTCC	TGGACACGGTCGTCTCTCGCGATAA
547	TGACGCGACGTGAGTAGTGGAAGCG	TCGCTTCCACTACTCACGTCGCGTC
548	TATGGTAGGGGCATTGGGCTTTCCT	TAGGAAAGCCCAATGCCCCTACCAT
549	TCCAAATATAGCCGCGCGGAGACAT	TATGTCTCCGCGCGGCTATATTTGG
550	TGCAAACCCTGATTGAATCGTGCCC	TGGGCACGATTCAATCAGGGTTTGC
551	TTAGCGTCTTGCGTGAAACCATGGG	TCCCATGGTTTCACGCAAGACGCTA
552	TCCACCCGACAGCGCTGGACTCTT	TAAGAGTCCAGCGCTGTCGGGGTGG
553	TACGAGCACTGAAGGCTGCTTTACG	TCGTAAAGCAGCCTTCAGTGCTCGT
554	TCATATCAGCGTCGTCTAGCTCGCG	TCGCGAGCTAGACGACGCTGATATG
555	TTGATCCCGGACCGGCTAGACTAAT	TATTAGTCTAGCCGGTCCGGGATCA
556	TGGCCCCGACACTACAGGGTAATCA	TTGATTACCCTGTAGTGTCGGGGCC
557	TGGCTCCAGGGCGAGATTATGAATG	TCATTCATAATCTCGCCCTGGAGCC
558	TCAAAATCCGATGGGCGGAAAATTA	TTAATTTTCCGCCCATCGGATTTTG
559	TCACAGGCGCATAGGGAGCAAGCTA	TTAGCTTGCTCCCTATGCGCCTGTG
560	TTAGCTATTGCCCCGATGGGCTACT	TAGTAGCCCATCGGGGCAATAGCTA
561	TTGGTACGCGGTCCATAGCAAGTCG	TCGACTTGCTATGGACCGCGTACCA
562	TGACGCTGTGGCTCGGAAACTGTTC	TGAACAGTTTCCGAGCCACAGCGTC
563	TCCTGGGTTCGCCGCGTGGTAACTG	TCAGTTACCACGCGGCGAACCCAGG
564	TTTCCCGCGTAGCCCAACAGCTATA	TTATAGCTGTTGGGCTACGCGGGAA

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Seq. ID	No.Decoder Sequence (5'-3') + 5'	T Probe Sequence (5'-3') + 5' T
565	TTTCGCGGATTGCTGCCGCATAACA	TTGTTATGCGGCAGCAATCCGCGAA
566	TAAAAATGGCACCGAAGTTGAGGCA	TTGCCTCAACTTCGGTGCCATTTTT
567	TCATTCCGCGCGAGTTGAAATCCAG	TCTGGATTTCAACTCGCGCGGAATG
568	TACGCACGTTTTTTGGCACGGTTAA	TTTAACCGTGCCAAAAAACGTGCGT
569	TTGTCCATGACGTCGTTTCTCTGGT	TACCAGAGAAACGACGTCATGGACA
570	TTCTCAGTCGGACTCGTATGCCAGA	TTCTGGCATACGAGTCCGACTGAGA
571	TCTCCAAACGCACACATCAAGCATC	TGATGCTTGATGTGTGCGTTTGGAG
572	TTTCAACCAAGCGGGTGTTCGTGA	TTCACGAACACCCCGCTTGGTTGAA
573	TGGTGTCGGAGGGTGGTGACCTCGA	TTCGAGGTCACCACCCTCCGACACC
574	TAGCGCTTTTGGTCATGATTTGCAA	TTTGCAAATCATGACCAAAAGCGCT
575	TCCGAGGACTTACGTCTGCCCAGGA	TTCCTGGGCAGACGTAAGTCCTCGG
576	TGCCCAATCCAGTTCTTATGCGCCC	TGGGCGCATAAGAACTGGATTGGGC
577	TCGGGTTAACCCACGCAAGTTATGA	TTCATAACTTGCGTGGGTTAACCCG
578	TTGATTAGCGCTCAATACACGCGTG	TCACGCGTGTATTGAGCGCTAATCA
579	TAAGGGCAGACCTTTGGTTCGACTG	TCAGTCGAACCAAAGGTCTGCCCTT
580	TGCGCCACAAGATTCACATGTCATT	TAATGACATGTGAATCTTGTGGCGC
581	TGCCATGTTCAAGGGCCTTTCGAAG	TCTTCGAAAGGCCCTTGAACATGGC
582	TCGCGGTGTTTTGTCTAGGTGCCGG	TCCGGCACCTAGACAAAACACCGCG
583	TCAACATTGTGGTGGCACTCCATCC	TGGATGGAGTGCCACCACAATGTTG
584	TCGATACGCGCCGGTTTGTTAAATC	TGATTTAACAAACCGGCGCGTATCG
585	TGGCTATAAACGTGCGGACTGCTCC	TGGAGCAGTCCGCACGTTTATAGCC
586	TTGGGTAAATCACTATTGCGCGGTT	TAACCGCGCAATAGTGATTTACCCA
587	TGTCTTCATCGGCCCGCGCAAGCTA	TTAGCTTGCGCGGGCCGATGAAGAC
588	TGCGACACCCTGTACTCTGATGC	TGCATCAGAGTACAGGGTGTGTCGC
589	TGTAGCAGGGTCCGCAAGACCAAGC	TGCTTGGTCTTGCGGACCCTGCTAC
590	TTCGCCAACGCAGGGTAACTGCCAT	TATGGCAGTTACCCTGCGTTGGCGA
591	TACTCCGAAGCTTCGAGCGGCACGA	TTCGTGCCGCTCGAAGCTTCGGAGT
12	TCATCGTCCCTTTCGATGGGATCAA	TTTGATCCCATCGAAAGGGACGATG
13	TGCACGGGAGCTGACGACGTGTCAA	TTTGACACGTCGTCAGCTCCCGTGC
594	TATCATCCCACGGCAGAGTGAAGAG	TCTCTTCACTCTGCCGTGGGATGAT
595	TCGCTGGACTGGCCTATCCGAGTCG	TCGACTCGGATAGGCCAGTCCAGCG
596	TCGGTCTCAGCAACACTGTCGCAAA	TTTTGCGACAGTGTTGCTGAGACCG
597	TCGAACGTTCTCCGATGTAATGGCC	TGGCCATTACATCGGAGAACGTTCG
598	TATACCGTGCGACAAGCCCCTCTGA	TTCAGAGGGGCTTGTCGCACGGTAT
599	TAGCTCATTCCCGAGACGGAACACC	TGGTGTTCCGTCTCGGGAATGAGCT
600	TTTTCATGCGGCCGTTGCAAATCAT	TATGATTTGCAACGGCCGCATGAAA
601	TACTCGAACGGACGTTCAATTCCCA	TTGGGAATTGAACGTCCGTTCGAGT

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TABLE 4-continued

Seq. ID	No.Decoder Sequence (5'-3') + 5	T Probe Sequence (5'-3') + 5' T
602	TCTGCATGGTGTGGGTGAGACTCCC	TGGGAGTCTCACCCACACCATGCAG
603	TCCGCGAGTGTGGATGGCGTGTTGA	TTCAACACGCCATCCACACTCGCGG
604	TAATGTGTCGGTCCTAAGCCGGGTG	TCACCCGGCTTAGGACCGACACATT
605	TTAAGACGAGCCTGCACAGCTTGCG	TCGCAAGCTGTGCAGGCTCGTCTTA
606	TGGCGTGGGAGGATAAGACGATGTC	TGACATCGTCTTATCCTCCCACGCC
607	TTGCTCCATGTTAGGAACGCACCAC	TGTGGTGCGTTCCTAACATGGAGCA
608	TCGGTGTTGGTCGGACTGACGACTG	TCAGTCGTCAGTCCGACCAACACCG
609	TCCGCGCGTATCTATCAGATCTGGG	TCCCAGATCTGATAGATACGCGCGG
610	TAAAGCATGCTCCACCTGGAGCGAG	TCTCGCTCCAGGTGGAGCATGCTTT
611	TACTTGCATCGCTGGGTAGATCCGG	TCCGGATCTACCCAGCGATGCAAGT
612	TTGCTTACGCAGTGGATTGGTCAGA	TTCTGACCAATCCACTGCGTAAGCA
613	TATGCAGATGAACAAATCGCCGAAT	TATTCGGCGATTTGTTCATCTGCAT
614	TGCAATTCTGGGCCATGTATTCGTC	TGACGAATACATGGCCCAGAATTGC
615	TAGGGTTCCTTACGCGTCGACATGG	TCCATGTCGACGCGTAAGGAACCCT
616	TGTGGAGCTAATCGCGAGCCTCAGA	TTCTGAGGCTCGCGATTAGCTCCAC
617	TTCGTAGTCTCACCGGCAATGATCC	TGGATCATTGCCGGTGAGACTACGA
618	TTTATAGCAGTGCGCCAATGCTTCG	TCGAAGCATTGGCGCACTGCTATAA
619	TCGAACAGTGCTGTCCGTCGCTCAA	TTTGAGCGACGGACAGCACTGTTCG
620	TTCCGCGTGGACTGTTAGACGCTAT	TATAGCGTCTAACAGTCCACGCGGA
621	TCATTAGCCCGCTGTCGGTAACTGT	TACAGTTACCGACAGCGGGCTAATG
622	TGGAAAGAAACTCAGACGCGCAATG	TCATTGCGCGTCTGAGTTTCTTTCC
623	TCGACTCGCTGGACAGGAGAATCGT	TACGATTCTCCTGTCCAGCGAGTCG
624	TCATGATCCTCTGTTTCACCCGCGG	TCCGCGGGTGAAACAGAGGATCATG
625	TGGCGTAGCGCTCTAAAAGCTTCGG	TCCGAAGCTTTTAGAGCGCTACGCC
626	TAGTGATGCCATCAGGCCCGTATAC	TGTATACGGGCCTGATGGCATCACT
627	TTATGGAAAGGGCAACAGCGCTATC	TGATAGCGCTGTTGCCCTTTCCATA
628	TCTGTGGTTGATGGAGGATCCACAC	TGTGTGGATCCTCCATCAACCACAG
629	TACTCGCTGGAATTTGCGCTGACAC	TGTGTCAGCGCAAATTCCAGCGAGT
630	TCAGGCCCGAACCACGCGGTTACAG	TCTGTAACCGCGTGGTTCGGGCCTG
631	TGGCGCAATGGGCGCATAAATACTA	TTAGTATTTATGCGCCCATTGCGCC
632	TGGTCAATTCGCGCTACATGCCCTA	TTAGGGCATGTAGCGCGAATTGACC
633	TGATGGTGGACTGGAGCCCTTCCGC	TGCGGAAGGGCTCCAGTCCACCATC
634	TCCGCGCATAGCGCAATAGGGGAGA	TTCTCCCCTATTGCGCTATGCGCGG
635	TTCTTCTGGCTGTCCGGCACCCGAA	TTTCGGGTGCCGGACAGCCAGAAGA
636	TGCGTTCGCAATTCACGGGCCCTTA	TTAAGGGCCCGTGAATTGCGAACGC
637	TTCGTTTCGGCCTTGGAGAGTATCG	TCGATACTCTCCAAGGCCGAAACGA
638	TAGGTGCAAGTGCAAGGCGAGAGGC	TGCCTCTCGCCTTGCACTTGCACCT

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TABLE 4-continued

Seq. II	No.Decoder Sequence (5	'-3') + 5'	T Probe	Sequence	(5'-3') +	5' Т
639	TCGCCAGTTTCGATGGCTG	ACGTTT	TAAACG	TCAGCCATC	GAAACTGGC	3
640	TGCTTTACCGCCGATCCC#	GATATC	TGATAT	'CTGGGATCG	GCGGTAAAG	3
641	TGTGCTTGACGAAGAGGCG	JAAATGT	TACATI	TCGCCTCTT	CGTCAAGCA	2
642	2 TCAGTCCGTGCGCTTCATG	TCCTCA	TTGAGG	ACATGAAGO	GCACGGACT	3
643	3 TTACGCGTAAGAGCCTACC	CTCGCG	TCGCGA	GGGTAGGCT	CTTACGCGT.	A
644	TGGCGAGTCTTGTGGGGAC	ATGTGT	TACACA	TGTCCCCAC	AAGACTCGC	С
645	TCCAAAGCGAAGCGAGCGT	GTCTAT	TATAGA	CACGCTCGC	TTCGCTTTG	3
646	TGCCGTAGGTTGCTCTTC	CCGAAC	TGTTCG	GTGAAGAGC	AACCTACGG	2
647	TAAATCCGCGATGTGCCGT	GAGGCT	TAGCCT	'CACGGCACA	TCGCGGATT'	Г
648	TGGCTTCGCACCCGTACCA	ATTTAG	TCTAAA	TTGGTACGG	GTGCGAAGC	2
649	TTGTAGAGTCCCACGTAGC	CGGCAT	TATGCC	GGCTACGTG	GGACTCTAC.	A
650	TCACTAGTCTGGGGCAAGG	TGCATT	TAATGO	ACCTTGCCC	CAGACTAGT	3
651	TTGTACTCGGCAGGCGCAA	TAGATT	TAATCI	'ATTGCGCCT	GCCGAGTAC.	A
652	? TAACGGGTATCGGAAGCGT	AAAAGC	TGCTTT	TACGCTTCC	GATACCCGT	Г
653	TCGGACTGCCCGTTTGCA	GTTGAG	TCTCAA	CTTGCAAAC	GGGCAGTCC	3
654	TATCGTTCAGCACTGGAGC	CCGTAA	TTTACG	GGCTCCAGI	'GCTGAACGA'	Г
655	TATGCATCGAACTAGTCGT	'GACGGC	TGCCGT	'CACGACTAG	TTCGATGCA	Г
656	TTTCCAGGCATTAAGGAGA	GGGAGC	TGCTCC	CTCTCCTTA	ATGCCTGGA.	A
657	TGTGCGACATCTACTCCAC	GATCCC	TGGGAT	CGTGGAGTA	GATGTCGCA	2
658	TCTCATCGTCCTAACACGA	GAGCCC	TGGGCT	CTCGTGTTA	GGACGATGA	3
659	TAATGGCACTTCGGCGGTG	ATGCAA	TTTGCA	TCACCGCCG	AAGTGCCAT	Г
660	TCCGTGGGAGGGAATCCAA	CCGAGG	TCCTCG	GTTGGATTC	CCTCCCACG	3
661	TAAATTCTCGTTGGTGACG	GCTCAT	TATGAG	CCGTCACCA	ACGAGAATT'	Г
662	2 TTTGCTCTTATCCTTGTCC	TGGGCG	TCGCCC	AGGACAAGG	ATAAGAGCA.	A
663	TTTAAGGATCAGGCGGAGC	TTGCAG	TCTGCA	AGCTCCGCC	TGATCCTTA	A
664	TCGCGACTAAGGTGCTGCA	ACTCGA	TTCGAG	TTGCAGCAC	CTTAGTCGC	3
665	TGCTCGATTTCACGGCCCG	TTGTTC	TGAACA	ACGGGCCGT	GAAATCGAG	2
666	TAGCAGAGTGCGTTGCAGA	GGCTAA	TTTAGC	CTCTGCAAC	GCACTCTGC	Г
667	TTGGAGGTGAGGACGACGT	GCACTA	TTAGTG	CACGTCGTC	CTCACCTCC.	A
668	TAACCGTTTAGGGTACATT	CGCGGT	TACCGC	GAATGTACC	CTAAACGGT	Г
669	TTATGATCGCTCGGCTCAC	AGTTTG	TCAAAC	TGTGAGCCG	AGCGATCAT.	A
670	TGACTTTTTGCGGAAACGT	CATGGT	TACCAT	GACGTTTCC	GCAAAAAGT	3
671	TTGTCGGTTATTCCACCTG	CAAGGA	TTCCTT	'GCAGGTGGA	ATAACCGAC.	A
672	? TCTATGGTTTGCACTGCGC	CGTCGA	TTCGAC	GGCGCAGTG	CAAACCATA	3
673	TAGCAGGGAAATTCAATCG	TTCGCA	TTGCGA	ACGATTGAA	TTTCCCTGC	Г
674	TCCTAACCGAGCGCTTAGC	ATTTCC	TGGAAA	TGCTAAGCG	CTCGGTTAG	3
675	TCCCGACCCTAACTCGCAT	'TGAATA	TTATTC	AATGCGAGT	TAGGGTCGG	3

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TABLE 4-continued

Seq. ID	No.Decoder Sequence (5'-3') + 5	' T Probe Sequence (5'-3') + 5' T
676	TTTGCTTAATGGTGACGCCACGGAT	TATCCGTGGCGTCACCATTAAGCAA
677	TGATGCTCGCCGTGTTTAGTTCACG	TCGTGAACTAAACACGGCGAGCATC
678	TTCGGATGACGAGTTTCCATGACGG	TCCGTCATGGAAACTCGTCATCCGA
679	TATGCGGTCTACTTTCTCGATCGGG	TCCCGATCGAGAAAGTAGACCGCAT
680	TTTGCGAGGCTAAGCACACGGTAAA	TTTTACCGTGTGCTTAGCCTCGCAA
681	TAACTTAATTACCGCCTCTGGCGCC	TGGCGCCAGAGGCGGTAATTAAGTT
682	TGTGACCGCGAACTTGTTCCGACAG	TCTGTCGGAACAAGTTCGCGGTCAC
683	TTGCGGATTACCGATTCGCTCTTAA	TTTAAGAGCGAATCGGTAATCCGCA
684	TTGATAGGGGGCCACGTTGATCAGA	TTCTGATCAACGTGGCCCCCTATCA
685	TTCGCTCCGTAGCGATTCATCGTAG	TCTACGATGAATCGCTACGGAGCGA
686	TTGTCAGCTGGTAGCCTCCGTTTGA	TTCAAACGGAGGCTACCAGCTGACA
687	TAGCGTCGCATGACGCTTACGGCAC	TGTGCCGTAAGCGTCATGCGACGCT
14	TAGACGCACCGCAACAGGCTGTCAA	TTTGACAGCCTGTTGCGGTGCGTCT
15	TCGTGTAGGGGTCCCGTGCTGTCAA	TTTGACAGCACGGGACCCCTACACG
690	TGTCGCATTCTGCACTGGCTTCGCC	TGGCGAAGCCAGTGCAGAATGCGAC
691	TTGATTAGGTGCGGTCCCGTAGTCC	TGGACTACGGGACCGCACCTAATCA
692	TAAGGGACCTTGGGTGACGGCGAGA	TTCTCGCCGTCACCCAAGGTCCCTT
693	TTCAAATGGCCACCGCGTGTCATTC	TGAATGACACGCGGTGGCCATTTGA
694	TCTCCGACGACCAATAAATAGCCGC	TGCGGCTATTTATTGGTCGTCGGAG
695	TGGCTATTCCCGTAGAGAGCGTCCA	TTGGACGCTCTCTACGGGAATAGCC
696	TTGGATAACCTCTCGGTCCATCCAC	TGTGGATGGACCGAGAGGTTATCCA
697	TGACCGCTGTACGGGAGTGTGCCTT	TAAGGCACACTCCCGTACAGCGGTG
698	TGCCACAGAGTTTTAGCAGGGACCC	TGGGTCCCTGCTAAAACTCTGTGGC
699	TCCCACGCTTTCCGACCACTGACCT	TAGGTCAGTGGTCGGAAAGCGTGGG
700	TCATTGACACAATGCGGGGACTGAT	TATCAGTCCCCGCATTGTGTCAATG
701	TAGCCACTCGACAGGGTTCCAAAGC	TGCTTTGGAACCCTGTCGAGTGGCT
702	TCAGGATGAGCAAAGCGACTCTCCA	TTGGAGAGTCGCTTTGCTCATCCTG
703	TCAAGGTATGGTCTGGGGCCTAAGG	TGCTTAGGCCCCAGACCATACCTTG
704	TGGTGTTCGGCCTAAACTCTTTCGG	TCCGAAAGAGTTTAGGCCGAACACC
705	TTTTAGTCGGACCCTGTGGCAATTC	TGAATTGCCACAGGGTCCGACTAAA
706	TCACACGTTTCCGACCAGCCTGAAC	TGTTCAGGCTGGTCGGAAACGTGTG
707	TCTGGACGAACTGGCTTCCTCGTAC	TGTACGAGGAAGCCAGTTCGTCCAG
708	TTTCACAATCCGCCGAAAACTGACC	TGGTCAGTTTTCGGCGGATTGTGAA
709	TAACAGGATATCCGCGATCACGACA	TTGTCGTGATCGCGGATATCCTGTT
710	TTACGTCGGATCCATTGCGCCGAGT	TACTCGGCGCAATGGATCCGACGTA
711	TCATGGATCTCTCGGTTTGATCGCC	TGGCGATCAAACCGAGAGATCCATG
712	TAGCCAGGCGCGTATATACGCTCGG	TCCGAGCGTATATACGCGCCTGGCT

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Seq. 1	ID No.De	coder	Sequence	(5'-3')	+ 5' T	Probe	Sequence	(5'-3')	+ 5' T
71	13 TA	TTTGGC	ACGTGTCG	rgccatgt	т	TAACAT	rggcacgac <i>i</i>	ACGTGCCA	AAT
71	L4 TC	CGCGTT	GCACCACT	TTGAGGTG	С	TGCAC	CTCAAAGTGG	TGCAACG	CGG
71	.5 TI	TGGACG	TGACAAGC	ATGGCGCT	С	TGAGCO	GCCATGCTTG	TCACGTC	CAA
71	16 TC	TGAATC	GCGCAAGT	AAATGGGG	G	TCCCC	CATTTACTT	CGCGATT	CAG
71	L7 TG	SATAAGG	TCCACCAG	ATTGCGCG	С	TGCGCC	GCAATCTGGT	GGACCTT	ATC
71	18 TC	TAACAA	TTGCCAAC	CGGGACGG	С	TGCCGT	CCCGGTTGG	CAATTGT	IAG
7 1	19 TG	GTAACC	TGGGTGCT	IGCAGGTT.	A	TTAACO	CTGCAAGCAC	CCAGGTT	ACC
72	20 TA	TCGGAG	CCACCATT	CGCATTGG	G	TCCCA	ATGCGAATGG	TGGCTCC	GAT
72	21 TG	TGAACT	GGCTTGCC	CCAGGATT	A	TTAATO	CCTGGGGCA	AGCCAGTT	CAC
72	22 TA	AGGCGAT	'AGCATGGT	CCCATATG	A	TTCATA	ATGGGACCAT	GCTATCG	CCT
72	23 TA	ACGGTA	TCGTGGCT	AATGCACG.	A	TTCGT	GCATTAGCCA	ACGATACC	GTT
72	24 TA	GTAGTG	GTCCTCCA	GATCGGCA	A	TTTGCC	CGATCTGGAG	GACCACT	ACT
72	25 TC	CGTTGA	ATTGGACG	GGAGGTTA	G	TCTAAC	CCTCCCGTCC	CAATTCAA	CGG
72	26 TG	CATAAG	TGCGGCAT	CGCGAAGG	G	TCCCTT	CGCGATGCC	GCACTTA	IGC
72	27 TC	GACAAG	ATGCAGCT	GCTACATG	С	TGCATO	GTAGCAGCTG	CATCTTG	ICG
72	?8 TT	CGCAGT	'GATTCCCG	ACCGATAA	G	TCTTAT	rcggtcggg <i>i</i>	ATCACTG	CGA
72	29 TC	AAGGCG	AGTCCACT	CGAGGGGA	С	TGTCC	CCTCGAGTGG	ACTCGCC	ITG
73	30 TG	CAACTT	'GCACGGCA'	FAAGTGGG	С	TGGCC	ACTTATGCCG	TGCAAGT'	IGC
73	31 TT	CCGAGC	TTGACGTT	CGCGACGT	С	TGACG	rcgcgaacgi	CAAGCTC	<b>GGA</b>
73	32 TA	AGCGCTG	GGCTGTGC	IGCCATCT	С	TGAGAT	rggcagcac <i>i</i>	AGCCCAGC	GCT
73	33 TT	TCATGT	CGCTGAGT	AACCCTCG	С	TGCGAG	GGTTACTC	AGCGACAT	GAA
73	34 TC	GAACCG	CTAATGCC	CATTGTCA	G	TCTGAG	CAATGGGCAT	TAGCGGT	ICG
73	35 TC	ACGGAA	GGTGGGAC	AAATCGCC	G	TCGGC	SATTTGTCCC	CACCTTCC	<b>GTG</b>
73	36 TC	CACAGAT	'GGAGACAA	ACGCGCCT	T	TAAGG	CGCGTTTGTC	TCCATCT	<b>GT</b> G
73	37 TT	TTTCGC	AACTCGCT	CCATAACC	С	TGGGT	FATGGAGCGA	GTTGCGA	AAA
73	38 TA	CGTTAC	GTTTCCGG	CGCCTCTA	A	TTTAG	AGGCGCCGG	AACGTAA	CGT
73	39 TT	ATCGGA	TTGCGTGG	GTTTCAAT	С	TGATTO	GAAACCCACG	CAATCCG	ATA
74	10 TC	TTCCAC	AATTGTCT	GCGACGCA	С	TGTGCC	STCGCAGACA	ATTGTGG	AAG
74	ll TT	GCACAA	AGGTATGG	CTGTCCGG	С	TGCCGC	GACAGCCATA	ACCTTTGT	3CA
74	12 TT	CCGATG	CCAGTCCC	ATCTTAAG.	A	TTCTT	AAGATGGGAC	TGGCATC	<b>3GA</b>
74	13 TC	TGAAAC	CGTGCGAA	rcgaggtg.	A	TTCACO	CTCGATTCGC	CACGGTTT	CAG
74	14 TO	GGTGTT	CCGCGTGT	CGAAAAAA	T	TATTT	TTTCGACACC	CGGAACA	CCG
74	15 TT	CTAGCA	GGCCTTTT(	GAATCGCC.	A	TTGGCC	GATTCAAAAG	GCCTGCT	AGA
74	16 TG	SAGTCAC	CTCTGAGA	CGGACGCC.	A	TTGGC	STCCGTCTC <i>I</i>	AGAGGTGA	CTC
74	ניד 7	CTTCTG	TCATCCTG	CAGCAGCA	T	TATGCT	rgctgcagg <i>i</i>	ATGACAGA	AGA
74	18 TG	CGGATG	AAACCTGA	AAGGGGCC	T	TAGGC	CCCTTTCAGG	TTTCATC	CGC
74	19 TG	GGGCCC	CAAACTGG	FATCAAGC	С	TGGCTT	rgataccag1	TTGGGGC	ccc

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TABLE 4-continued

TOTAL	Sea. ID	No. Decoder Sequence (5'-3') + 5'	
TAGGEGGCCCAACTGTGAGGTCTTG TCAAGACCTCACAGTTGGCCGCCTC TACACCATGTGCTCCCGCGCTGCAGT TACTGCAGCGCGGGAGCACATGGTGT TACACCATGTGCTCCCGCGCTGCAGT TACTGCAGCGCGGGAGCACATGGTGT TACACCATGTGCTCCCGCTCCAGT TACACCATGTCATGT		No. Becoder bequence (5 -5 ) 1 5	Tillobe bequence (5 = 5 )   5 I
TACACCATGTGCTCCGGGTGCAGT TACGATGGGGGGGAGCACATGGTGT TACGATGAACATGAATCGGAGTCG TCGACTCCCGATTCATGTTCATCGT TCGACTCCCGATTCATGTTCATCGT TCGACTCCCGATTCATGTTCATCGT TTTGACACCACTGTAGCAGCGCTCCG TCGGAGGGCTGCTACAGGGATGCAC TCGCAGTGCGAATTCAGTTCAAAAG TCTTTTAAACTGAAATACGGCAC TGCAGTTTAAGCGACTCCATTACCG TTAGGTGACCTTAAGCCTTGACGG TCGCAACACACCCACTA TTAGGTACCTTAAGCGTTCAAAAG TCGCACTAAGCACACGCACCCACACACCACAC	750	TGCATTGGCTTCGGATTCTCCTACA	TTGTAGGAGAATCCGAAGCCAATGC
Tagartagartagartagartagartagartagartagar	751	TAGGCGGCCCAACTGTGAGGTCTTG	TCAAGACCTCACAGTTGGGCCGCCT
TETGCATCCCTGTAGCAGCGCTCCG TEGGAGCGCTGTACAGGGATGCAG TSS TGTGCCGTATTTCGACCTGTGGTT TAACGCACAGGTGAAATACGGCAC TGCAGTTCTAAAAG TCTTTTGACTGAAGTGCCACTGC TGCAGTTCAAAAG TCTTTTGACTGAAGTGCCTTAACGC TGCAGTGCCACTTCAGTCAAAAG TCTCTAAGCCACAGGTCAAGTCCCTA TGCAGTTTAAGCGATGCCTTGACG TCGCCAAGCAAGCATAGCCTAAGCCT TTAAGTGACCTAGCCTGTGCGG TCGCCAAGCAAGCAAGCCTAGGTCACCTA TGCACTAGCCTACCTAGCT TCCCCTTACGGCTCGTCTATGC TGCACAGCACA	752	TACACCATGTGCTCCGCGCTGCAGT	TACTGCAGCGCGGAGCACATGGTGT
TAACGCACAGGTCGAATTCGACCTGTGCGTT TAACGCACAGGTCGAATTACGGCAC TGCAGTGCGCACTTCAGTTCAAAAG TCTTTTGAACTGAAGTGCCCCTGC TGCGATTTTAAGCGATGCCTTGACG TCGCAAGCAAGCACGCCTAGGTCACTA TTAGGTGACCTAGGCTTGCTTGCGG TCGCCAAGCAAGCAAGCCAAGGTATCCAG TCGCAAGCAAGCAAGCCAAGGATACCAG TCCCCTTACGCTCGTCTCTATGC TGCGCAAGCAAGCAAGCAAGGATACCAG TCCCCTTACGCCTGCTCTATGC TGCAAGCAAGCAAGCAAGGGAAAGCC TCCCCTTACGGCTCGATGCATTAA TTAATGCATCGCATGCGAAGCAA TGCGCTGAGGGAGCGCTTAAGGA TGCGCTGAGGGAGCGCTAAGGGG TTTCTTGGAACGCCTGGGGTTCA TTCAAACCCATTCCAGCAACCAACCAACACAAAA TTCATCCTTACCGCTCACCTCAC	753	TACGATGAACATGAATCGGGAGTCG	TCGACTCCCGATTCATGTTCATCGT
TGCAGTGCGCACTTCAGTTCAAAAG TCTTTTGAACTGAAGTGCGCACTGC TGCGATTTTAAGCGATGCCTTGACG TCGCAAGCAAGCAAGCCTAGGCTCCTTAAATCGC TTAGGTGACCTAGGCTTGCTGTGCGG TCGCCAAGCAAGCAAGCCTAGGTCACCTA TTAGGTGACCTAGCCTGTGCGGGCG TGCGCCGCACAGGCAAGCAAGCCTAAGGGG TCCCCTTACGGCTCGTCTCTTATGC TGCATAGCGACGAGGCAAGCGAAGCG	754	TCTGCATCCCTGTAGCAGCGCTCCG	TCGGAGCGCTGCTACAGGGATGCAG
TGGCATTTTAAGCGATGCCTTGACG TGGCAAGCAAGCCTAAAAATCGC TTAGTGACCTAGGCTTGCTTGCGG TCCGCAAGCAAGCCTAGGCTACCTA TTTGGATACCTTGCCTGTGCGGCGC TGCGCCGCACAGGCAAGGCA	755	TGTGCCGTATTTCGACCTGTGCGTT	TAACGCACAGGTCGAAATACGGCAC
TTAGGTGACCTAGGCTTGCTTGCGG TCCGCAAGCAAGCCTAGGTCACTA TTAGACCACAGCCTAGGTCACTA TCTGGATACCTTGCCTGTGCGCCC TGCGCCGCACAGGCAGGCAGGCAGGCAGGC TCCCCTTACGGCTCGTCTATGC TGCATAGACGAGCCAGGCAGGCATAAGGG TGCCTTACGGCTCATTAC TTAATGCATCGCATC	756	TGCAGTGCGCACTTCAGTTCAAAAG	TCTTTTGAACTGAAGTGCGCACTGC
TCTGGATACCTTGCCTGTGCGGCCC TGCGCCGACAGGCAAGGTATCCAG TCCCCTTACGCTCGTCGTCTATGC TGCATAGACGACGAGCCGTAAGGGG TGCATAGACGACGAGCCGTAAGGGG TGCATAGACGACGAGCCGTAAGGGG TGCATAGACGACGAGCCGTAAGGGG TGCATAGACGACCAGGCCGTAAGGGG TTTTCTGTAAGCGCCTGGGGTTCA TTGAACCCCAGGCCGCTTACAGAAA TGGCTGAGGTGAGCGGTAAGGATGA TTCATCCTTACCGCTCACCTCAGCC TTTCTTGCCCCGATCTAATTTG TCAAATTAGATCGGGGAGGCCAAGAA TTCCTACGTACACGGGGTTACCTCC TGAGGGTAACGCCGTGTACGTAAGGA TTCCTACGTACACGGGGTTACCTCC TGAAACCCATTCCAGCAGACGCCTG TCAAACCCATTCCAGCAGACGCCTG TCAAACCCATTCCAGCAGACGCCTG TCAACGCCGGAATTGCTATATT TTTGAGGAGGAATTTGCCATGGGGCG TCAACGCCGCAAAATGGATTAC TCAAACCCATTCCAGCAGCCTC TGAGGCTGACCAAAATTCCTCCTA TTTTCAAGGAGGATTTGCCACGGCGTTG TCAACGCCGGGCACACACTCTCCTAT TCTGCAAGTGCTTAGCTCGTCAGCCTC TGAGGCTGACGAGCCAAACCCTAT TCTGGCTGTGTCGCCCAACCCAG TTCTTAACGTCGTCTCGCCCAACCCAG TTCTTAACGTCGTCTCCCCCAGC TGCTCGGGGACAACGTTTATGAAAA TTTTTCATAAACGTTGTCCCCGAGC TGCTCGGGGACAACGTTTATGAAAA TTAGCAAGGAGGAGCACACCCCCTC TGAGGCGAGGACAACGTTTATGAAAA TTAGCAAGAGCACATCCTCCCTCC TGAGCGAGGACAACGTTTATGAAAA TTAGCAAGCACATCATCATTATA TTAGCCCACGGAGCAAGGCATCACT TAACCGCTACTGAATCACA TTTGGATTCCCTGCACCAACCCAG TTCTCAAGCACCATCATTATA TTAACATTCCCTGCCTCCAGCT TTACATTCCCTGCCTCCAGCT TAACCCCACGAGGCATCAATCAA TTATAATGAGTCTCAACCAA TTATAATGCCAAGCCATCAATCAA TTATAATGCAAGCCATCAATCAA TTATAATGCCAAGCCATCAATCAA TTATAATGCCAAGCCATCAATCAA TTATAATGCCAAGCCATCAATCAA TTATAATGCCAAGCCATCAATCAA TTATAATGCCAAGCCATCAATCAA TTATACCCTTCAAGCCATCAATCAA TTATAACGCCACGAGCCTTCCAACCT TCACCGCCTTCAAAACCC TCACCCCACGAGCCTTCCAACCACACCAC	757	TGCGATTTTAAGCGATGCCTTGACG	TCGTCAAGGCATCGCTTAAAATCGC
Teccettacegetegetetatec Teccettacegetegetetatec Teccettacegetegetetatec Teccettacegetegetetatec Teccettacegetegetetatec Teccetacegetegetetatec Teccettacegetegetetatec Tecatacecacegetegetetatec Tecatacecacegetegetatec Tecatacecacecetacecetec Tecatacecacecetacecetec Tecatacecacecetacecetec Tecatacecacecacecetacecetec Tecatacecacecacecacetacecetec Tecatacecacecacecacetacecetec Tecatacecacecacacacecetecetec Tecatacecacecacacacacecetecacetecacetecacetecacetecacecac	758	TTAGGTGACCTAGGCTTGCTTGCGG	TCCGCAAGCAAGCCTAGGTCACCTA
THATGCATCGCATCCCGATGCATTA TTAATGCATCGCATCG	759	TCTGGATACCTTGCCTGTGCGGCGC	TGCGCCGCACAGGCAAGGTATCCAG
TTTTCTGTAAGCGCCTGGGGTTCA TTGAACCCCAGGCCGCTTACAGAAA TGGTGAGGTGA	760	TCCCCTTACGGCTCGTCGTCTATGC	TGCATAGACGACGAGCCGTAAGGGG
TGCTGAGGTGAGGTGAGGATGA TTCATCCTTACCGCTCACCTCAGCC TG4 TTCTTGGCCTCCCCGATCTAATTTG TCAAATTAGATCGGGGAGGCCAGA TG5 TGGAGGTAACGCCGTGTACGTAGGA TTCCTACGTACACGGCGTTACCTCC TG6 TGTAATCCATTTGTGGCTGCGTCAA TTTGACGCCACCACAAATGGATTAC TCAAACCCATTCCAGCAGACGCCTG TCAGGCGTCTGCTGGAATGGGTTG TCAAACCCATTCCAGCAGACGCCTG TCAGGCGTCTGCTGGAATGGGTTG TTAGGAGGAATTTGGCATGCGGGCG TCGCCCGCATGCCAAAATTCCTCCTA TG79 TATAGGTAGGATGTCCCGGCGTTG TCAACGCCGGGCACACCCTACCTAT TTTO TGCAAGTGCTTAGCCTCC TGAGGCTGACGAGCCACACCTCACCT	761	TGCGCTTGCCCGATGCGATGCATTA	TTAATGCATCGCATCGGGCAAGCGC
TCAAATTAGATCGGGAGGCCAAGA TTCTTGGCCTCCCCGATCTAATTTG TCAAACTAGATCGGGGAGGCCAAGA TTCTACGTACACGGCGTTACCTCC TGGAGGTAACGCCGTGTACGTAGGA TTTGACGCAGCCACAAATGGATTAC TCAAACCCATTCCAGCAGACGCCTG TCAGGCGTCTGCTAGAATGGGTTTG TCAAACCCATTCCAGCAGACGCCTG TCAGGCGTCTGCTAGAATTCCTCCTA TTTGAGGAGGAATTTGGCATGCGGCGG TCGCCCGCATGCCAAATTCCTCCTA TATAGGTAGGATGTGCCCGGCGTTG TCAACGCCGGCACACCCTACCTAT TCTGCAAGTGCTTAGCCTCGTCAGCCTC TGAAGGCTGACACACCCTACCTAT TCTGCAGTGTTAGCTCGTCAGCCTC TGAGGCTGACAGACCACCACACCA	762	TTTTCTGTAAGCGGCCTGGGGTTCA	TTGAACCCCAGGCCGCTTACAGAAA
TGGAGGTAACGCCGTGTACGTAGA TTCCTACGTACACGGCGTTACCTCC TGAACCCATTCCAGCAGCGCTCAA TTTGACGCAGCCACAAATGGATTAC TCAAACCCATTCCAGCAGACGCCTG TCAGGCGTCTGCTGGAATGGGTTG TCAGACCCATTCCAGCAGACGCCTG TCAGGCGTCTGCTGGAATGGGTTG TCAAACCCATTCCAGCAGACGCCTG TCAGGCGTCTGCTGGAATGGGTTG TTAGGAGGAATTTGGCATGCGGGCG TCGCCCGCATGCCAAATTCCTCCTA TGGAAGTGCTTAGCTCGCGCGTTG TCAACGCCGGGCACATCCTACCTAT TTT TCTGGCTGTGTCGCCACCTC TGAGGCTGACGAGCCACACCTCACCT	763	TGGCTGAGGTGAGCGGTAAGGATGA	TTCATCCTTACCGCTCACCTCAGCC
TTTGACGCAGCCACAAATGGATTAC TCAAACCCATTCCAGCAGACGCCTG TCAGGCGTCTGCTGGAATGGGTTTG TCAGACCCATTCCAGCAGACGCCTG TCAGGCGTCTGCTGGAATGGGTTTG TTAGGAGGAATTTGGCATGCGGGCG TCGCCCGCATGCCAAATTCCTCCTA TTTGACGCGGCGTTG TCAACGCCGGGCACACTCCTACCTAT TTTGCAAGTGCTTAGCTCGTCAGCCTC TGAGGCTGACGAGCCACACTCTACCTAT TCTGGCTGTGTCGCATCTCGTTAAC TGTTAACGAGATGCGACACACCAGCCAG TTTTTTCATAAACGTTGTCCCCGAGC TGCTCGGGGACAACGCTTAG TTTTTCATAAACGTTGTCCCCGAGC TGGAGCGGAGACAACGTTTATGAAAA TTAGCAGGAGGAGACCTCCGCTCC TGGAGCGGAGACACCTCCGCTC TTTCAAGCACCATCGTGCAATCCAA TTTGGATTGCACGATGGTGCTTGAA TAGCCGTCGCCAGTGATCCAAA TTTGGATTGCACGATGGTGCTTGAA TCACCTAGCGATCACTGTGCAATCCAA TTTGAATTCCCTGCCTCCGTGGGCTT TAACCCCACGGAGGCAGGGAATGTA TTACATTCCCTGCCTCCGTGGGCTT TAACCCCACGGAGCAGGGAATGTA TTTCGAGCAGCGTTCGACACCTCATTATA TTATAATGAGTGTCGACGCGAACCGGAACCGCGAACCGCAAAACCGTTTCAAACACCGAAAGCC TTCTGAGCAGCCAGCGCTCCAGCT TTACAATTCCCTGCCTCCGAAAGCC TGGCTTTCAGGGCCTTGCCAAAACCC TGGCTTTCAGGGCCTTGCCAAAACCC TGGCTTTCAGGGCCTTGCCAAAACCC TTTTGAATTGCCAAGCCCTGAAAAGCC TGGCTTTCAGGGCCTTGCCAAAACCC TTTTGAATTGCCAAGCCCTGAAAACCC TTTTTGAATTGCCAAGCCCTGAAAACCC TTTTTAGCACGCGTTGCCAAAAACCC TTTTTTAGCACGCGTTGCCAAAAACCC TTTTTTAGCACGCGTTGCCAAAAACCC TTTTTTAGCACGCGTTGCCAAAAACCC TTTTTTTTTT	764	TTCTTGGCCTCCCCGATCTAATTTG	TCAAATTAGATCGGGGAGGCCAAGA
TCAAACCCATTCCAGCAGACGCCTG TCAGGCGTCTGCTGGAATGGGTTTG TTAGGAGGAATTTGGCATGCGGGCG TCGCCCGCATGCCAAATTCCTCCTA TTAGGAGGAATTTGGCATGCGGGCG TCAACGCCGGGCACACCCTACCTAT TCAACGCCGGGCACACCCTACCTAT TCTGGCTGTTAGCTCGTCAGCCTC TGAGGCTGACGAGCCTAAGCACTTGC TCTAACGTCGTCTCGCCATCCTTAAC TCTAACGTCGTCTCGCGCAATCACT TAGTGATTGCCGGAGACGACGACGTTAG TTTTTCATAAACGTTGTCCCCGAGC TGCTCGGGGACAACGTTTATGAAAA TAGCAGGAGGACGACCTCCGCTCC TGGAGCGGAGACACGTTTATGAAAA TTTTCAAGCACCATCGTGCAATCCAA TTTGGATTGCACGATGGTCCTCGCT TTACATTCCCTGCCTCCGTGGGCTT TAAGCCCACGGAGGCAGGAATGAT TTACATTCCCTGCCTCCGTGGGCTT TAAGCCCACGGAGGCAGGGAATGTA TCGCTTCGCGTATTCAGTAGCGGTT TAACCCCACGGAGGCAGGGAATGTA TTTCGGACGCGTCGACACTCATTATA TTATAATGAGTGTCGACGCGTCCGA TTCTGAGCAGCCAGCGCTCCAGCT TAGCTTGGACGCGTGGCCTCCAGC TTGCTTCAGGGCTTGGCAATCCAA TTTTTAAATGAGTGTCGACGCTCCAGA TTTTTGAATTGCCAAGCCCTGAAAGCC TGGCTTTCAGGGCTTGGCAATCCAA TTTTTAAATGAGTGTCGACGCTTCAGA TTTTTTTCAAGGCCACGCGTTCCAGA TTTTTTTTTT	765	TGGAGGTAACGCCGTGTACGTAGGA	TTCCTACGTACACGGCGTTACCTCC
TAGGAGGAATTTGGCATGCGGGCG TCGCCCGCATGCCAAATTCCTCCTA TAGGTAGGATGTGCCCGGCGTTG TCAACGCCGGGCACATCCTACCTAT TTO TGCAAGTGCTTAGCTCGTCAGCCTC TGAGGCTGACGAGCTAAGCACTTGC TCTGGCTGTGCGCATCTCGTTAAC TGTTAACGAGATGCGACACAGCCAG TTO TCTGGCTGTCTCGCGCAATCACT TAGTGATTGCGCGAGACGACGCTTAG TTTTTCATAAACGTTGTCCCCGAGC TGCTCGGGGACAACGTTTATGAAAA TTAGCAGGAGGACGACCTCCGCTCC TGGAGCGGAGGTTCGTCCTCCTGCT TTTCAAGCACCATCGTGCAATCCAA TTTGGATTGCACGATGGTGCTTGAA TTAGCATCGCCAGTGATCGCTAGTGG TCCACTAGCGATCACTGGCGACCT TTACATTCCCTGCCTCCGTGGGCTT TAACCCCCACGGAGGCAGGGAATGTA TTACATTCCCTGCCTCCGTGGGCTT TAACCCCCACGGAGGCAGGGAATGTA TTACATTCCCTGCCTCCGTGGGCTT TAACCGCTACTGAATACGCGAAGCG TTTCGGACGCGTCGACACTCATTATA TTATAATGAGTGTCGACGCGTCCGA TAGCTTGAGCAGCCTTGAAAGCC TGGCTTTCAGGGCCTTGCAAATCCAA TTTTGAATTGCCAAGCCCTGAAAGCC TGGCTTTCAGGGCTTGGCAATCCAA TTTTTAAATGAGTGTTCGCAAGCCTTAGAA TTTTTAAATTGCCTTGCAATCCAA TTTTTAAATTGCCAAGCCCTGAAAACC TGGCTTTCAGGGCTTTGCAAATCCAA TTTTTAAATTGCCAAGCCCTTGAAAACC TTGCTTTCAGGGCTTTCAAGGCCAAAACCT TTACCCGACGCATCAATCAA TTTTTAACATTCCCTTGCTTGATGCGTTGGTTAAA TTTTTAGCACGCGTTGCCAATCAAACC TTTTTAGCACGCGTTGCCAATCAAACCC TTTTTAGCACGCGTTGCCAATCAAACCC TTTTTAGCACGCGTTGCCAAAACCT TTTTAGCACGCGTTGCCAATCAAAACCT TTTTAGCACGCGTTGGCCAATCAAAACCC TTTTTAGCACGCGTTGCCAATCAAAACCT TTTTAGCACGCGTTGGCCAATCAAAACCT TTTTAGCACGCGTTGGCCAATTCAAACCT TTTTAGCACGCGTTGGCCAATTCAAAACCT TTTTAGCACGCGTTGGCCTATGAAACCT TTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGCCTATGAAACCT TTTTTAGCACGCGTTGCCTATGAAACCT TTTTTAGCACGCGTTGCCTATTAGAACCT TTTTTAGCACGCGTTGCTATGAAACCT TTTTTAGCACGCGTTGCTTTTTTTTTT	766	TGTAATCCATTTGTGGCTGCGTCAA	TTTGACGCAGCCACAAATGGATTAC
TATAGGTAGGATGTGCCCGGCGTTG TCAACGCCGGGCACATCCTACCTAT TGCAAGTGCTTAGCTCGTCAGCCTC TGAGGCTGACGAGCTAAGCACTTGC TTTTTACCGAGCTGTCGCATCTCGTTAAC TGTTAACGAGATGCGACACAGCCAG TCTAACGTCGTCTCGCGCAATCACT TAGTGATTGCGCGAGACGACGACGATGG TTTTTTCATAAACGTTGTCCCCGAGC TGCTCGGGGGACACACGTTTATGAAAA TAGCAGGAGGACGACCTCCGCTCC TGGAGCGGAGGATCGTCCTCTGCT TTTCAAGCACCATCGTGCAATCCAA TTTGGATTGCACGATGGTGCTTGAA TAGCGTCGCCAGTGATCGCTAGTGG TCCACTAGCGATCACTGGCGACCT TAACCCCCACGGAGGCAGGCAATCTA TAGCTTCCCTGCCTCCGTGGGCTT TAACCCCCACGGAGGCAGGGAATGTA TTGGATTCCCTGCGTCGACACTCATTATA TTATAATGAGTGTCGACGCGTCCGA TTCTGAGCAGCCCTGAAGCC TGGCTTTCAGGGCTTGCAATCCAA TTTTGAATTGCCAAGCCCTGAAAGCC TGGCTTTCAGGGCTTGGCAATCCAA TTTTGAATTGCCAAGCCCTGAAAGCC TGGCTTTCAGGGCTTGGCAATCCAA TTTTTAGATTGCCAAGCCCTTGATGCGTGG TCACCGACGCATCAAGGCGAAAACT TTTTAGCACGCGTGGCCTATGAAAC TTTTTAGCACGCGTGGCCTATGAAAC TTTTTAGCACGCGTTGGCAATCCAA TTTTTAGCACGCGTTGGCAATCCAA TTTTTAGCACGCGTTGGCAATCCAA TTTTTAGCACGCGTTGGCAAAACCT TTTTTAGCACGCGTTGGCAAAACCT TTTTTAGCACGCGTTGGCAAAACCT TTTTTAGCACGCGTTGGCAAAACCT TTTTTAGCACGCGTTGGCAAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATTGAAACCT TTTTTAGCACGCGTTGGCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATTGAAACCT TTTTTAGCACGCGTTGGCCTATTGAAACCT TTTTTAGCACGCGTTGGCTATGAAACCT TTTTTAGCACGCGTTGGCTATTGAAACCT TTTTTAGCACGCGTTGCTATTGAAACCT TTTTTAGCACGCGTTGCTATTGAAACCT TTTTTAGCACGCGTTGCTATTGAAACCT TTTTTAGCACGCGTTGCTATTGAAACCT TTTTTAGCACGCGTTGCTATTGAAACCT TTTTTAGCACGCGTTGCTATGAAACCT TTTTTAGCACGCGTTGCTATTGAAACCT TTTTTAGCACGCGTTGCTATGAAACCT TTTTTAGCACGCGTTGCTATGAAACCT TTTTTAGCACGCGTTGCTATGAAACCT TTTTTAGCACGCGTTGCTATGAAACCT TTTTTAGCACGCGTTGCTATGAAACCT TTTTAGCACGCGTTGCTATGAAACCT TTTTTAGCACGCGTTGCTATGAACCT TTTTTAGCACGCTTTTTTTTTT	767	TCAAACCCATTCCAGCAGACGCCTG	TCAGGCGTCTGCTGGAATGGGTTTG
TGCAAGTGCTTAGCTCGTCAGCCTC TGAGGCTGACGAGCTAAGCACTTGC TCTGCTGTGTCGCATCTCGTTAAC TGTTAACGAGATGCGACACAGCCAG TCTAACGTCGTCTCGCGCAATCACT TAGTGATTGCGCGAGACGACGCTTAG TTTTTCATAAACGTTGTCCCCGAGC TGCTCGGGGACAACGTTTATGAAAA TAGCAGGAGGACGAACCTCCGCTCC TGGAGCGGAGGACACGTTTATGAAAA TTTCAAGCACCACTCGTGCAATCCAA TTTGGATTGCACGATGGTCCTTGAA TAGCATGCCCAGTGGATCGCTAGTGG TCCACTAGCGATCACTGGCGACGCT TAACCCCACGGAGGCAGGGAATGTA TACATTCCCTGCCTCCGTGGGCTT TAACCCCACGGAGGCAGGGAATGTA TTCGGACGCGTATTCAGTAGCGGTT TAACCGCTACTGAATACGCGAAGCG TTCTGGACGCGTCCGACACTCATTATA TTATAATGAGTGTCGACGCGTCCGAA TAGCTTGGACGCGTCCAGCT TAGCTTGGAGCAGCCTTGAAAGCC TGGCTTTCAGGGCTTGGCAATCCAA TAGCTTGAGCAGCCTTGAAAACC TGGCTTTCAGGGCTTGGCAATCCAA TAGTTTCATAGGCCACGCGTGCTAAA TCACCGACGCATCAAGGCGAAAACT TTTTAGCACGCGTTGGCCAAAACCT TTTTAGCACGCGTTGGCAAAACCT TTTTAGCACGCGTTGGCCTATGAAACCT TTTTAGCACGCGTTGGCCTATGAAACCT TTTTAGCACGCGTTGGCCTATGAAACCT TTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTTAGAAACCT TTTTTAGCACGCGTTGGCCTTAGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTTAGAAACCT TTTTTAGCACGCGTTGGCCTTAGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCAATCAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTTAGCACGCGTTGGCCTATGAAACCT TTTTAGCACGCGTTGCCTATGAAACCT TTTTAGCACGCGTTGCTATGAAACCT TTTTAGCACGCGTTGCTATGAAACCT TTTTAGCACGCTTAGAAACCT TTTTAGCACGCTTAGAAACCT TTTTAGCACGCTTAGAAACCT TTTTAGCACGCTTAGAACCT TTTTAGCACGCTTAGAAACCT TTTTAGCACGCTTAGAACCT TTTTAGCACGCTTAGAAACCT TTTTAGCACGCTAGAACCT	768	TTAGGAGGAATTTGGCATGCGGGCG	TCGCCCGCATGCCAAATTCCTCCTA
TCTGGCTGTGTCGCATCTCGTTAAC TGTTAACGAGATGCGACACAGCCAG TCTTAACGTCGTCTCGCGCAATCACT TAGTGATTGCGCGAGACGACGACGTTAG TTTTTCATAAACGTTGTCCCCGAGC TGCTCGGGGACAACGTTTATGAAAA TAGCAGGAGGACGACCTCCGCTCC TGGAGCGGAGGTTCGTCCTCTGCT TTTCAAGCACCATCGTGCAATCCAA TTTGGATTGCACGATGGTGCTTGAA TAGCGTCGCCAGTGATCGCTAGTGG TCCACTAGCGATCACTGGCGACGCT TTACATTCCCTGCCTCCGTGGGCTT TAACCGCCACGGAGGCAGGGAATGTA TCGCTTCGCGTATTCAGTAGCGGTT TAACCGCTACTGAATACGCGAAGCG TTCTGAGCAGCCACCACTCATTATA TTATAATGAGTGTCGACGCGTCCAGA TTCTGAGCAGGCCAGCCCTCCAGCT TAGCTTCGAGCAGCCTCCAGCT TAGCTGGAGCCCTGCAAAGCC TGGCTTTCAGGGCTTGGCAATCCAA TAGTTTTCATAGGCCAAGCCCTGAAAACCT TCACCGACGCATCAAGGCGAAAACT TCACCGACGCATCAAGGCGAAAACCT TTTTAGCACGCGTGGCCTATGAAACC TTTTTAGCACGCGTGGCCTATGAAACCT TTTTAGCACGCGTGGCCTATGAAACCT TTTTAGCACGCGTGGCCTATGAAACCT TTTTTAGCACGCGTGGCCTATGAAACCT TTTTAGCACGCGTGGCCTATGAAACCT TTTTAGCACGCGTGGCCTATGAAACCT TTTTAGCACGCGTGGCCTATGAAACCT TTTTAGCACGCGTGGCCTATGAAACCT TTTTTAGCACGCGTGGCCTATGAAACCT TTTTTAGCACGCGTGCCTATGAAACCT TTTTTAGCACGCGTGGCCTATGAAACCT TTTTTAGCACGCGTGGCCTATGAAACCT TTTTTAGCACGCGTGGCCTATGAAACCT TTTTTAGCACGCGTGCCTATGAAACCT TTTTTAGCACGCGTGCCTATGAAACCT TTTTTAGCACGCGTGCTATGAAACCT TTTTTAGCACGCGTGCTATGAAACCT TTTTTAGCACGCGTGCTATGAAACCT TTTTTAGCACGCGTGCTATGAAACCT TTTTTAGCACGCTAGCGCTAGCACTAGAACT TTTTTAGCACGCTAGAACCTAGACCTAGAACCTAGACCTAGACCTAGACCTAGAACCTAGACTAGACCTAGAACCTAGACCTAGAACCTAGACACACAC	769	TATAGGTAGGATGTGCCCGGCGTTG	TCAACGCCGGGCACATCCTACCTAT
TCTAACGTCGTCTCGCGCAATCACT TAGTGATTGCGCGAGACGACGTTAG TTTTTCATAAACGTTGTCCCCGAGC TGCTCGGGGACAACGTTTATGAAAA TAGCAGGAGGACGACCTCCGCTCC TGGAGCGGAGGTTCGTCCTCCTGCT TTTCAAGCACCATCGTGCAATCCAA TTTGGATTGCACGATGGTGCTTGAA TCCACTAGCGATCACTGGCGACCT TTACATTCCCTGCCTCCGTGGGCTT TAAGCCCCACGGAGGCAGGGAATGTA TGCTTCGCGTATTCAGTAGCGGTT TAACCCCACGGAGGCAGGGAATGTA TTTGGACGCGTCGACACTCATTATA TTATAATGAGTGTCGACGCGTCCAGA TTCTGAGCAGGCCAGCGCTCCAGCT TAGCTTGGAGCGCTTGCCAGA TTTTGAATTGCCAAGCCCTGAAAGCC TGGCTTTCAGGGCTTGGCAATTCAA TAGTTTTCATAGGCCACGCGTAAACCT TCACCGACGCATCAAAGCC TGGCTTTCAGGGCTTGGCAAACCT TTTTGAATTGCCAAGCCCTGAAAGCC TTCTTCAGGGCTTGGCAATCCAA TTTTTACATTGCCAAGCCCTTGATGCGTCGTG TCACCGACGCATCAAGGCCGAAAACCT TTTTTACATTGCCATGAAAACCT TTTTTACATTGCCATGAAAACCT TTTTTAGCACGCGTGGCCTATGAAACCT TTTTTAGCACGCGTGGCTATGAAACCT TTTTTAGCACGCGTGGCTATGAAACCT TTTTTAGCACGCGTGCTATGAAACCT TTTTTAGCACGCGTGCTATGAAACCT TTTTTTTTTT	770	TGCAAGTGCTTAGCTCGTCAGCCTC	TGAGGCTGACGAGCTAAGCACTTGC
TTTTCATAAACGTTGTCCCCGAGC TGCTCGGGGACAACGTTTATGAAAA TAGCAGGAGGACGAACCTCCGCTCC TGGAGCGGAGGTTCGTCCTCCTGCT TTTCAAGCACCATCGTGCAATCCAA TTTGGATTGCACGATGGTGCTTGAA TAGCGTCGCCAGTGATCGCTAGTGG TCCACTAGCGATCACTGGCGACGCT TAAGCCCCACGGAGGCAGGGAATGTA TACATTCCCTGCCTCCGTGGGCTT TAAGCCCACGGAGGCAGGGAATGTA TCGCTTCGCGTATTCAGTAGCGGTT TAACCGCTACTGAATACGCGAAGCG TTCTGAGCAGGCCAGCGCTCCAGCT TAGCTGGAGCGCTGGCACACTCATTATA TTATAATGAGTGTCGACGCGTCCAGA TTCTGAGCAGGCCAGCGCTCCAGCT TAGCTGGAGCGCTTGGCAATCCAA TAGCTTCAGGGCTTGGCAATCCAA TAGCTTCAGGGCTTGGCAATCCAA TTTTAAATGAGTGTCGACGCAAAACCT TGGCTTTCAGGGCTTGGCAAAACCT TTTTAACATTCCCAAGCCCTGAAAACCT TTTTAGCACGCGTGGCAAAACCT TTTTAGCACGCGTTGGCAAAACCT TTTTAGCACGCGTGGCCTATGAAAACCT	771	TCTGGCTGTGTCGCATCTCGTTAAC	TGTTAACGAGATGCGACACAGCCAG
TAGCAGGAGGACGAACCTCCGCTCC TGGAGCGGAGGTTCGTCCTCTGCT TTTCAAGCACCATCGTGCAATCCAA TTTGGATTGCACGATGGTGCTTGAA TTTGGATTGCACGATGGTGCTTGAA TTTGATTCCCTGCCTCGTGGGCTT TAACCCCACGGAGGCAGGGAATGTA TTTGGATTCGCGTATTCAGTAGCGGTT TAACCGCTACTGAATACGCGAAGCG TTTCGGACGCGTCGACACTCATTATA TTATAATGAGTGTCGACGCGTCCAGA TTCTGAGCAGGCCAGCGCTCCAGCT TAGCTTCGGGCTTGAAAGCC TGGCTTTCAGGGCTTGCACACTCAATACAA TAGCTTCAGGGCTTGCCAAAACCC TGGCTTTCAGGGCTTGGCAAAACCT TTTTGAATTGCCAAGCCCTGAAAACCC TGGCTTTCAGGGCTTGGCAAAACCT TCACCGACGCATCAAGGCGAAAACCT TTTTAGCACGCGTGGCCAAAACCT TTTTAGCACGCGTGGCCAAAACCT TTTTAGCACGCGTGGCCAAAACCT TTTTAGCACGCGTGGCCTATGAAAACCT TTTTAGCACGCGTGGCCTATGAAAACCT TTTTAGCACGCGTGGCCTATGAAAACCT TTTTAGCACGCGTGGCCTATGAAAACCT TTTTAGCACGCGTGGCCTATGAAAACCT TTTTAGCACGCGTGGCCTATGAAAACCT	772	TCTAACGTCGTCTCGCGCAATCACT	TAGTGATTGCGCGAGACGACGTTAG
TTTCAAGCACCATCGTGCAATCCAA  TTTGGATTGCACGATGGTGCTTGAA  TTGGATTGCACGATGGTGCTTGAA  TCACTAGCGATCACTGGCGACGCT  TTACATTCCCTGCCTCCGTGGGCTT  TAAGCCCACGGAGGCAGGGAATGTA  TTACATTCCCTGCCTCCGTGGGCTT  TAACCGCTACTGAATACGCGAAGCG  TTCTGGACGCGTCGACACTCATTATA  TTATAATGAGTGTCGACGCGTCCAGA  TTCTGAGCAGGCCAGCGCTCCAGCT  TAGCTGGAGCGCTGGCAATCCA  TTTTGAATTGCCAAGCCCTGAAAGCC  TGGCTTTCAGGGCTTGGCAATTCAA  TCACCGACGCATCAAGGCGAAAACT  TCACCGACGCATCAAGGCGAAAACT  TTTTAGCACGCGTGGCCTATGAAACC  TGTTTCATAGGCCACGCGTGCTAAA  TTTTAGCACGCGTGGCCTATGAAACC	773	TTTTCATAAACGTTGTCCCCGAGC	TGCTCGGGGACAACGTTTATGAAAA
TTTCAAGCACCATCGTGCAATCCAA  TTTGGATTGCACGATGGTGCTTGAA  TTAGCTTGCCCAGTGATCGCTAGTGG  TCCACTAGCGATCACTGGCGACGCT  TTACATTCCCTGCCTCCGTGGGCTT  TAAGCCCACGGAGGCAGGGAATGTA  TTAGCTTCGCGTATTCAGTAGCGGTT  TAACCGCTACTGAATACGCGAAGCG  TTCTGGACGCGTCGACACTCATTATA  TTATAATGAGTGTCGACGCGTCCAGA  TTTTGAATTGCCAAGCCCTGAAAGCC  TGGCTTTCAGGGCTTGGCAATTCAA  TAGTTTTCATAGGCCACGCGTCGAAACT  TCACCGACGCATCAAGGCC  TGGCTTTCAGGGCTTGGCAAAACT  TCACCGACGCATCAAGGCCGAAAACT  TTTTAGCACGCGTGGCCATGAAAACT  TTTTAGCACGCGTGGCCTATGAAACC	774	TAGCAGGAGGACGAACCTCCGCTCC	TGGAGCGGAGGTTCGTCCTCCTGCT
TCACTAGCGATCACTGGCGACGCT  TAGCGTCGCCAGTGATCGCTAGTGG  TCACTAGCGATCACTGGCGACGCT  TAACCCCACGGAGGCAGGGAATGTA  TAACCCCACGGAGGCAGGGAATGTA  TAACCGCTACTGAATACGCGAAGCG  TTCGGACGCTCGACACTCATTATA  TTATAATGAGTGTCGACGCGTCCAGA  TTCTGAGCAGGCCAGCGCTCCAGCT  TAGCTGGAGGCCTGGCACATTCAA  TTTTGAATTGCCAAGCCCTGAAAGCC  TGGCTTTCAGGGCTTGGCAATTCAA  TAGTTTTCGCCTTGATGCGTCGTG  TCACCGACGCATCAAGGCGAAAACT  TTTTAGCACGCGTGGCCTAGAAACC  TGTTTCATAGGCCACGCGTGCTAAA  TTTTAGCACGCGTGGCCTATGAAACC	775	TTTCAAGCACCATCGTGCAATCCAA	ТТТGGAТТGCACGAТGGTGCТТGAA
TTACATTCCCTGCCTCCGTGGGCTT TAAGCCCACGGAGGCAGGGAATGTA TTACATTCCCTGCCTCCGTGGGCTT TAACCGCTACTGAATACGCGAAGCG TTCGGACGCGTCGACACTCATTATA TTATAATGAGTGTCGACGCGTCCGA TTCTGAGCAGGCCAGCGCTCCAGCT TAGCTGGAGGCCTGGCAGCTCCAGA TTTTGAATTGCCAAGCCCTGAAAGCC TGGCTTTCAGGGCTTGGCAATTCAA TAGTTTTCGCCTTGATGCGTCGGTG TCACCGACGCATCAAGGCGAAAACT TTTTAGCACGCGTGGCCTATGAAAC TTTTTAGCACGCGTGGCCTATGAAAC			
TAACCGCTACTGAATACGCGAAGCG  TTATAATGAGTGTCGACGCGTCCGA  TTATAATGAGTGTCGACGCGTCCGA  TTATAATGAGTGTCGACGCGTCCGA  TTATAATGAGTGTCGACGCGTCCGA  TTATAATGAGTGTCGACGCGTCCGA  TTATAATGAGTGTCGACGCGTCCAGA  TTATAATGAGTGTCGACGCGTCCAGA  TTAGCTGGAGCCTTGCACAGCC  TGGCTTTCAGGGCTTGGCAATTCAA  TAGCTTTCAGGGCTTGCCAAAGCC  TGCCTTTCAGGGCTTGGCAAAACT  TCACCGACGCATCAAGGCCGAAAACT  TTAGCACGCGTGGCCTATGAAAC  TTTTAGCACGCGTGGCCTATGAAAC			
TTATAATGAGTGTCGACGCGTCCGA TTCTGAGCAGGCCAGCGTCCAGCT TAGCTGGAGGCCTGCAGACTCATTATA TTATAATGAGTGTCGACGCGTCCAGA TTCTGAGCAGGCCAGCGCTCCAGCT TAGCTTGGAGCCCTGCAAAGCC TGGCTTTCAGGGCTTGGCAATTCAA TAGTTTTCGCCTTGATGCGTCGGTG TCACCGACGCATCAAGGCGAAAACT TTTTAGCACGCGTGGCCTATGAAAC TTTTAGCACGCGTGGCCTATGAAAC			
780 TTCTGAGCAGGCCAGCGCTCCAGCT TAGCTGGAGCGCTGGCCTGCTCAGA 781 TTTGAATTGCCAAGCCCTGAAAGCC TGGCTTTCAGGGCTTGGCAATTCAA 782 TAGTTTTCGCCTTGATGCGTCGGTG TCACCGACGCATCAAGGCGAAAACT 783 TGTTTCATAGGCCACGCGTGCTAAA TTTTAGCACGCGTGGCCTATGAAAC			
781 TTTGAATTGCCAAGCCCTGAAAGCC TGGCTTTCAGGGCTTGGCAATTCAA 782 TAGTTTTCGCCTTGATGCGTCGTG TCACCGACGCATCAAGGCGAAAACT 783 TGTTTCATAGGCCACGCGTGCTAAA TTTTAGCACGCGTGGCCTATGAAAC			
782 TAGTTTTCGCCTTGATGCGTCGGTG TCACCGACGCATCAAGGCGAAAACT 783 TGTTTCATAGGCCACGCGTGCTAAA TTTTAGCACGCGTGGCCTATGAAAC			
783 TGTTTCATAGGCCACGCGTGCTAAA TTTTAGCACGCGTGGCCTATGAAAC			
	782	TAGTTTTCGCCTTGATGCGTCGGTG	TCACCGACGCATCAAGGCGAAAACT
16 TCATCGCTGCAAGTACCGCACTCAA TTTGAGTGCGGTACTTGCAGCGATG	783	TGTTTCATAGGCCACGCGTGCTAAA	TTTTAGCACGCGTGGCCTATGAAAC
	16	TCATCGCTGCAAGTACCGCACTCAA	TTTGAGTGCGGTACTTGCAGCGATG

We claim:

- 1. An oligonucleotide array comprising an array of at least 25 different addresses, each address comprising a different capture probe selected from the group consisting of the sequences set forth in Table 1, Table 2, Table 3 and Table 4.
- 2. An array according to claim 1, wherein said capture probes are microspheres.
- 3. An array according to claim 1 or 2 wherein said array is a liquid array.
- **4**. An array according to claim 1 or **2**, wherein said array further comprises a solid support.
- 5. An array according to claim 1, wherein said addresses are microspheres and wherein said solid support comprises wells into which said microspheres are individually distributed.
- **6**. An array according to claim 1, wherein each address is a different known location, and said wherein each capture probe is attached to one of said known locations.
- 7. An array according to claim 1, wherein said array comprises at least 50 different addresses, each address comprising a different capture probe selected from the group consisting of the sequences set forth in Table 1, Table 2, Table 3 and Table 4.
- 8. An array according to claim 1 wherein said array comprises at least 100 different addresses, each address comprising a different capture probe selected from the group consisting of the sequences set forth in Table 1, Table 2, Table 3 and Table 4.
- 9. A kit comprising at least twenty-five nucleic acids selected from the group consisting of sequences substantially complementary to the sequences set forth in Table I, Table II, Table III and Table IV or their complement.
- 10. A kit according to claim 9, wherein said kit comprises at least 50 nucleic acids selected from the group consisting of the sequences substantially complementary to the sequences set forth in Table II, Table III, Table III and Table IV or their complement.
- 11. A kit according to claim 9, wherein said kit comprises at least 100 nucleic acids selected from the group consisting of the sequences substantially complementary to the sequences set forth in Table I, Table II, Table III and Table IV or their complement.
- 12. A kit according to claim 9, wherein said nucleic acids further comprise at least a first universal priming sequence.
- 13. A kit according to claim 9, wherein said nucleic acid sequence further comprises a sequence substantially complementary to a target domain.
- 14. A method of immobilizing a target nucleic acid sequence, said method comprising:
  - a) attaching a first adapter nucleic acid to a first target nucleic acid sequence to form a modified first target nucleic acid sequence, wherein said first adapter nucleic acid comprises a sequence substantially complementary to a sequence selected from the sequences set forth in Table I, Table II, Table III, and Table IV;

- b) contacting said modified first target nucleic acid sequence with an array comprising an array of at least 25 different addresses, each address comprising a different capture probe selected from the group consisting of the sequences set forth in Table 1, Table 2, Table 3 and Table 4, whereby said target nucleic acid sequence is immobilized.
- 15. A method of detecting a target nucleic acid sequence, said method comprising:
  - a) attaching a first adapter nucleic acid to a first target nucleic acid sequence to form a modified first target nucleic acid sequence, wherein said first adapter nucleic acid comprises a sequence substantially complementary to a sequence selected from the sequences set forth in Table I, Table II, Table III, and Table IV;
  - b) contacting said modified first target nucleic acid sequence with an array comprising: an array of at least 25 different addresses, each address comprising a different capture probe selected from the group consisting of the sequences set forth in Table 1, Table 2, Table 3 and Table 4; and
  - c) detecting the presence of said modified first target nucleic acid sequence.
- **16.** A method of detecting a target nucleic acid, said method comprising:
  - a) hybridizing a first adapter probe with a first target nucleic acid, said first adapter probe comprising a first domain that is complementary to said first target nucleic acid and a second domain, said second domain comprising a first sequence substantially complementary to a selected from the group consisting of the sequences set forth in Table I, Table II, Table III and Table IV to form a first hybridization complex;
  - b) contacting said first hybridization complex with an enzyme such that when said first domain of said adapter probe is perfectly complementary with said first target nucleic acid, said first adapter probe is altered resulting in a modified first adapter probe;
  - c) contacting said modified first adapter probe with a population of microspheres comprising at least a first subpopulation comprising a first capture probe, such that said first capture probe and said modified first adapter probe form a second hybridization complex; and
  - d) detecting the presence of said modified first adapter probe as an indication of the presence of said target nucleic acid.

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